Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10149	GM_157_B1_D09_MR	g2335061	BLASTN	446	4e-13	64	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
10150	GM_157_B1_E02_T7	g3212855	BLASTX	184	6e-13	41	(AC004005) hypothetical protein [Arabidopsis thaliana]
10151	GM_157_B1_E04_T7	g3789709	BLASTN	424	4e-12	64	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
10152	GM_157_B1_E05_T7	g1142699	BLASTN	617	1e-21	84	Glycine max satellite STR120-A.1.
10153	GM_157_B1_E08_MR	g4063760	BLASTX	229	5e-17	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10154	GM_157_B1_E10_MR	g170029	BLASTN	380	4e-10	79	Glycine max cv. Dare nodulin 26 gene fragment.
10155	GM_157_B1_E11_MR	g2827711	BLASTX	236	8e-18	68	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]
10156	GM_157_B1_F01_MR	g2914707	BLASTX	160	7e-10	34	(AC003974) putative disease resistance protein (Cf-2.2) [Arabidopsis thaliana] gi 3298554 (AC004681) putative disease resistance protein [Arabidopsis thaliana]
10157	GM_157_B1_F01_T7	g1272349	BLASTX	253	2e-20	47	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
10158	GM_157_B1_F09_T7	g18559	BLASTN	801	3e-29	73	G.max gene for catalase
10159	GM_157_B1_F11_MR	g3695395	BLASTX	211	2e-15	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
10160	GM_157_B1_G05_T7	g2522227	BLASTX	272	6e-23	45	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
10161	GM_157_B1_G09_MR	g3746060	BLASTX	238	2e-19	70	(AC005311) unknown protein [Arabidopsis thaliana]
10162	GM_157_B1_G09_T7	g3063446	BLASTX	177	3e-11	89	(AC003981) F22O13.8 [Arabidopsis thaliana]
10163	GM_157_B1_G11_MR	g507910	BLASTN	362	9e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10164	GM_157_B1_H01_MR	g3047060	BLASTN	377	5e-10	63	Arabidopsis thaliana BAC F7N22
10165	GM_157_B1_H04_MR	g2160158	BLASTX	207	2e-15	81	(AC000132) Similar to elongation factor 1-gamma (gb EF1G_XENLA). ESTs gb T20564,gb T45940,gb T04527 come from this gene. [Arabidopsis thaliana]
10166	GM_157_B1_H05_MR	g3097320	BLASTN	762	2e-27	74	Glycine max gene for Bd 30K, complete cds
10167	GM_157_B1_H07_MR	g2864621	BLASTX	215	3e-16	46	hypothetical protein [Arabidopsis thaliana]
10168	GM_157_B1_H09_MR	g507910	BLASTN	361	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10169	GM_157_B1_H11_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10170	GM_157_B1_H12_T7	g4063760	BLASTX	444	7e-40	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10171	GM_158_A1_A03_T7	g3695395	BLASTX	201	7e-18	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
10172	GM_158_A1_A04_T7	g3021270	BLASTX	266	2e-37	66	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10173	GM_158_A1_A11_MR	g905361	BLASTX	565	6e-54	91	(U22103) gag-protease polyprotein [Glycine max]
10174	GM_158_A1_A12_MR	g4063760	BLASTX	219	7e-16	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10175	GM_158_A1_B06_MR	g2264320	BLASTN	649	3e-22	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
10176	GM_158_A1_B08_T7	g3873182	BLASTN	405	3e-11	65	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
10177	GM_158_A1_B12_MR	g3097320	BLASTN	655	1e-22	73	Glycine max gene for Bd 30K, complete cds
10178	GM_158_A1_C02_MR	g3645899	BLASTX	216	5e-23	51	(U68408) 5' end not determined experimentally [Zea mays]
10179	GM_158_A1_C12_T7	g507910	BLASTN	445	2e-13	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10180	GM_158_A1_D03_T7	g18559	BLASTN	1072	1e-41	77	G.max gene for catalase
10181	GM_158_A1_D04_T7	g3097320	BLASTN	489	4e-15	77	Glycine max gene for Bd 30K, complete cds
10182	GM_158_A1_D05_MR	g100484	BLASTX	259	2e-20	54	hypothetical protein - garden snapdragon
10183	GM_158_A1_D05_T7	g3319363	BLASTX	203	2e-14	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
10184	GM_158_A1_E04_MR	g13767	BLASTN	336	5e-09	67	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
10185	GM_158_A1_E05_MR	g1769898	BLASTX	294	2e-24	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10186	GM_158_A1_E06_MR	g3063446	BLASTX	250	5e-19	90	(AC003981) F22O13.8 [Arabidopsis thaliana]
10187	GM_158_A1_E07_T7	g421955	BLASTX	282	2e-27	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10188	GM_158_A1_E08_T7	g3150402	BLASTX	151	2e-09	90	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]
10189	GM_158_A1_E09_T7	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10190	GM_158_A1_E12_MR	g131150	BLASTX	520	3e-49	79	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 gi 81515 pir S00445 photosystem I protein A2 - spinach chloroplast gi 12271 (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia oleracea] gi 225422 prf 1303218B gene psaB [Spinacia oleracea]
10191	GM_158_A1_F01_T7	g3142328	BLASTN	2008	2e-84	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10192	GM_158_A1_F02_T7	g4038056	BLASTX	289	2e-23	46	(AC005897) putative transposon [Arabidopsis thaliana]
10193	GM_158_A1_F03_MR	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10194	GM_158_A1_F03_T7	g4098865	BLASTN	352	5e-09	62	Dictyostelium discoideum unknown protein gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10195	GM_158_A1_F04_MR	g3033389	BLASTX	164	3e-10	35	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
10196	GM_158_A1_F05_MR	g3142328	BLASTN	1189	6e-47	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10197	GM_158_A1_F06_T7	g507910	BLASTN	576	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10198	GM_158_A1_F07_T7	g3600045	BLASTN	361	3e-10	74	Arabidopsis thaliana BAC F2P3
10199	GM_158_A1_F12_T7	g1813979	BLASTX	190	4e-23	70	(Y10860) hypothetical protein [Musa acuminata]
10200	GM_158_A1_G03_MR	g4063760	BLASTX	385	1e-33	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10201	GM_158_A1_G03_T7	g3645899	BLASTX	228	6e-17	52	(U68408) 5' end not determined experimentally [Zea mays]
10202	GM_158_A1_G04_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10203	GM_158_A1_G04_T7	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10204	GM_158_A1_G06_T7	g2351063	BLASTN	410	2e-11	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19
10205	GM_158_A1_H01_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10206	GM_158_A1_H02_MR	g3241923	BLASTN	476	2e-14	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]
10207	GM_158_A1_H04_MR	g4056432	BLASTX	146	1e-08	43	(AC005990) Similar to gi 2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb Z97341. ESTs gb T20778 and gb AA586281 come from this gene. [Arabidopsis thaliana]
10208	GM_158_A1_H06_MR	g507910	BLASTN	413	5e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10209	GM_158_A2_A01_T7	g14227	BLASTN	424	5e-13	67	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
10210	GM_158_A2_A04_MR	g3777527	BLASTX	273	8e-24	52	(AF053008) gag-pol polyprotein [Glycine max]
10211	GM_158_A2_A05_MR	g4063760	BLASTX	212	4e-15	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10212	GM_158_A2_A06_T7	g3097320	BLASTN	431	2e-12	68	Glycine max gene for Bd 30K, complete cds
10213	GM_158_A2_A11_MR	g3845197	BLASTN	447	4e-13	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10214	GM_158_A2_A12_T7	g3777527	BLASTX	559	6e-52	91	(AF053008) gag-pol polyprotein [Glycine max]
10215	GM_158_A2_B03_T7	g3142328	BLASTN	616	7e-21	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10216	GM_158_A2_B05_T7	g2760839	BLASTX	178	7e-12	36	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10217	GM_158_A2_B12_T7	g130582	BLASTX	171	1e-10	34	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10218	GM_158_A2_C02_T7	g4063760	BLASTX	214	2e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10219	GM_158_A2_C03_T7	g3097320	BLASTN	464	6e-14	73	Glycine max gene for Bd 30K, complete cds
10220	GM_158_A2_C04_T7	g4063760	BLASTX	454	5e-41	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10221	GM_158_A2_C06_T7	g2129559	BLASTX	158	8e-10	62	cellulase homolog OR16pep - Arabidopsis thaliana gi 1022807 (U37702) cellulase [Arabidopsis thaliana] gi 3493633 (AF074092) cellulase [Arabidopsis thaliana] gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
10222	GM_158_A2_C08_T7	g3645899	BLASTX	308	2e-25	55	(U68408) 5' end not determined experimentally [Zea mays]
10223	GM_158_A2_C09_MR	g2995405	BLASTX	226	3e-18	41	(Y12432) polyprotein [Ananas comosus]
10224	GM_158_A2_C10_MR	g3763969	BLASTN	361	3e-09	66	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
10225	GM_158_A2_C12_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10226	GM_158_A2_D02_MR	g133917	BLASTX	108	2e-11	80	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
10227	GM_158_A2_D04_MR	g2129618	BLASTX	178	1e-11	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10228	GM_158_A2_D06_MR	g3930515	BLASTX	115	8e-12	46	(AF059674) putative gag protein [Nicotiana tabacum]
10229	GM_158_A2_E02_T7	g130582	BLASTX	207	3e-31	56	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10230	GM_158_A2_E03_MR	g2522227	BLASTX	214	8e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10231	GM_158_A2_E06_T7	g1171046	BLASTX	144	2e-09	59	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493) metallothionein-like protein [Trifolium repens]
10232	GM_158_A2_E07_T7	g507910	BLASTN	548	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10233	GM_158_A2_E08_T7	g1136741	BLASTX	168	6e-11	50	(D42052) predicted protein of 548 amino acids [Homo sapiens]
10234	GM_158_A2_E12_MR	g2282576	BLASTX	133	3e-11	59	(U77700) HsGCN1 [Homo sapiens]
10235	GM_158_A2_F03_T7	g3426334	BLASTN	366	1e-09	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10236	GM_158_A2_F04_T7	g4038056	BLASTX	333	3e-28	45	(AC005897) putative transposon [Arabidopsis thaliana]
10237	GM_158_A2_F12_T7	g2769655	BLASTN	492	3e-15	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
10238	GM_158_A2_G01_MR	g4063770	BLASTX	195	1e-13	39	(AB004906) transposase [Ipomoea purpurea]
10239	GM_158_A2_G01_T7	g1142703	BLASTN	248	2e-12	72	Glycine max satellite STR120-B.1.
10240	GM_158_A2_G05_MR	g2583130	BLASTX	187	2e-12	35	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
10241	GM_158_A2_H01_T7	g4063760	BLASTX	272	1e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10242	GM_158_A2_H02_MR	g1524103	BLASTN	376	6e-10	65	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
10243	GM_158_A2_H09_T7	g505129	BLASTN	403	3e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10244	GM_158_B1_A02_MR	g82166	BLASTX	174	7e-12	87	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B, chloroplast - common tobacco (fragment)
10245	GM_158_B1_A02_T7	g1171583	BLASTN	539	2e-17	69	P.falciparum complete gene map of plastid-like DNA (IR-A)
10246	GM_158_B1_A09_MR	g3461840	BLASTX	349	1e-29	46	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
10247	GM_158_B1_A09_T7	g4098966	BLASTN	1562	1e-64	82	Glycine max putative reistance gene analog genomic sequence
10248	GM_158_B1_A10_T7	g3176795	BLASTN	346	5e-09	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
10249	GM_158_B1_A12_MR	g1708464	BLASTX	164	2e-10	58	PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD) (2,3-DIHYDROXY ACID HYDROLYASE) gi 1213255 (Z69795) unknown [Schizosaccharomyces pombe]
10250	GM_158_B1_B03_T7	g3650035	BLASTX	171	7e-11	42	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
10251	GM_158_B1_B07_T7	g2462058	BLASTX	211	2e-16	61	(Y13389) reverse transcriptase [Antirrhinum majus]
10252	GM_158_B1_B12_T7	g13597	BLASTN	373	5e-10	66	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10253	GM_158_B1_C05_T7	g507910	BLASTN	596	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10254	GM_158_B1_C08_MR	g1769898	BLASTX	507	7e-48	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10255	GM_158_B1_C11_T7	g1480927	BLASTN	872	8e-33	80	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
10256	GM_158_B1_C12_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10257	GM_158_B1_C12_T7	g2769655	BLASTN	519	2e-16	71	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
10258	GM_158_B1_D03_T7	g507910	BLASTN	514	1e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence
10259	GM_158_B1_D08_T7	g1136228	BLASTX	210	5e-15	40	(U32986) UV-damaged DNA binding factor [Homo sapiens] gi 1588524 prf 2208446A xeroderma pigmentosum group E-binding factor [Homo sapiens]
10260	GM_158_B1_D12_T7	g2244840	BLASTX	173	2e-12	52	(Z97337) hypothetical protein [Arabidopsis thaliana]
10261	GM_158_B1_E03_T7	g2244840	BLASTX	235	4e-19	46	(Z97337) hypothetical protein [Arabidopsis thaliana]
10262	GM_158_B1_F03_MR	g4115365	BLASTX	244	2e-18	53	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
10263	GM_158_B1_F07_MR	g1171591	BLASTN	367	9e-12	65	P.falciparum complete gene map of plastid-like DNA (IR-B)
10264	GM_158_B1_F08_MR	g4115365	BLASTX	329	1e-27	56	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
10265	GM_158_B1_G04_T7	g2760830	BLASTX	506	1e-47	75	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
10266	GM_158_B1_G08_T7	g2564048	BLASTN	395	8e-11	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
10267	GM_158_B1_G11_T7	g3600044	BLASTX	189	1e-12	43	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
10268	GM_158_B1_H07_T7	g3860242	BLASTN	501	1e-15	72	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence [Arabidopsis thaliana]
10269	GM_158_B1_H08_MR	g3549672	BLASTX	162	1e-10	38	(AL031394) putative protein [Arabidopsis thaliana]
10270	GM_158_B1_H09_MR	g2522227	BLASTX	186	9e-14	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
10271	GM_158_B1_H10_MR	g2522230	BLASTX	270	1e-22	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10272	GM_158_B1_H10_T7	g18768	BLASTN	455	3e-14	81	Soybean Tgm6 transposable element 3' end
10273	GM_158_B2_B07_T7	g3777527	BLASTX	154	2e-11	49	(AF053008) gag-pol polyprotein [Glycine max]
10274	GM_158_B2_B08_T7	g2583130	BLASTX	172	8e-11	42	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
10275	GM_158_B2_C01_T7	g905361	BLASTX	429	3e-39	95	(U22103) gag-protease polyprotein [Glycine max]
10276	GM_158_B2_C06_T7	g18559	BLASTN	348	1e-08	69	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10277	GM_158_B2_C10_T7	g3941442	BLASTX	173	7e-12	57	(AF062875) putative transcription factor [Arabidopsis thaliana]
10278	GM_158_B2_D06_T7	g3142300	BLASTX	269	4e-21	56	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T88158, gb N38703 and gb AA651043 come from this gene. [Arabidopsis thaliana]
10279	GM_158_B2_D09_T7	g2290780	BLASTX	231	1e-18	52	(AF002667) heat shock cognate protein [Solanum commersonii]
10280	GM_158_B2_E02_T7	g1370287	BLASTX	93	4e-11	100	(Z73553) core protein [Pisum sativum]
10281	GM_159_A1_A02_T7	g507910	BLASTN	501	5e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10282	GM_159_A1_A03_MR	g2864621	BLASTX	150	4e-09	46	hypothetical protein [Arabidopsis thaliana]
10283	GM_159_A1_A04_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10284	GM_159_A1_A07_T7	g2129675	BLASTX	120	4e-16	75	probable chlorophyll synthetase G4 - Arabidopsis thaliana gi 972938 (U19382) putative chlorophyll synthetase [Arabidopsis thaliana] gi 3068709 (AF049236) putative chlorophyll synthetase [Arabidopsis thaliana]
10285	GM_159_A1_A10_T7	g4063760	BLASTX	105	1e-08	30	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10286	GM_159_A1_B03_T7	g18559	BLASTN	393	9e-11	71	G.max gene for catalase
10287	GM_159_A1_B05_T7	g507910	BLASTN	557	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10288	GM_159_A1_B06_MR	g507910	BLASTN	426	1e-12	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10289	GM_159_A1_B06_T7	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10290	GM_159_A1_B07_MR	g905361	BLASTX	257	2e-20	87	(U22103) gag-protease polyprotein [Glycine max]
10291	GM_159_A1_B08_T7	g2832611	BLASTN	355	5e-09	61	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
10292	GM_159_A1_B09_MR	g3378224	BLASTX	197	5e-15	66	(AJ001213) reverse transcriptase [Lycopersicon chilense]
10293	GM_159_A1_B10_T7	g1769897	BLASTX	171	3e-11	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10294	GM_159_A1_C01_T7	g20035	BLASTN	440	7e-13	75	Tobacco anther-specific gene TA-29 and stem-specific gene TSJT1
10295	GM_159_A1_C04_MR	g4063756	BLASTN	476	2e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10296	GM_159_A1_D03_MR	g507910	BLASTN	374	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10297	GM_159_A1_D03_T7	g507910	BLASTN	560	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10298	GM_159_A1_D05_T7	g3757543	BLASTN	360	3e-09	60	Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence [Homo sapiens]
10299	GM_159_A1_D06_T7	g2924777	BLASTX	170	1e-10	42	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
10300	GM_159_A1_D08_MR	g2832612	BLASTX	198	4e-15	38	(AL021711) putative protein (fragment) [Arabidopsis thaliana]
10301	GM_159_A1_D08_T7	g3080374	BLASTX	276	3e-22	40	(AL022580) putative protein [Arabidopsis thaliana]
10302	GM_159_A1_E02_T7	g3810596	BLASTX	371	3e-32	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10303	GM_159_A1_E04_MR	g130582	BLASTX	437	4e-39	66	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10304	GM_159_A1_E07_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10305	GM_159_A1_E10_T7	g3142379	BLASTX	430	1e-39	74	(AF053008) envelope-like [Glycine max]
10306	GM_159_A1_E11_T7	g3645899	BLASTX	203	3e-14	60	(U68408) 5' end not determined experimentally [Zea mays]
10307	GM_159_A1_F02_T7	g2129618	BLASTX	215	1e-15	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10308	GM_159_A1_F03_MR	g2501496	BLASTX	152	8e-10	58	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 7 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 7) gi 542017 pir S41953 UTP-glucose glucosyltransferase - cassava gi 453253 (X77464) UTP-glucose glucosyltransferase [Manihot esculenta]
10309	GM_159_A1_F03_T7	g1906826	BLASTX	158	1e-09	84	(Y11827) heat shock protein [Arabidopsis thaliana]
10310	GM_159_A1_F04_T7	g2982459	BLASTX	225	6e-18	81	(AL022223) putative protein [Arabidopsis thaliana]
10311	GM_159_A1_F05_T7	g531389	BLASTX	290	2e-23	40	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
10312	GM_159_A1_F08_MR	g1076570	BLASTX	245	4e-20	81	homeotic protein CHB6 - carrot
10313	GM_159_A1_F11_T7	g2708743	BLASTX	209	1e-14	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
10314	GM_159_A1_G01_T7	g4063760	BLASTX	263	1e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10315	GM_159_A1_G04_MR	g99755	BLASTX	283	3e-23	47	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
10316	GM_159_A1_G08_MR	g3142328	BLASTN	1062	4e-41	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10317	GM_159_A1_G08_T7	g505129	BLASTN	402	3e-11	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10318	GM_159_A1_G11_MR	g3142379	BLASTX	221	6e-17	72	(AF053008) envelope-like [Glycine max]
10319	GM_159_A1_G11_T7	g18559	BLASTN	367	1e-09	63	G.max gene for catalase
10320	GM_159_A1_H04_MR	g905361	BLASTX	168	7e-11	37	(U22103) gag-protease polyprotein [Glycine max]
10321	GM_159_A1_H04_T7	g414863	BLASTN	285	4e-10	61	A.longa plastid genes for ribosomal proteins and tRNAs
10322	GM_159_A1_H05_MR	g507910	BLASTN	350	3e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10323	GM_159_A1_H05_T7	g4063760	BLASTX	388	5e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10324	GM_159_A1_H07_T7	g3777527	BLASTX	777	3e-75	97	(AF053008) gag-pol polyprotein [Glycine max]
10325	GM_159_A2_B01_MR	g3097320	BLASTN	448	3e-13	73	Glycine max gene for Bd 30K, complete cds
10326	GM_159_A2_B02_MR	g507910	BLASTN	349	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10327	GM_159_A2_B02_T7	g4063760	BLASTX	351	6e-30	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10328	GM_159_A2_B03_T7	g2244753	BLASTX	385	3e-34	52	(Z97335) hypothetical protein [Arabidopsis thaliana]
10329	GM_159_A2_B04_MR	g2129618	BLASTX	176	2e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10330	GM_159_A2_B05_MR	g1142702	BLASTN	1147	3e-45	98	Glycine max satellite STR120-A.4.
10331	GM_159_A2_B07_T7	g905360	BLASTN	979	1e-37	87	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
10332	GM_159_A2_B11_MR	g2665890	BLASTX	195	6e-14	66	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]
10333	GM_159_A2_C09_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10334	GM_159_A2_C09_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10335	GM_159_A2_D04_T7	g3142328	BLASTN	796	4e-29	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10336	GM_159_A2_D05_MR	g2995405	BLASTX	452	3e-42	62	(Y12432) polyprotein [Ananas comosus]
10337	GM_159_A2_D06_MR	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10338	GM_159_A2_D08_T7	g3097320	BLASTN	1393	4e-56	83	Glycine max gene for Bd 30K, complete cds
10339	GM_159_A2_D09_T7	g2982550	BLASTN	353	7e-09	66	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence [Plasmodium falciparum]
10340	GM_159_A2_D10_MR	g3033400	BLASTX	155	7e-13	56	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
10341	GM_159_A2_D10_T7	g3319353	BLASTX	162	4e-19	45	(AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]
10342	GM_159_A2_E04_T7	g3097320	BLASTN	719	2e-25	74	Glycine max gene for Bd 30K, complete cds
10343	GM_159_A2_E11_MR	g3980264	BLASTX	215	6e-17	95	(AJ011383) 20S proteasome beta subunit [Cicer arietinum]
10344	GM_159_A2_E12_T7	g507910	BLASTN	625	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10345	GM_159_A2_F02_MR	g662924	BLASTX	173	2e-12	55	(Z46952) heat shock transcription factor 21 [Glycine max]
10346	GM_159_A2_F04_T7	g18559	BLASTN	985	1e-37	76	G.max gene for catalase
10347	GM_159_A2_F05_MR	g3142328	BLASTN	650	2e-22	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10348	GM_159_A2_G01_T7	g18559	BLASTN	373	7e-10	72	G.max gene for catalase
10349	GM_159_A2_G02_MR	g1666236	BLASTX	157	3e-10	31	(U76261) unknown [Hordeum vulgare]
10350	GM_159_A2_G03_T7	g1572819	BLASTX	150	3e-13	40	(U70855) similar to the RAS gene family [Caenorhabditis elegans]
10351	GM_159_A2_G08_T7	g4038056	BLASTX	354	1e-30	52	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10352	GM_159_A2_G09_MR	g4063760	BLASTX	518	8e-48	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10353	GM_159_A2_G12_T7	g2462134	BLASTX	252	4e-20	40	(Y13368) reverse transcriptase [Beta vulgaris]
10354	GM_159_A2_H01_MR	g4063760	BLASTX	182	6e-12	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10355	GM_159_A2_H01_T7	g507910	BLASTN	635	4e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10356	GM_159_A2_H03_MR	g905361	BLASTX	693	2e-67	96	(U22103) gag-protease polyprotein [Glycine max]
10357	GM_159_A2_H03_T7	g3142328	BLASTN	532	4e-17	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10358	GM_159_A2_H07_T7	g4063770	BLASTX	148	4e-20	45	(AB004906) transposase [Ipomoea purpurea]
10359	GM_159_B2_A02_T7	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10360	GM_159_B2_A08_MR	g2392762	BLASTN	352	7e-09	69	Arabidopsis thaliana BAC T32N15 from chromsome V, complete sequence [Arabidopsis thaliana]
10361	GM_159_B2_A09_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
10362	GM_159_B2_A09_T7	g507910	BLASTN	379	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10363	GM_159_B2_A11_T7	g2522230	BLASTX	267	2e-22	41	(AB007467) retrotransposon-like gene, the first amino acid was determined to be leucine [Vicia faba]
10364	GM_159_B2_B03_MR	g3097320	BLASTN	806	2e-29	78	Glycine max gene for Bd 30K, complete cds
10365	GM_159_B2_B03_T7	g3142328	BLASTN	689	3e-24	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10366	GM_159_B2_B08_MR	g2209031	BLASTX	258	9e-21	49	(AB001569) ORF of 1.56 kb [Daucus carota]
10367	GM_159_B2_B09_MR	g3142328	BLASTN	843	3e-31	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10368	GM_159_B2_B12_T7	g1666236	BLASTX	201	4e-15	39	(U76261) unknown [Hordeum vulgare]
10369	GM_159_B2_C02_MR	g3319362	BLASTX	189	9e-24	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10370	GM_159_B2_C07_T7	g3319362	BLASTX	220	4e-16	49	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10371	GM_159_B2_C11_MR	g4038056	BLASTX	326	2e-27	57	(AC005897) putative transposon [Arabidopsis thaliana]
10372	GM_159_B2_D02_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10373	GM_159_B2_D03_MR	g4092471	BLASTN	446	4e-13	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
10374	GM_159_B2_D04_MR	g3426334	BLASTN	384	2e-10	66	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10375	GM_159_B2_D07_T7	g3097320	BLASTN	459	9e-14	78	Glycine max gene for Bd 30K, complete cds
10376	GM_159_B2_D08_MR	g18695	BLASTN	417	5e-12	72	Soybean nodulin 22 gene
10377	GM_159_B2_D09_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10378	GM_159_B2_D09_T7	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10379	GM_159_B2_E01_MR	g2522228	BLASTX	245	1e-19	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
10380	GM_159_B2_E04_MR	g1769898	BLASTX	338	3e-29	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10381	GM_159_B2_F04_MR	g18559	BLASTN	558	3e-18	75	G.max gene for catalase
10382	GM_159_B2_F08_MR	g905361	BLASTX	176	1e-11	40	(U22103) gag-protease polyprotein [Glycine max]
10383	GM_159_B2_F10_T7	g507910	BLASTN	574	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10384	GM_159_B2_F11_MR	g3645899	BLASTX	344	2e-29	59	(U68408) 5' end not determined experimentally [Zea mays]
10385	GM_159_B2_G04_MR	g905360	BLASTN	1146	2e-45	91	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
10386	GM_159_B2_G06_MR	g3645899	BLASTX	327	2e-27	57	(U68408) 5' end not determined experimentally [Zea mays]
10387	GM_159_B2_G06_T7	g3097320	BLASTN	418	7e-12	69	Glycine max gene for Bd 30K, complete cds
10388	GM_159_B2_H01_MR	g3142330	BLASTX	548	4e-52	95	(U96295) envelope-like [Glycine max]
10389	GM_159_B2_H03_T7	g1524103	BLASTN	489	5e-15	64	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
10390	GM_159_B2_H05_T7	g4063760	BLASTX	192	2e-27	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10391	GM_159_B2_H06_T7	g4050011	BLASTN	395	8e-11	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
10392	GM_159_B2_H07_MR	g3777527	BLASTX	390	6e-34	66	(AF053008) gag-pol polyprotein [Glycine max]
10393	GM_159_B2_H11_MR	g3522945	BLASTX	180	3e-12	49	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]
10394	GM_159_B2_H11_T7	g4006885	BLASTN	355	5e-09	63	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2
10395	GM_160_A1_A02_T7	g2462936	BLASTX	273	5e-23	56	(Y12321) open reading frame 2 [Brassica oleracea]
10396	GM_160_A1_A07_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10397	GM_160_A1_A09_T7	g905361	BLASTX	232	1e-17	34	(U22103) gag-protease polyprotein [Glycine max]
10398	GM_160_A1_A12_T7	g226407	BLASTX	165	5e-10	45	retrotransposon del1-46 [Lilium henryi]
10399	GM_160_A1_B01_T7	g3176774	BLASTN	339	5e-09	61	Homo sapiens allele 3 fragile site locus (FRA10B) minisatellite, 3' sequence
10400	GM_160_A1_B05_MR	g3142328	BLASTN	1756	8e-73	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10401	GM_160_A1_B07_T7	g2443320	BLASTX	221	5e-16	43	(D85597) polyprotein [Oryza australiensis]
10402	GM_160_A1_B09_T7	g3913525	BLASTX	165	3e-10	100	DNA POLYMERASE DELTA CATALYTIC CHAIN >gi 2895198 (AF020193) DNA polymerase delta [Glycine max]
10403	GM_160_A1_C06_T7	g3097320	BLASTN	1014	7e-39	79	Glycine max gene for Bd 30K, complete cds
10404	GM_160_A1_C07_T7	g505129	BLASTN	383	2e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10405	GM_160_A1_D02_T7	g1666236	BLASTX	221	2e-17	33	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10406	GM_160_A1_D05_T7	g2982431	BLASTX	233	2e-17	52	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
10407	GM_160_A1_D07_T7	g2244899	BLASTX	189	6e-13	60	(Z97338) similar to UFD1 protein [Arabidopsis thaliana]
10408	GM_160_A1_E08_T7	g2832258	BLASTN	392	8e-11	74	Medicago sativa ENOD40-2 promoter sequence
10409	GM_160_A1_E10_T7	g1666236	BLASTX	162	9e-11	36	(U76261) unknown [Hordeum vulgare]
10410	GM_160_A1_F01_T7	g4115365	BLASTX	149	2e-10	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
10411	GM_160_A1_F04_MR	g3097320	BLASTN	961	2e-36	80	Glycine max gene for Bd 30K, complete cds
10412	GM_160_A1_F04_T7	g226407	BLASTX	389	6e-34	47	retrotransposon del1-46 [Lilium henryi]
10413	GM_160_A1_F05_MR	g1142703	BLASTN	474	6e-15	88	Glycine max satellite STR120-B.1.
10414	GM_160_A1_F06_T7	g3142328	BLASTN	879	6e-42	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10415	GM_160_A1_F10_T7	g3367587	BLASTX	152	7e-10	35	(AL031135) putative protein [Arabidopsis thaliana]
10416	GM_160_A1_G04_MR	g3142328	BLASTN	761	2e-27	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10417	GM_160_A1_G09_MR	g905361	BLASTX	674	2e-65	87	(U22103) gag-protease polyprotein [Glycine max]
10418	GM_160_A1_G09_T7	g3142328	BLASTN	1702	2e-70	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10419	GM_160_A1_G12_T7	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10420	GM_160_A1_H01_T7	g2088656	BLASTX	171	6e-11	36	(AF002109) DNA-directed RNA polymerase II isolog [Arabidopsis thaliana]
10421	GM_160_A1_H04_T7	g3777527	BLASTX	231	3e-20	45	(AF053008) gag-pol polyprotein [Glycine max]
10422	GM_160_A1_H09_T7	g116162	BLASTX	218	3e-17	63	G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) gi 2146780 pir S74672 mitotic-specific cyclin S13-7 - soybean (fragment) gi 829266 (X62303) mitotic cyclin [Glycine max]
10423	GM_160_A2_B11_MR	g2181938	BLASTX	149	6e-10	87	(Y13477) mitochondrial elongation factor G [Leishmania mexicana]
10424	GM_160_A2_C03_MR	g18559	BLASTN	1043	3e-40	74	G.max gene for catalase
10425	GM_160_A2_C05_MR	g3777527	BLASTX	405	1e-35	58	(AF053008) gag-pol polyprotein [Glycine max]
10426	GM_160_A2_C09_MR	g1142702	BLASTN	634	4e-22	78	Glycine max satellite STR120-A.4.
10427	GM_160_A2_C12_MR	g4063760	BLASTX	474	4e-43	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10428	GM_160_A2_D03_MR	g18559	BLASTN	1000	3e-38	74	G.max gene for catalase
10429	GM_160_A2_D04_T7	g342952	BLASTN	340	3e-09	66	paramecium species 1,168 mt dna dimer: replication init. region.
10430	GM_160_A2_D05_MR	g3142328	BLASTN	1560	7e-64	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10431	GM_160_A2_D06_MR	g2809253	BLASTX	171	2e-11	32	(AC002560) F21B7.22 [Arabidopsis thaliana]
10432	GM_160_A2_D11_MR	g4063760	BLASTX	152	9e-09	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10433	GM_160_A2_E04_MR	g2995405	BLASTX	296	2e-24	52	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10434	GM_160_A2_E09_T7	g100484	BLASTX	215	9e-16	55	hypothetical protein - garden snapdragon
10435	GM_160_A2_F04_MR	g1666236	BLASTX	221	2e-17	31	(U76261) unknown [Hordeum vulgare]
10436	GM_160_A2_F06_MR	g3023817	BLASTX	259	8e-39	83	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (G6PD) gi 1480344 gnl PID e254807 (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
10437	GM_160_A2_F08_MR	g3142328	BLASTN	635	9e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10438	GM_160_A2_F09_T7	g4063760	BLASTX	149	3e-13	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10439	GM_160_A2_G03_MR	g541936	BLASTX	199	3e-15	62	4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL14) - soybean (fragment)
10440	GM_160_A2_G06_MR	g905361	BLASTX	119	3e-13	33	(U22103) gag-protease polyprotein [Glycine max]
10441	GM_160_A2_G10_MR	g507910	BLASTN	522	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10442	GM_160_A2_G11_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10443	GM_160_A2_H02_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
10444	GM_160_A2_H06_MR	g1769897	BLASTX	156	3e-11	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10445	GM_160_B1_A04_T7	g4063760	BLASTX	334	3e-28	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10446	GM_160_B1_A08_MR	g3777527	BLASTX	318	3e-26	57	(AF053008) gag-pol polyprotein [Glycine max]
10447	GM_160_B1_A10_T7	g3142328	BLASTN	600	4e-20	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10448	GM_160_B1_B06_MR	g2522228	BLASTX	393	9e-36	79	(AB007466) reverse transcriptase-like protein [Vicia faba]
10449	GM_160_B1_B06_T7	g2104945	BLASTN	384	2e-10	70	Glycine max copia-like retrotransposon Tgmr, complete sequence
10450	GM_160_B1_B09_MR	g2462834	BLASTX	138	9e-09	36	(AF000657) hypothetical protein [Arabidopsis thaliana]
10451	GM_160_B1_C09_MR	g421955	BLASTX	173	4e-14	43	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10452	GM_160_B1_D02_MR	g18559	BLASTN	975	3e-37	77	G.max gene for catalase
10453	GM_160_B1_D06_MR	g2995405	BLASTX	255	6e-20	52	(Y12432) polyprotein [Ananas comosus]
10454	GM_160_B1_D12_MR	g3097320	BLASTN	1277	8e-51	81	Glycine max gene for Bd 30K, complete cds
10455	GM_160_B1_D12_T7	g3142328	BLASTN	1240	3e-49	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10456	GM_160_B1_E10_T7	g4038056	BLASTX	283	6e-23	44	(AC005897) putative transposon [Arabidopsis thaliana]
10457	GM_160_B1_F01_MR	g3142293	BLASTX	348	5e-31	64	(AC002411) Contains similarity to myosin IB heavy chain gb X70400 from Gallus gallus. [Arabidopsis thaliana]
10458	GM_160_B1_F05_T7	g3810584	BLASTN	402	4e-11	66	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10459	GM_160_B1_F08_MR	g2443320	BLASTX	327	2e-27	46	(D85597) polyprotein [Oryza australiensis]
10460	GM_160_B1_F09_T7	g4063760	BLASTX	204	3e-25	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10461	GM_160_B1_G01_MR	g4063770	BLASTX	298	8e-26	56	(AB004906) transposase [Ipomoea purpurea]
10462	GM_160_B1_G03_MR	g3386604	BLASTX	223	1e-16	47	(AC004665) putative protein kinase [Arabidopsis thaliana]
10463	GM_160_B1_G06_MR	g629693	BLASTX	211	5e-16	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10464	GM_160_B1_H02_MR	g2501353	BLASTX	188	7e-21	81	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
10465	GM_160_B1_H06_T7	g3287679	BLASTX	229	5e-17	74	(AC003979) T22J18.6 [Arabidopsis thaliana]
10466	GM_160_B2_A02_T7	g3142328	BLASTN	588	1e-19	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10467	GM_160_B2_A10_T7	g4063760	BLASTX	109	1e-12	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10468	GM_160_B2_B02_MR	g2264320	BLASTN	454	2e-13	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
10469	GM_160_B2_B04_MR	g1666236	BLASTX	182	5e-13	30	(U76261) unknown [Hordeum vulgare]
10470	GM_160_B2_B06_MR	g1666236	BLASTX	148	3e-09	27	(U76261) unknown [Hordeum vulgare]
10471	GM_160_B2_B07_MR	g20861	BLASTN	432	1e-12	69	P.sativum retrotransposon
10472	GM_160_B2_B09_T7	g2522227	BLASTX	209	3e-16	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
10473	GM_160_B2_B10_T7	g507910	BLASTN	389	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10474	GM_160_B2_C09_T7	g3249064	BLASTX	154	3e-16	60	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana]
10475	GM_160_B2_D01_T7	g3377855	BLASTX	306	2e-26	71	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
10476	GM_160_B2_D03_MR	g507910	BLASTN	378	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10477	GM_160_B2_E01_T7	g3426334	BLASTN	366	1e-09	62	Pisum sativum pectin methylesterase (repme1) gene, complete cds
10478	GM_160_B2_E03_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10479	GM_160_B2_E03_T7	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10480	GM_160_B2_E07_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
10481	GM_160_B2_E09_T7	g4063760	BLASTX	426	5e-38	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10482	GM_160_B2_E10_T7	g4106408	BLASTN	430	1e-12	73	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1
10483	GM_160_B2_E11_MR	g3097320	BLASTN	1076	1e-41	82	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10484	GM_160_B2_F03_MR	g4063760	BLASTX	218	2e-19	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10485	GM_160_B2_F06_MR	g905361	BLASTX	566	2e-56	98	(U22103) gag-protease polyprotein [Glycine max]
10486	GM_160_B2_F12_MR	g130582	BLASTX	159	2e-09	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10487	GM_160_B2_G05_MR	g2495155	BLASTX	233	6e-18	60	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) gi 1694926 gnl PID d1009544 (D50407) glutamyl-tRNA reductase [Cucumis sativus]
10488	GM_160_B2_G06_T7	g3142328	BLASTN	1376	2e-55	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10489	GM_160_B2_G08_MR	g507910	BLASTN	551	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10490	GM_160_B2_G08_T7	g507910	BLASTN	462	3e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10491	GM_160_B2_H07_MR	g3142328	BLASTN	746	8e-27	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10492	GM_161_A1_A03_T7	g4050011	BLASTN	533	4e-17	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
10493	GM_161_A1_A05_T7	g226407	BLASTX	171	1e-10	31	retrotransposon del1-46 [Lilium henryi]
10494	GM_161_A1_A08_T7	g507910	BLASTN	360	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10495	GM_161_A1_A09_T7	g421954	BLASTX	299	7e-25	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
10496	GM_161_A1_A10_MR	g3777527	BLASTX	583	2e-54	96	(AF053008) gag-pol polyprotein [Glycine max]
10497	GM_161_A1_A11_MR	g3142328	BLASTN	526	8e-17	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10498	GM_161_A1_A11_T7	g3777527	BLASTX	176	3e-11	35	(AF053008) gag-pol polyprotein [Glycine max]
10499	GM_161_A1_B03_T7	g3142328	BLASTN	639	6e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10500	GM_161_A1_B05_T7	g342965	BLASTN	345	5e-09	61	paramecium species 7,227 mt dna dimer: replication init. region.
10501	GM_161_A1_B09_MR	g3449333	BLASTN	355	5e-09	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]
10502	GM_161_A1_B10_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10503	GM_161_A1_D02_T7	g1732513	BLASTX	186	8e-14	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
10504	GM_161_A1_D03_T7	g3097320	BLASTN	525	1e-16	74	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10505	GM_161_A1_D05_MR	g3402749	BLASTX	148	5e-11	43	(AL031187) putative protein [Arabidopsis thaliana]
10506	GM_161_A1_D08_T7	g563247	BLASTX	646	9e-63	90	(U16279) acetolactate synthase precursor [Xanthium sp.]
10507	GM_161_A1_D10_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10508	GM_161_A1_D10_T7	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
10509	GM_161_A1_D12_MR	g17918	BLASTN	359	4e-10	64	B.oleracea encoding S-receptor kinase protein.
10510	GM_161_A1_E05_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10511	GM_161_A1_E06_MR	g629693	BLASTX	169	2e-11	35	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10512	GM_161_A1_E06_T7	g1076755	BLASTX	528	1e-49	79	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
10513	GM_161_A1_E08_MR	g3377848	BLASTX	149	2e-12	49	(AF076274) contains similarity to reverse transcriptases (Pfam. rvt.hmm, score: 12.22) [Arabidopsis thaliana]
10514	GM_161_A1_F07_T7	g421955	BLASTX	193	4e-30	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10515	GM_161_A1_F08_MR	g114532	BLASTX	432	6e-40	88	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
10516	GM_161_A1_G10_T7	g507910	BLASTN	367	6e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10517	GM_161_A1_G12_T7	g3142328	BLASTN	724	8e-26	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10518	GM_161_A1_H01_MR	g4063760	BLASTX	257	6e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10519	GM_161_A1_H02_T7	g905361	BLASTX	241	1e-18	41	(U22103) gag-protease polyprotein [Glycine max]
10520	GM_161_A1_H03_T7	g3142328	BLASTN	1499	4e-61	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10521	GM_161_A1_H05_MR	g1769898	BLASTX	199	3e-21	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10522	GM_161_A1_H08_MR	g4063760	BLASTX	373	2e-32	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10523	GM_161_A1_H09_MR	g507910	BLASTN	378	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence
10524	GM_161_A2_B04_MR	g2183226	BLASTN	343	7e-09	62	Dictyostelium discoideum calmodulin-like protein (calB) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10525	GM_161_A2_B07_MR	g130398	BLASTX	183	4e-12	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
10526	GM_161_A2_B08_MR	g4063760	BLASTX	432	1e-38	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10527	GM_161_A2_B10_T7	g4150930	BLASTN	385	2e-10	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
10528	GM_161_A2_B11_MR	g4063760	BLASTX	155	8e-16	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10529	GM_161_A2_B11_T7	g3176795	BLASTN	424	8e-13	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
10530	GM_161_A2_B12_T7	g3845148	BLASTN	376	6e-10	61	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence
10531	GM_161_A2_C02_MR	g1532163	BLASTX	206	5e-16	64	(U63815) similar to glutaredoxin encoded by GenBank Accession Number Z49699; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop c...
10532	GM_161_A2_C02_T7	g2961349	BLASTX	128	5e-09	34	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
10533	GM_161_A2_C03_T7	g507910	BLASTN	483	3e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10534	GM_161_A2_C06_MR	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10535	GM_161_A2_C06_T7	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10536	GM_161_A2_C09_T7	g1769898	BLASTX	117	5e-10	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10537	GM_161_A2_C11_MR	g2764526	BLASTN	742	2e-26	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
10538	GM_161_A2_D04_MR	g3513745	BLASTX	156	5e-09	32	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
10539	GM_161_A2_D06_MR	g4063760	BLASTX	232	3e-17	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10540	GM_161_A2_D07_MR	g3777527	BLASTX	208	5e-30	88	(AF053008) gag-pol polyprotein [Glycine max]
10541	GM_161_A2_D07_T7	g1167523	BLASTX	358	1e-30	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
10542	GM_161_A2_D10_MR	g3777527	BLASTX	579	4e-54	94	(AF053008) gag-pol polyprotein [Glycine max]
10543	GM_161_A2_D12_T7	g4056486	BLASTX	300	2e-25	47	(AC005896) hypothetical protein [Arabidopsis thaliana]
10544	GM_161_A2_E03_MR	g3426048	BLASTX	353	2e-31	82	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]
10545	GM_161_A2_E06_T7	g3777527	BLASTX	489	1e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
10546	GM_161_A2_E08_MR	g507910	BLASTN	625	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10547	GM_161_A2_E12_MR	g3426334	BLASTN	354	5e-09	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10548	GM_161_A2_F06_MR	g3777527	BLASTX	703	2e-67	95	(AF053008) gag-pol polyprotein [Glycine max]
10549	GM_161_A2_F07_MR	g507910	BLASTN	364	8e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10550	GM_161_A2_F08_MR	g3142328	BLASTN	763	1e-27	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10551	GM_161_A2_F09_T7	g4063760	BLASTX	163	6e-10	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10552	GM_161_A2_F10_MR	g99730	BLASTX	244	3e-26	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
10553	GM_161_A2_F11_MR	g2462134	BLASTX	166	9e-11	42	(Y13368) reverse transcriptase [Beta vulgaris]
10554	GM_161_A2_G01_MR	g3142328	BLASTN	905	5e-34	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10555	GM_161_A2_G02_T7	g1041029	BLASTN	370	5e-10	69	Mouse 921-L mRNA for presynaptic protein, complete cds
10556	GM_161_A2_G05_T7	g2995405	BLASTX	537	2e-50	65	(Y12432) polyprotein [Ananas comosus]
10557	GM_161_A2_G08_MR	g505129	BLASTN	389	1e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10558	GM_161_A2_H04_MR	g1840106	BLASTN	519	2e-17	63	Human fragile site locus (FRA16B) minisatellite repeat
10559	GM_161_A2_H06_MR	g3779030	BLASTX	129	5e-15	37	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
10560	GM_161_A2_H10_T7	g541936	BLASTX	233	7e-19	76	4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL14) - soybean (fragment)
10561	GM_161_A2_H11_MR	g3859610	BLASTN	386	2e-10	65	Arabidopsis thaliana BAC T9E19
10562	GM_161_A2_H12_MR	g170080	BLASTN	386	1e-23	65	Soybean seed lectin gene transposable element tgm1.
10563	GM_161_A2_H12_T7	g100484	BLASTX	399	1e-35	52	hypothetical protein - garden snapdragon
10564	GM_161_B1_A01_MR	g905361	BLASTX	225	6e-17	41	(U22103) gag-protease polyprotein [Glycine max]
10565	GM_161_B1_A03_MR	g1769899	BLASTX	202	2e-15	79	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10566	GM_161_B1_A03_T7	g3645899	BLASTX	284	6e-23	58	(U68408) 5' end not determined experimentally [Zea mays]
10567	GM_161_B1_A04_T7	g170605	BLASTN	434	7e-13	58	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
10568	GM_161_B1_A05_T7	g4063760	BLASTX	139	5e-18	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10569	GM_161_B1_A08_MR	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10570	GM_161_B1_A08_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10571	GM_161_B1_A09_T7	g4092471	BLASTN	524	1e-16	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
10572	GM_161_B1_B04_MR	g2995405	BLASTX	284	5e-23	52	(Y12432) polyprotein [Ananas comosus]
10573	GM_161_B1_B05_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
10574	GM_161_B1_B05_T7	g507910	BLASTN	391	5e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10575	GM_161_B1_B08_T7	g18559	BLASTN	863	4e-32	76	G.max gene for catalase
10576	GM_161_B1_B09_MR	g18559	BLASTN	1342	7e-54	86	G.max gene for catalase
10577	GM_161_B1_B10_MR	g2443320	BLASTX	308	3e-25	52	(D85597) polyprotein [Oryza australiensis]
10578	GM_161_B1_C11_MR	g3319363	BLASTX	137	2e-15	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
10579	GM_161_B1_D01_MR	g507910	BLASTN	389	6e-11	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10580	GM_161_B1_D02_MR	g1666236	BLASTX	149	3e-09	28	(U76261) unknown [Hordeum vulgare]
10581	GM_161_B1_D03_MR	g3645899	BLASTX	199	9e-27	50	(U68408) 5' end not determined experimentally [Zea mays]
10582	GM_161_B1_D03_T7	g2129618	BLASTX	216	1e-15	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10583	GM_161_B1_D08_MR	g99729	BLASTX	212	4e-20	46	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
10584	GM_161_B1_D08_T7	g18559	BLASTN	1213	5e-48	82	G.max gene for catalase
10585	GM_161_B1_E01_MR	g3860167	BLASTX	195	3e-13	42	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]
10586	GM_161_B1_E04_T7	g3645899	BLASTX	358	6e-39	62	(U68408) 5' end not determined experimentally [Zea mays]
10587	GM_161_B1_E07_MR	g2129618	BLASTX	163	4e-10	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10588	GM_161_B1_E11_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10589	GM_161_B1_F02_MR	g3097320	BLASTN	493	3e-15	75	Glycine max gene for Bd 30K, complete cds
10590	GM_161_B1_F04_MR	g3094012	BLASTX	164	2e-11	89	(AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
10591	GM_161_B1_F09_MR	g18559	BLASTN	819	4e-30	80	G.max gene for catalase
10592	GM_161_B1_G04_MR	g4063760	BLASTX	470	9e-43	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10593	GM_161_B1_G08_MR	g3777526	BLASTN	442	6e-13	62	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
10594	GM_161_B1_G09_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10595	GM_161_B1_H01_MR	g3142328	BLASTN	1251	9e-50	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10596	GM_161_B1_H03_MR	g3319362	BLASTX	152	4e-16	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10597	GM_161_B1_H11_MR	g342963	BLASTN	422	2e-12	69	paramecium species 5,87 mt dna dimer: replication init. region.
10598	GM_161_B1_H11_T7	g1658062	BLASTX	230	7e-18	68	ACC synthase [Malus domestica]
10599	GM_161_B2_A03_T7	g3777527	BLASTX	175	4e-11	38	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10600	GM_161_B2_A05_T7	g3097320	BLASTN	438	9e-13	70	Glycine max gene for Bd 30K, complete cds
10601	GM_161_B2_A07_MR	g342963	BLASTN	395	3e-11	64	paramecium species 5.87 mt dna dimer: replication init. region.
10602	GM_161_B2_B11_T7	g3021357	BLASTX	254	4e-21	77	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]
10603	GM_161_B2_B12_T7	g2443320	BLASTX	235	2e-17	49	(D85597) polyprotein [Oryza australiensis]
10604	GM_161_B2_C01_MR	g3777527	BLASTX	302	1e-35	93	(AF053008) gag-pol polyprotein [Glycine max]
10605	GM_161_B2_C01_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10606	GM_161_B2_C04_MR	g3386534	BLASTX	230	6e-18	61	(AF078934) mariner transposase [Glycine max]
10607	GM_161_B2_C04_T7	g99922	BLASTX	295	2e-47	83	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10608	GM_161_B2_C09_T7	g2264309	BLASTN	602	4e-20	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
10609	GM_161_B2_D01_MR	g905361	BLASTX	497	9e-47	90	(U22103) gag-protease polyprotein [Glycine max]
10610	GM_161_B2_D04_MR	g100484	BLASTX	159	7e-10	38	hypothetical protein - garden snapdragon
10611	GM_161_B2_D07_MR	g1142701	BLASTN	1103	2e-43	87	Glycine max satellite STR120-A.3.
10612	GM_161_B2_D10_MR	g4063760	BLASTX	267	5e-21	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10613	GM_161_B2_D10_T7	g1480927	BLASTN	784	9e-29	89	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
10614	GM_161_B2_E01_MR	g507910	BLASTN	374	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10615	GM_161_B2_E01_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10616	GM_161_B2_E03_MR	g3702738	BLASTN	311	5e-10	79	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWJ3, complete sequence [Arabidopsis thaliana]
10617	GM_161_B2_E03_T7	g1906825	BLASTN	395	6e-11	88	A.thaliana hsp81.2 gene
10618	GM_161_B2_E04_MR	g3687234	BLASTX	224	2e-16	39	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
10619	GM_161_B2_F06_T7	g2462058	BLASTX	257	2e-21	62	(Y13389) reverse transcriptase [Antirrhinum majus]
10620	GM_161_B2_F07_MR	g2129618	BLASTX	173	4e-11	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10621	GM_161_B2_F07_T7	g18559	BLASTN	674	2e-23	79	G.max gene for catalase
10622	GM_161_B2_F12_MR	g1946279	BLASTX	163	2e-11	36	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
10623	GM_161_B2_G01_T7	g100484	BLASTX	318	7e-27	57	hypothetical protein - garden snapdragon
10624	GM_161_B2_G03_T7	g3142328	BLASTN	941	1e-35	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10625	GM_161_B2_G07_T7	g3142328	BLASTN	1506	2e-61	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10626	GM_161_B2_H03_T7	g100484	BLASTX	334	1e-28	59	hypothetical protein - garden snapdragon
10627	GM_161_B2_H09_MR	g507910	BLASTN	499	6e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
10628	GM_161_B2_H09_T7	g507910	BLASTN	357	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
10629	GM_161_B2_H10_T7	g18559	BLASTN	762	2e-27	78	G.max gene for catalase
10630	GM_161_B2_H11_MR	g1142701	BLASTN	1205	4e-48	85	Glycine max satellite STR120-A.3.
10631	GM_162_A1_A05_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10632	GM_162_A1_A05_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10633	GM_162_A1_A06_T7	g2522228	BLASTX	218	1e-16	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
10634	GM_162_A1_A07_T7	g3426261	BLASTX	294	7e-24	44	(U81378) disease resistance gene homolog Mi-copy1 [Lycopersicon esculentum]
10635	GM_162_A1_A09_MR	g320564	BLASTX	107	6e-09	42	transposon copia - Arabidopsis thaliana (fragment)
10636	GM_162_A1_B02_MR	g3334349	BLASTX	156	2e-09	47	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS) gi 2564215 gnl PID e1181897 (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]
10637	GM_162_A1_B04_MR	g3560028	BLASTN	394	7e-11	67	Schistosoma intercalatum ribosomal intergenic spacer DNA
10638	GM_162_A1_B05_T7	g2443320	BLASTX	281	2e-22	45	(D85597) polyprotein [Oryza australiensis]
10639	GM_162_A1_B10_MR	g3097320	BLASTN	804	2e-29	73	Glycine max gene for Bd 30K, complete cds
10640	GM_162_A1_B11_T7	g2352492	BLASTX	181	3e-12	41	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] gi 2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
10641	GM_162_A1_C02_MR	g1666236	BLASTX	86	8e-09	26	(U76261) unknown [Hordeum vulgare]
10642	GM_162_A1_C03_MR	g3142328	BLASTN	961	1e-36	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10643	GM_162_A1_C05_MR	g507910	BLASTN	612	5e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10644	GM_162_A1_C10_MR	g1769898	BLASTX	305	1e-25	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10645	GM_162_A1_D02_MR	g2129618	BLASTX	156	3e-09	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10646	GM_162_A1_D09_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10647	GM_162_A1_E05_MR	g2244915	BLASTX	240	3e-18	40	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
10648	GM_162_A1_E10_MR	g3402711	BLASTX	166	6e-11	48	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]
10649	GM_162_A1_E10_T7	g3193221	BLASTN	1282	5e-51	75	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
10650	GM_162_A1_E11_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10651	GM_162_A1_E12_T7	g3426334	BLASTN	351	7e-09	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10652	GM_162_A1_F02_T7	g3777527	BLASTX	215	2e-15	45	(AF053008) gag-pol polyprotein [Glycine max]
10653	GM_162_A1_G05_T7	g531389	BLASTX	156	4e-09	31	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
10654	GM_162_A1_G07_MR	g170029	BLASTN	360	3e-09	76	Glycine max cv. Dare nodulin 26 gene fragment.
10655	GM_162_A1_G08_T7	g3097320	BLASTN	711	4e-25	75	Glycine max gene for Bd 30K, complete cds
10656	GM_162_A1_H01_MR	g507910	BLASTN	530	2e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10657	GM_162_A1_H01_T7	g3645899	BLASTX	221	1e-20	41	(U68408) 5' end not determined experimentally [Zea mays]
10658	GM_162_A1_H03_T7	g2522228	BLASTX	369	3e-33	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
10659	GM_162_A1_H04_MR	g100484	BLASTX	355	7e-31	61	hypothetical protein - garden snapdragon
10660	GM_162_A1_H06_T7	g2351065	BLASTN	475	2e-14	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15
10661	GM_162_A1_H07_T7	g2618693	BLASTX	103	4e-09	27	(AC002510) putative zinc-finger protein [Arabidopsis thaliana]
10662	GM_162_A1_H08_T7	g507910	BLASTN	593	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10663	GM_162_A1_H09_T7	g3097320	BLASTN	457	1e-13	76	Glycine max gene for Bd 30K, complete cds
10664	GM_162_A1_H11_T7	g2160156	BLASTX	256	8e-24	66	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb Z73100). [Arabidopsis thaliana]
10665	GM_162_A2_A05_T7	g4115359	BLASTX	150	7e-10	41	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
10666	GM_162_A2_A10_MR	g3947433	BLASTN	451	2e-13	63	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
10667	GM_162_A2_B03_MR	g2443320	BLASTX	192	2e-14	35	(D85597) polyprotein [Oryza australiensis]
10668	GM_162_A2_B06_MR	g3845197	BLASTN	368	1e-09	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10669	GM_162_A2_B09_MR	g3152629	BLASTN	567	1e-18	67	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
10670	GM_162_A2_C02_T7	g100484	BLASTX	290	7e-24	60	hypothetical protein - garden snapdragon
10671	GM_162_A2_C03_MR	g4160362	BLASTN	355	5e-09	63	Saccharomyces cerevisiae complete mitochondrial genome
10672	GM_162_A2_C05_MR	g226407	BLASTX	244	2e-18	46	retrotransposon del1-46 [Lilium henryi]
10673	GM_162_A2_C10_MR	g4140712	BLASTX	331	1e-39	59	(AF110183) putative integrase [Oryza sativa]
10674	GM_162_A2_C12_MR	g2114040	BLASTN	383	7e-11	81	Vigna vexillata DNA for TY1-copia-like retrotransposable element
10675	GM_162_A2_D08_MR	g1769897	BLASTX	137	4e-10	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10676	GM_162_A2_D11_MR	g4063760	BLASTX	388	2e-39	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10677	GM_162_A2_D12_MR	g3820757	BLASTN	377	3e-10	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
10678	GM_162_A2_E03_MR	g3746069	BLASTX	171	9e-11	40	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10679	GM_162_A2_E05_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10680	GM_162_A2_E05_T7	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10681	GM_162_A2_E07_MR	g99729	BLASTX	342	2e-30	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
10682	GM_162_A2_E08_MR	g4063760	BLASTX	175	3e-11	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10683	GM_162_A2_E12_MR	g1167523	BLASTX	103	1e-11	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
10684	GM_162_A2_F01_MR	g507910	BLASTN	393	4e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10685	GM_162_A2_F07_MR	g99922	BLASTX	277	3e-31	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10686	GM_162_A2_F09_T7	g3777527	BLASTX	243	3e-18	47	(AF053008) gag-pol polyprotein [Glycine max]
10687	GM_162_A2_G01_T7	g3142328	BLASTN	973	4e-37	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10688	GM_162_A2_G10_T7	g829300	BLASTX	210	2e-16	81	(X01647) open reading frame (ORF 704) [Marchantia polymorpha]
10689	GM_162_B1_A03_MR	g3924609	BLASTX	263	4e-27	59	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
10690	GM_162_B1_A04_T7	g3142328	BLASTN	925	6e-35	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10691	GM_162_B1_A05_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
10692	GM_162_B1_A05_T7	g507910	BLASTN	359	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10693	GM_162_B1_A10_MR	g14227	BLASTN	449	2e-14	61	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
10694	GM_162_B1_B03_T7	g1769898	BLASTX	234	1e-19	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10695	GM_162_B1_B05_MR	g2335061	BLASTN	471	3e-14	61	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
10696	GM_162_B1_B10_T7	g1666236	BLASTX	180	9e-13	29	(U76261) unknown [Hordeum vulgare]
10697	GM_162_B1_B11_MR	g3915022	BLASTX	167	5e-25	60	SUCROSE-PHOSPHATE SYNTHASE 2 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2) >gi 2190350 gnl PID e310970 (Y11795) sucrose-phosphate synthase [Craterostigma plantagineum]
10698	GM_162_B1_C01_T7	g3097320	BLASTN	879	9e-33	75	Glycine max gene for Bd 30K, complete cds
10699	GM_162_B1_C02_MR	g905361	BLASTX	608	2e-58	93	(U22103) gag-protease polyprotein [Glycine max]
10700	GM_162_B1_C04_T7	g3777527	BLASTX	672	5e-64	94	(AF053008) gag-pol polyprotein [Glycine max]
10701	GM_162_B1_C06_T7	g3738114	BLASTN	427	3e-12	65	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10702	GM_162_B1_D01_MR	g2213582	BLASTX	158	3e-09	34	(AC000348) T7N9.2 [Arabidopsis thaliana]
10703	GM_162_B1_D01_T7	g1431738	BLASTN	519	1e-16	88	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
10704	GM_162_B1_D02_MR	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10705	GM_162_B1_D06_MR	g2979597	BLASTN	403	4e-11	60	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
10706	GM_162_B1_E01_MR	g12212	BLASTN	1145	3e-50	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
10707	GM_162_B1_E01_T7	g2734665	BLASTX	495	1e-46	70	(U48752) ribosomal protein subunit 2 [Euphrasia sp.]
10708	GM_162_B1_E03_T7	g4063760	BLASTX	268	4e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10709	GM_162_B1_E06_MR	g2708743	BLASTX	203	4e-14	34	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
10710	GM_162_B1_E09_T7	g2443320	BLASTX	350	8e-30	55	(D85597) polyprotein [Oryza australiensis]
10711	GM_162_B1_F01_T7	g3319362	BLASTX	183	3e-12	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10712	GM_162_B1_F05_MR	g4063760	BLASTX	366	2e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10713	GM_162_B1_F06_T7	g2828278	BLASTN	439	9e-13	65	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)
10714	GM_162_B1_F07_T7	g3777526	BLASTN	1381	2e-55	88	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
10715	GM_162_B1_G01_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10716	GM_162_B1_G06_T7	g1518388	BLASTX	210	1e-26	76	(X91172) korean-radish isoperoxidase [Raphanus sativus]
10717	GM_162_B1_G09_MR	g3645899	BLASTX	213	4e-18	44	(U68408) 5' end not determined experimentally [Zea mays]
10718	GM_162_B1_H06_MR	g507910	BLASTN	463	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
10719	GM_162_B1_H06_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10720	GM_162_B1_H08_MR	g3097320	BLASTN	1246	2e-49	83	Glycine max gene for Bd 30K, complete cds
10721	GM_162_B1_H10_MR	g507910	BLASTN	362	9e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10722	GM_162_B1_H11_MR	g4063760	BLASTX	390	4e-34	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10723	GM_162_B1_H11_T7	g8540	BLASTN	365	2e-10	63	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb M29744 DROSAT02 Drosophila satellite DNA fragment 1.672-614.
10724	GM_162_B2_A03_MR	g226407	BLASTX	432	2e-38	46	retrotransposon del1-46 [Lilium henryi]
10725	GM_162_B2_A05_T7	g2129652	BLASTX	210	4e-15	35	myosin heavy chain homolog - Arabidopsis thaliana (fragment) gi 699495 (U19616) myosin heavy chain homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10726	GM_162_B2_A07_MR	g4063760	BLASTX	293	9e-24	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10727	GM_162_B2_A07_T7	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10728	GM_162_B2_A09_MR	g100484	BLASTX	180	8e-14	47	hypothetical protein - garden snapdragon
10729	GM_162_B2_B06_T7	g3777527	BLASTX	563	1e-57	80	(AF053008) gag-pol polyprotein [Glycine max]
10730	GM_162_B2_B08_T7	g3142328	BLASTN	427	2e-20	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10731	GM_162_B2_B11_MR	g99922	BLASTX	533	1e-50	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10732	GM_162_B2_B12_MR	g507910	BLASTN	391	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10733	GM_162_B2_B12_T7	g3097320	BLASTN	446	4e-13	70	Glycine max gene for Bd 30K, complete cds
10734	GM_162_B2_C03_MR	g2275089	BLASTN	650	4e-29	93	Swietenia humilis DNA for simple tandem repeat (340bp)
10735	GM_162_B2_C04_T7	g505337	BLASTN	379	4e-10	61	Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.
10736	GM_162_B2_C08_MR	g2738982	BLASTX	187	5e-13	44	(AF022157) CYP71A10 [Glycine max]
10737	GM_162_B2_C08_T7	g225282	BLASTX	474	3e-55	72	RNA polymerase beta [Nicotiana tabacum]
10738	GM_162_B2_C10_MR	g4063760	BLASTX	205	8e-32	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10739	GM_162_B2_E01_MR	g505129	BLASTN	502	9e-16	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10740	GM_162_B2_E04_T7	g3645899	BLASTX	133	5e-16	41	(U68408) 5' end not determined experimentally [Zea mays]
10741	GM_162_B2_E07_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10742	GM_162_B2_E08_MR	g4038056	BLASTX	278	2e-22	44	(AC005897) putative transposon [Arabidopsis thaliana]
10743	GM_162_B2_E10_T7	g2522230	BLASTX	365	9e-33	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10744	GM_162_B2_E11_MR	g507910	BLASTN	345	6e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10745	GM_162_B2_F01_T7	g4063760	BLASTX	461	1e-41	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10746	GM_162_B2_F05_T7	g2522230	BLASTX	341	3e-30	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10747	GM_162_B2_F08_T7	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10748	GM_162_B2_F09_T7	g4063760	BLASTX	208	5e-31	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10749	GM_162_B2_F11_T7	g3645899	BLASTX	292	8e-24	48	(U68408) 5' end not determined experimentally [Zea mays]
10750	GM_162_B2_G01_MR	g4063760	BLASTX	486	2e-44	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10751	GM_162_B2_G09_MR	g3645899	BLASTX	288	1e-26	41	(U68408) 5' end not determined experimentally [Zea mays]
10752	GM_162_B2_G09_T7	g100484	BLASTX	267	1e-25	56	hypothetical protein - garden snapdragon
10753	GM_163_A1_A02_T7	g4038056	BLASTX	233	4e-23	48	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10754	GM_163_A1_A07_T7	g1335695	BLASTX	248	2e-20	42	(X02600) unidentified open reading frame II (146 aa) [Drosophila melanogaster]
10755	GM_163_A1_A09_T7	g3513747	BLASTX	258	7e-20	47	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
10756	GM_163_A1_B03_T7	g4063760	BLASTX	132	6e-09	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10757	GM_163_A1_B07_T7	g1172441	BLASTX	96	3e-09	81	POSSIBLE TRANSCRIPTION FACTOR POSF21 gi 99685 pir S21883 DNA-binding protein POSF21 - Arabidopsis thaliana gi 16429 (X61031) posF21 gene product [Arabidopsis thaliana]
10758	GM_163_A1_B08_T7	g3650039	BLASTX	258	2e-20	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
10759	GM_163_A1_C06_T7	g3142328	BLASTN	1827	4e-76	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10760	GM_163_A1_D03_T7	g2443320	BLASTX	135	1e-16	37	(D85597) polyprotein [Oryza australiensis]
10761	GM_163_A1_D07_T7	g3377856	BLASTX	236	9e-18	38	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
10762	GM_163_A1_D11_T7	g3738133	BLASTN	353	7e-09	69	Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence [Homo sapiens]
10763	GM_163_A1_E01_T7	g2244802	BLASTX	378	1e-32	50	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
10764	GM_163_A1_E04_T7	g629693	BLASTX	254	5e-21	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10765	GM_163_A1_E07_T7	g4063760	BLASTX	341	6e-29	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10766	GM_163_A1_E12_T7	g3522932	BLASTN	383	3e-10	62	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
10767	GM_163_A1_F02_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10768	GM_163_A1_F05_T7	g1045614	BLASTX	185	8e-13	51	(U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]
10769	GM_163_A1_G12_T7	g3097320	BLASTN	468	4e-14	73	Glycine max gene for Bd 30K, complete cds
10770	GM_163_A1_H04_T7	g4063760	BLASTX	281	1e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10771	GM_163_A1_H06_T7	g18559	BLASTN	469	3e-14	75	G.max gene for catalase
10772	GM_163_A1_H12_T7	g4038056	BLASTX	356	9e-31	54	(AC005897) putative transposon [Arabidopsis thaliana]
10773	GM_163_A2_C05_MR	g18559	BLASTN	1372	3e-55	79	G.max gene for catalase
10774	GM_163_A2_E05_MR	g1236920	BLASTN	436	8e-13	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10775	GM_163_A2_F04_MR	g1335861	BLASTN	374	7e-10	68	Glycine max clathrin heavy chain mRNA, complete cds
10776	GM_163_A2_F10_MR	g522302	BLASTX	260	3e-20	47	(L35053) endonuclease [Magnaporthe grisea]
10777	GM_163_A2_H03_MR	g3738114	BLASTN	352	7e-09	64	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
10778	GM_163_B1_A02_MR	g1480927	BLASTN	1056	2e-41	88	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
10779	GM_163_B1_A07_MR	g3851527	BLASTN	406	2e-11	67	Hordeum vulgare cultivar Bomi starch branching enzyme IIb (sbeIIb) gene, nuclear gene encoding plastid protein, partial cds
10780	GM_163_B1_A11_T7	g508826	BLASTN	381	3e-10	68	Drosophila melanogaster Oregon-R mitochondrial A+T region.
10781	GM_163_B1_B04_MR	g3319362	BLASTX	446	2e-40	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10782	GM_163_B1_B05_MR	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10783	GM_163_B1_B08_MR	g4063760	BLASTX	204	2e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10784	GM_163_B1_C05_T7	g3777527	BLASTX	471	7e-51	88	(AF053008) gag-pol polyprotein [Glycine max]
10785	GM_163_B1_C12_MR	g905361	BLASTX	174	2e-11	34	(U22103) gag-protease polyprotein [Glycine max]
10786	GM_163_B1_D05_T7	g3142328	BLASTN	1099	7e-43	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10787	GM_163_B1_D07_T7	g4063756	BLASTN	418	8e-12	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10788	GM_163_B1_D09_T7	g3047114	BLASTX	305	2e-26	78	(AF058919) No definition line found [Arabidopsis thaliana]
10789	GM_163_B1_E01_MR	g99922	BLASTX	232	1e-18	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10790	GM_163_B1_E03_T7	g4063760	BLASTX	160	1e-09	30	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10791	GM_163_B1_E05_T7	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10792	GM_163_B1_E06_MR	g4038030	BLASTX	229	2e-17	71	(AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]
10793	GM_163_B1_E09_MR	g3560028	BLASTN	362	2e-09	64	Schistosoma intercalatum ribosomal intergenic spacer DNA
10794	GM_163_B1_E09_T7	g4092471	BLASTN	437	1e-12	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
10795	GM_163_B1_F01_MR	g3449319	BLASTN	494	3e-15	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQP15, complete sequence [Arabidopsis thaliana]
10796	GM_163_B1_F05_T7	g507910	BLASTN	416	3e-12	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10797	GM_163_B1_F06_MR	g507910	BLASTN	478	5e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence
10798	GM_163_B1_F09_T7	g1769898	BLASTX	358	1e-34	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10799	GM_163_B1_F11_MR	g1666236	BLASTX	195	2e-14	30	(U76261) unknown [Hordeum vulgare]
10800	GM_163_B1_F12_MR	g507910	BLASTN	511	2e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10801	GM_163_B1_G05_T7	g226407	BLASTX	310	2e-25	50	retrotransposon del1-46 [Lilium henryi]
10802	GM_163_B1_G06_T7	g3176799	BLASTN	387	3e-11	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence
10803	GM_163_B1_G09_MR	g18559	BLASTN	1141	1e-44	77	G.max gene for catalase
10804	GM_163_B1_G11_T7	g2462054	BLASTX	173	2e-12	40	(Y13373) reverse transcriptase [Allium cepa]
10805	GM_163_B1_H02_MR	g1769898	BLASTX	264	4e-21	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10806	GM_163_B1_H02_T7	g3650039	BLASTX	174	2e-11	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
10807	GM_163_B1_H03_MR	g2827713	BLASTX	152	2e-09	82	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]
10808	GM_163_B1_H07_MR	g3142379	BLASTX	277	4e-23	75	(AF053008) envelope-like [Glycine max]
10809	GM_163_B1_H09_T7	g2085783	BLASTN	365	2e-09	67	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
10810	GM_163_B1_H10_MR	g1220442	BLASTN	350	7e-09	61	Plasmodium falciparum clone HB3 d-aminolevulinic acid synthetase gene, complete cds
10811	GM_163_B1_H12_MR	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10812	GM_163_B2_A02_T7	g18559	BLASTN	365	2e-09	71	G.max gene for catalase
10813	GM_163_B2_A03_T7	g2194136	BLASTX	281	9e-28	56	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
10814	GM_163_B2_A04_MR	g3097320	BLASTN	430	2e-12	70	Glycine max gene for Bd 30K, complete cds
10815	GM_163_B2_A05_T7	g18559	BLASTN	530	5e-17	72	G.max gene for catalase
10816	GM_163_B2_A06_MR	g18559	BLASTN	877	1e-32	73	G.max gene for catalase
10817	GM_163_B2_A09_MR	g2443320	BLASTX	155	5e-09	26	(D85597) polyprotein [Oryza australiensis]
10818	GM_163_B2_A10_MR	g3914056	BLASTX	125	2e-13	78	DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
10819	GM_163_B2_B02_MR	g3142328	BLASTN	878	1e-60	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10820	GM_163_B2_B02_T7	g3777527	BLASTX	258	7e-20	37	(AF053008) gag-pol polyprotein [Glycine max]
10821	GM_163_B2_B04_T7	g3319362	BLASTX	260	2e-20	34	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10822	GM_163_B2_B05_MR	g3777527	BLASTX	416	9e-37	47	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10823	GM_163_B2_B05_T7	g629693	BLASTX	164	3e-25	39	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10824	GM_163_B2_B11_T7	g18559	BLASTN	497	2e-15	76	G.max gene for catalase
10825	GM_163_B2_B12_T7	g2651294	BLASTN	384	3e-10	64	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]
10826	GM_163_B2_C02_MR	g1707017	BLASTX	678	5e-66	82	(U78721) RNA helicase isolog [Arabidopsis thaliana]
10827	GM_163_B2_C08_T7	g1171591	BLASTN	409	2e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-B)
10828	GM_163_B2_C10_MR	g3461846	BLASTX	422	2e-37	56	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
10829	GM_163_B2_C10_T7	g4063770	BLASTX	494	7e-46	56	(AB004906) transposase [Ipomoea purpurea]
10830	GM_163_B2_C12_MR	g3645899	BLASTX	142	2e-12	49	(U68408) 5' end not determined experimentally [Zea mays]
10831	GM_163_B2_D04_T7	g1076389	BLASTX	164	4e-25	84	protein phosphatase 2A pDF1 - Arabidopsis thaliana gi 683502 (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]
10832	GM_163_B2_D06_MR	g1769898	BLASTX	339	2e-29	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10833	GM_163_B2_D07_T7	g505129	BLASTN	302	2e-09	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10834	GM_163_B2_D09_T7	g1370199	BLASTN	622	3e-22	71	L.japonicus mRNA for small GTP-binding protein, RAC1
10835	GM_163_B2_E05_MR	g1769897	BLASTX	258	3e-23	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10836	GM_163_B2_E06_MR	g13767	BLASTN	370	1e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
10837	GM_163_B2_E10_MR	g3097320	BLASTN	471	3e-14	71	Glycine max gene for Bd 30K, complete cds
10838	GM_163_B2_E12_MR	g2129618	BLASTX	245	8e-19	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10839	GM_163_B2_E12_T7	g3097320	BLASTN	1012	8e-39	76	Glycine max gene for Bd 30K, complete cds
10840	GM_163_B2_F03_MR	g3250688	BLASTX	251	1e-20	43	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
10841	GM_163_B2_F05_MR	g3875246	BLASTX	135	3e-09	50	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...
10842	GM_163_B2_F07_T7	g2586082	BLASTX	422	2e-37	50	(U72725) retrofit [Oryza longistaminata]
10843	GM_163_B2_F09_T7	g18559	BLASTN	495	2e-15	73	G.max gene for catalase
10844	GM_163_B2_F12_MR	g3810596	BLASTX	243	1e-18	37	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10845	GM_163_B2_G01_T7	g905361	BLASTX	433	8e-40	95	(U22103) gag-protease polyprotein [Glycine max]
10846	GM_163_B2_G03_T7	g4063760	BLASTX	593	7e-56	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10847	GM_163_B2_G06_MR	g507910	BLASTN	575	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10848	GM_163_B2_G10_MR	g507910	BLASTN	642	2e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10849	GM_163_B2_G10_T7	g3777527	BLASTX	411	3e-36	49	(AF053008) gag-pol polyprotein [Glycine max]
10850	GM_163_B2_G12_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10851	GM_163_B2_H05_T7	g4038056	BLASTX	276	3e-22	37	(AC005897) putative transposon [Arabidopsis thaliana]
10852	GM_163_B2_H06_MR	g507910	BLASTN	372	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10853	GM_164_A1_A01_T7	g1769898	BLASTX	406	9e-39	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10854	GM_164_A1_A02_T7	g131772	BLASTX	109	2e-13	79	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) - maize
10855	GM_164_A1_A03_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10856	GM_164_A1_A05_T7	g3645899	BLASTX	199	8e-14	49	(U68408) 5' end not determined experimentally [Zea mays]
10857	GM_164_A1_B06_MR	g3097320	BLASTN	1195	4e-47	81	Glycine max gene for Bd 30K, complete cds
10858	GM_164_A1_B07_T7	g170029	BLASTN	383	3e-10	80	Glycine max cv Dare nodulin 26 gene fragment.
10859	GM_164_A1_B09_MR	g1572834	BLASTN	377	5e-10	62	Caenorhabditis elegans cosmid T01C4
10860	GM_164_A1_C06_MR	g2443320	BLASTX	367	1e-31	54	(D85597) polyprotein [Oryza australiensis]
10861	GM_164_A1_C06_T7	g2708743	BLASTX	171	2e-11	37	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
10862	GM_164_A1_C10_T7	g2921625	BLASTN	348	1e-08	69	Lupinus luteus leghemoglobin (LbI) gene, complete cds
10863	GM_164_A1_C11_T7	g3645899	BLASTX	168	8e-12	50	(U68408) 5' end not determined experimentally [Zea mays]
10864	GM_164_A1_D03_MR	g18559	BLASTN	1017	4e-39	73	G.max gene for catalase
10865	GM_164_A1_D07_T7	g3341443	BLASTX	150	9e-10	82	(AJ223074) acid phosphatase [Glycine max]
10866	GM_164_A1_D10_T7	g4150930	BLASTN	400	5e-11	62	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
10867	GM_164_A1_E01_MR	g1769898	BLASTX	472	4e-44	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10868	GM_164_A1_E04_MR	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10869	GM_164_A1_E05_MR	g3777527	BLASTX	747	4e-72	95	(AF053008) gag-pol polyprotein [Glycine max]
10870	GM_164_A1_E10_MR	g3142328	BLASTN	873	1e-32	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10871	GM_164_A1_F02_MR	g2995405	BLASTX	251	1e-19	57	(Y12432) polyprotein [Ananas comosus]
10872	GM_164_A1_F04_MR	g1769898	BLASTX	183	2e-12	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10873	GM_164_A1_F08_T7	g3142379	BLASTX	289	1e-24	69	(AF053008) envelope-like [Glycine max]
10874	GM_164_A1_G01_T7	g905361	BLASTX	223	9e-17	34	(U22103) gag-protease polyprotein [Glycine max]
10875	GM_164_A1_G03_MR	g905361	BLASTX	389	8e-35	91	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10876	GM_164_A1_G04_MR	g4063756	BLASTN	567	1e-18	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10877	GM_164_A1_G11_T7	g1769901	BLASTX	206	3e-15	68	(X95737) proline transporter 1 [Arabidopsis thaliana] gi 2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]
10878	GM_164_A1_H07_T7	g2462744	BLASTX	225	3e-17	36	(AC002292) Hypothetical protein [Arabidopsis thaliana]
10879	GM_164_A1_H08_MR	g3201554	BLASTX	185	1e-12	63	(AJ006501) beta-D-glucosidase [Tropaeolum majus]
10880	GM_164_A1_H09_MR	g3845139	BLASTN	311	5e-09	64	Plasmodium falciparum chromosome 2, section 21 of 73 of the complete sequence
10881	GM_164_A1_H10_MR	g3319362	BLASTX	249	3e-19	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10882	GM_164_A2_A03_T7	g2642431	BLASTX	258	6e-20	36	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
10883	GM_164_A2_A04_T7	g2980640	BLASTN	446	4e-13	71	Arabidopsis thaliana mRNA for putative MRP protein
10884	GM_164_A2_A07_T7	g2586082	BLASTX	184	5e-27	46	(U72725) retrofit [Oryza longistaminata]
10885	GM_164_A2_A08_MR	g114734	BLASTX	166	1e-18	85	AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
10886	GM_164_A2_A09_MR	g2959781	BLASTX	113	3e-15	79	(AJ223508) Zwille protein [Arabidopsis thaliana]
10887	GM_164_A2_A10_MR	g3142328	BLASTN	952	3e-36	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10888	GM_164_A2_A11_MR	g18559	BLASTN	793	6e-29	73	G.max gene for catalase
10889	GM_164_A2_B01_T7	g1666236	BLASTX	118	2e-13	30	(U76261) unknown [Hordeum vulgare]
10890	GM_164_A2_B02_T7	g2864621	BLASTX	101	5e-10	26	hypothetical protein [Arabidopsis thaliana]
10891	GM_164_A2_B06_MR	g3643603	BLASTX	225	1e-16	60	(AC005395) unknown protein [Arabidopsis thaliana]
10892	GM_164_A2_B09_MR	g2522228	BLASTX	157	6e-10	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
10893	GM_164_A2_C02_T7	g4049647	BLASTN	351	8e-09	61	Melanoplus sanguinipes entomopoxvirus, complete genome
10894	GM_164_A2_C03_T7	g3763850	BLASTN	789	1e-28	78	Glycine max GmENOD93 gene for early nodulin, complete cds
10895	GM_164_A2_C04_T7	g421954	BLASTX	183	2e-12	37	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
10896	GM_164_A2_C09_T7	g3820757	BLASTN	390	8e-11	64	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
10897	GM_164_A2_D02_MR	g4063756	BLASTN	516	3e-16	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10898	GM_164_A2_D03_T7	g4140712	BLASTX	465	2e-43	61	(AF110183) putative integrase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10899	GM_164_A2_D04_T7	g3249105	BLASTX	224	2e-23	80	(AC003114) Contains similarity to protein phosphatase 2C (AB11) gb X78886 from A. thaliana. [Arabidopsis thaliana]
10900	GM_164_A2_D08_MR	g2129618	BLASTX	168	1e-10	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10901	GM_164_A2_D11_MR	g2443320	BLASTX	149	6e-12	40	(D85597) polyprotein [Oryza australiensis]
10902	GM_164_A2_D11_T7	g18559	BLASTN	1056	7e-41	74	G.max gene for catalase
10903	GM_164_A2_D12_T7	g1906830	BLASTX	176	7e-17	68	(Y11829) heat shock protein [Arabidopsis thaliana]
10904	GM_164_A2_E05_MR	g2218024	BLASTN	208	6e-10	60	Apis mellifera mitochondrial tRNA-Leu gene
10905	GM_164_A2_E06_T7	g336279	BLASTN	350	9e-09	60	Apis mellifera ligustica complete mitochondrial genome
10906	GM_164_A2_E08_T7	g2781348	BLASTX	220	2e-16	47	(AC003113) F24O1.4 [Arabidopsis thaliana]
10907	GM_164_A2_E09_T7	g3142328	BLASTN	978	2e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10908	GM_164_A2_F01_T7	g18559	BLASTN	1007	1e-38	76	G.max gene for catalase
10909	GM_164_A2_F02_MR	g3097320	BLASTN	1280	6e-51	80	Glycine max gene for Bd 30K, complete cds
10910	GM_164_A2_F04_MR	g1076498	BLASTX	186	6e-18	78	zinc-finger protein (C-terminal) - soybean gi 558543 (Z36749) C-terminal zinc-finger [Glycine max]
10911	GM_164_A2_F11_T7	g100484	BLASTX	383	6e-34	52	hypothetical protein - garden snapdragon
10912	GM_164_A2_G01_T7	g226407	BLASTX	332	8e-28	40	retrotransposon del1-46 [Lilium henryi]
10913	GM_164_A2_G10_T7	g3377848	BLASTX	156	1e-11	38	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
10914	GM_164_A2_H07_T7	g2443320	BLASTX	363	4e-31	50	(D85597) polyprotein [Oryza australiensis]
10915	GM_164_B1_A02_T7	g3650039	BLASTX	222	1e-16	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
10916	GM_164_B1_A04_T7	g2129618	BLASTX	211	4e-15	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10917	GM_164_B1_A05_T7	g2586082	BLASTX	137	5e-09	56	(U72725) retrofit [Oryza longistaminata]
10918	GM_164_B1_A10_MR	g4063770	BLASTX	172	4e-11	43	(AB004906) transposase [Ipomoea purpurea]
10919	GM_164_B1_B01_T7	g18559	BLASTN	434	1e-12	70	G.max gene for catalase
10920	GM_164_B1_B02_T7	g3201608	BLASTN	359	3e-09	62	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence.
10921	GM_164_B1_B06_MR	g4063760	BLASTX	217	1e-15	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10922	GM_164_B1_B06_T7	g3097320	BLASTN	963	1e-36	82	Glycine max gene for Bd 30K, complete cds
10923	GM_164_B1_B07_T7	g3193221	BLASTN	947	7e-36	70	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
10924	GM_164_B1_B09_MR	g3746070	BLASTX	145	2e-13	73	(AC005311) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10925	GM_164_B1_B10_T7	g4063760	BLASTX	234	1e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10926	GM_164_B1_C10_MR	g3023281	BLASTX	343	3e-30	59	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
10927	GM_164_B1_C10_T7	g2997694	BLASTX	283	4e-24	49	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
10928	GM_164_B1_C11_T7	g2464905	BLASTX	203	1e-15	67	(Z99708) minor allergen [Arabidopsis thaliana]
10929	GM_164_B1_D03_MR	g4140712	BLASTX	158	3e 29	45	(AF110183) putative integrase [Oryza sativa]
10930	GM_164_B1_D03_T7	g4038062	BLASTX	192	8e-16	44	(AC005897) putative transposon MuDR [Arabidopsis thaliana]
10931	GM_164_B1_D05_MR	g3845197	BLASTN	361	3e-09	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10932	GM_164_B1_D06_T7	g342964	BLASTN	523	1e-17	66	paramecium species 5.311 mt dna dimer: replication init. region.
10933	GM_164_B1_D08_MR	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10934	GM_164_B1_D10_MR	g3142328	BLASTN	856	8e-32	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10935	GM_164_B1_D12_MR	g3142328	BLASTN	847	2e-31	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10936	GM_164_B1_E02_MR	g13773	BLASTN	443	6e-14	65	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
10937	GM_164_B1_E02_T7	g3980359	BLASTN	358	4e-09	64	Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence [Homo sapiens]
10938	GM_164_B1_E04_T7	g1769899	BLASTX	190	3e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10939	GM_164_B1_E07_T7	g2764526	BLASTN	501	1e-15	67	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
10940	GM_164_B1_E08_T7	g1666236	BLASTX	103	2e-11	36	(U76261) unknown [Hordeum vulgare]
10941	GM_164_B1_E10_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10942	GM_164_B1_E10_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10943	GM_164_B1_F01_T7	g2224933	BLASTX	472	4e-44	68	(AF004216) ethylene-insensitive3 [Arabidopsis thaliana] gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]
10944	GM_164_B1_F02_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10945	GM_164_B1_F02_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10946	GM_164_B1_F03_T7	g2065531	BLASTX	172	1e-20	83	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
10947	GM_164_B1_F05_MR	g3845197	BLASTN	474	2e-14	66	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10948	GM_164_B1_F10_T7	g4063760	BLASTX	535	1e-49	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10949	GM_164_B1_G02_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10950	GM_164_B1_G02_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10951	GM_164_B1_G04_MR	g100484	BLASTX	374	6e-33	62	hypothetical protein - garden snapdragon
10952	GM_164_B1_G04_T7	g2462134	BLASTX	235	3e-18	41	(Y13368) reverse transcriptase [Beta vulgaris]
10953	GM_164_B1_G09_T7	g4063760	BLASTX	166	6e-12	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10954	GM_164_B1_H04_T7	g1769898	BLASTX	415	8e-38	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10955	GM_164_B1_H07_T7	g2462936	BLASTX	402	1e-36	52	(Y12321) open reading frame 2 [Brassica oleracea]
10956	GM_164_B1_H09_MR	g2262178	BLASTX	178	5e-12	55	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]
10957	GM_164_B1_H12_T7	g507910	BLASTN	531	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10958	GM_164_B2_A02_T7	g2462732	BLASTX	292	3e-24	47	(AC002292) Hypothetical Protein [Arabidopsis thaliana]
10959	GM_164_B2_A03_T7	g2244807	BLASTX	253	6e-25	52	(Z97336) hypothetical protein [Arabidopsis thaliana]
10960	GM_164_B2_A07_MR	g3869063	BLASTN	382	3e-10	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]
10961	GM_164_B2_A07_T7	g130582	BLASTX	221	2e-31	45	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10962	GM_164_B2_A08_T7	g3426334	BLASTN	535	3e-17	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10963	GM_164_B2_B03_T7	g3845197	BLASTN	470	3e-14	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10964	GM_164_B2_B06_T7	g2764526	BLASTN	635	1e-21	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
10965	GM_164_B2_B07_MR	g3522943	BLASTX	403	2e-35	71	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
10966	GM_164_B2_B07_T7	g4063760	BLASTX	128	4e-14	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10967	GM_164_B2_C06_T7	g4063760	BLASTX	707	4e-68	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10968	GM_164_B2_C07_MR	g170605	BLASTN	425	2e-12	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
10969	GM_164_B2_C08_T7	g18559	BLASTN	435	1e-12	63	G.max gene for catalase
10970	GM_164_B2_C09_MR	g3550435	BLASTN	524	1e-16	63	Hordeum vulgare Hotr1 gene
10971	GM_164_B2_C10_T7	g3096930	BLASTX	276	1e-22	65	(AL023094) Homeodomain - like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
10972	GM_164_B2_D01_T7	g3249105	BLASTX	218	3e-24	58	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
10973	GM_164_B2_D04_MR	g1769898	BLASTX	330	3e-37	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10974	GM_164_B2_D09_MR	g18559	BLASTN	361	3e-09	64	G max gene for catalase
10975	GM_164_B2_D10_MR	g507910	BLASTN	382	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10976	GM_164_B2_D10_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10977	GM_164_B2_E01_T7	g2213608	BLASTX	187	1e-12	32	(AC000103) F21J9.2 [Arabidopsis thaliana]
10978	GM_164_B2_E03_MR	g4063760	BLASTX	170	1e-10	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10979	GM_164_B2_E03_T7	g3928142	BLASTX	231	7e-29	95	(AJ131045) protein phosphatase [Cicer arietinum]
10980	GM_164_B2_E07_T7	g905361	BLASTX	149	8e-09	83	(U22103) gag-protease polyprotein [Glycine max]
10981	GM_164_B2_E09_T7	g2961349	BLASTX	394	4e-38	48	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
10982	GM_164_B2_E12_T7	g4160362	BLASTN	425	4e-14	58	Saccharomyces cerevisiae complete mitochondrial genome
10983	GM_164_B2_F03_MR	g629693	BLASTX	352	2e-31	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10984	GM_164_B2_F05_MR	g4063760	BLASTX	254	1e-19	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10985	GM_164_B2_F05_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10986	GM_164_B2_F06_T7	g507910	BLASTN	469	1e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10987	GM_164_B2_F07_T7	g905361	BLASTX	160	5e-10	31	(U22103) gag-protease polyprotein [Glycine max]
10988	GM_164_B2_F10_T7	g3128168	BLASTX	362	4e-37	75	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]
10989	GM_164_B2_G01_MR	g2522230	BLASTX	132	1e-13	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10990	GM_164_B2_G02_MR	g2462936	BLASTX	127	7e-13	42	(Y12321) open reading frame 2 [Brassica oleracea]
10991	GM_164_B2_G04_MR	g1778823	BLASTX	177	7e-13	87	(U82810) early light-induced protein [Glycine max]
10992	GM_164_B2_G05_MR	g4049647	BLASTN	366	2e-09	60	Melanoplus sanguinipes entomopoxvirus, complete genome
10993	GM_164_B2_G05_T7	g2961373	BLASTX	144	6e-14	43	(AL022141) putative disease resistance protein [Arabidopsis thaliana]
10994	GM_164_B2_G06_T7	g2352492	BLASTX	200	6e-24	50	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] gi 2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
10995	GM_164_B2_G08_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
10996	GM_164_B2_G09_T7	g3643604	BLASTX	180	8e-12	37	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
10997	GM_164_B2_G10_T7	g507910	BLASTN	603	1e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
10998	GM_164_B2_H01_T7	g4038056	BLASTX	336	1e-28	43	(AC005897) putative transposon [Arabidopsis thaliana]
10999	GM_164_B2_H04_T7	g2583130	BLASTX	184	4e-12	30	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11000	GM_164_B2_H07_T7	g2522228	BLASTX	667	8e-65	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
11001	GM_164_B2_H08_T7	g2443320	BLASTX	146	2e-23	43	(D85597) polyprotein [Oryza australiensis]
11002	GM_164_B2_H09_T7	g4063760	BLASTX	423	4e-69	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11003	GM_164_B2_H12_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11004	GM_165_A2_A02_MR	g3776577	BLASTX	144	2e-09	54	(AC005388) T22H22.24 [Arabidopsis thaliana]
11005	GM_165_A2_A07_MR	g2392895	BLASTX	232	3e-17	44	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]
11006	GM_165_A2_A10_MR	g18559	BLASTN	914	2e-34	77	G.max gene for catalase
11007	GM_165_A2_B03_MR	g3269282	BLASTX	167	3e-10	38	(AL030978) putative protein [Arabidopsis thaliana]
11008	GM_165_A2_B04_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11009	GM_165_A2_B04_T7	g507910	BLASTN	351	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11010	GM_165_A2_B09_MR	g507910	BLASTN	379	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11011	GM_165_A2_C02_MR	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
11012	GM_165_A2_C02_T7	g507910	BLASTN	549	3e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11013	GM_165_A2_C04_MR	g629693	BLASTX	172	1e-11	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11014	GM_165_A2_C05_T7	g3660471	BLASTX	194	1e-13	82	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
11015	GM_165_A2_C07_MR	g585416	BLASTX	122	3e-15	82	LIPOXYGENASE gi 467565 (X71344) lipoxygenase [Lens culinaris]
11016	GM_165_A2_C08_T7	g507910	BLASTN	504	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11017	GM_165_A2_D01_MR	g629693	BLASTX	296	2e-31	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11018	GM_165_A2_D05_MR	g2598589	BLASTX	115	4e-12	54	(Y15367) MtN19 [Medicago truncatula]
11019	GM_165_A2_D05_T7	g2598589	BLASTX	213	4e-16	45	(Y15367) MtN19 [Medicago truncatula]
11020	GM_165_A2_D07_T7	g2104945	BLASTN	792	7e-29	67	Glycine max copia-like retrotransposon Tgmr, complete sequence
11021	GM_165_A2_D10_MR	g3650039	BLASTX	293	3e-24	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11022	GM_165_A2_E02_MR	g3702736	BLASTN	446	4e-13	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]
11023	GM_165_A2_E03_T7	g3695394	BLASTN	349	1e-08	63	Arabidopsis thaliana BAC T5H22
11024	GM_165_A2_E05_T7	g507910	BLASTN	535	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11025	GM_165_A2_E07_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11026	GM_165_A2_E07_T7	g507910	BLASTN	343	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11027	GM_165_A2_E12_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11028	GM_165_A2_F01_MR	g170030	BLASTN	1405	1e-56	95	Soybean nodulin-35 (N-35) gene encoding a subunit of uricase II, complete cds.
11029	GM_165_A2_F08_MR	g99922	BLASTX	371	2e-33	79	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11030	GM_165_A2_F10_MR	g1705678	BLASTX	323	3e-27	76	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) gi 862480 (U20213) valosin-containing protein [Glycine max]
11031	GM_165_A2_G01_T7	g3142328	BLASTN	918	1e-34	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11032	GM_165_A2_G05_MR	g507910	BLASTN	389	6e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11033	GM_165_A2_G05_T7	g507910	BLASTN	358	1e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
11034	GM_165_A2_H01_MR	g2443320	BLASTX	382	3e-33	52	(D85597) polyprotein [Oryza australiensis]
11035	GM_165_A2_H02_MR	g4063760	BLASTX	376	4e-34	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11036	GM_165_A2_H08_MR	g905361	BLASTX	427	4e-39	95	(U22103) gag-protease polyprotein [Glycine max]
11037	GM_165_A2_H11_T7	g3142328	BLASTN	531	5e-17	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11038	GM_165_A2_H12_MR	g3645899	BLASTX	199	2e-29	46	(U68408) 5' end not determined experimentally [Zea mays]
11039	GM_165_B1_A12_MR	g3599418	BLASTN	573	6e-19	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11040	GM_165_B1_B07_T7	g3142328	BLASTN	907	4e-34	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11041	GM_165_B1_D08_MR	g4063760	BLASTX	253	1e-20	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11042	GM_165_B1_E02_T7	g18559	BLASTN	354	5e-09	74	G.max gene for catalase
11043	GM_165_B1_F02_T7	g507910	BLASTN	488	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11044	GM_165_B1_F04_T7	g3650039	BLASTX	177	9e-12	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11045	GM_165_B1_F05_T7	g3810595	BLASTX	159	1e-15	45	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
11046	GM_165_B1_F07_T7	g2995405	BLASTX	245	7e-19	63	(Y12432) polyprotein [Ananas comosus]
11047	GM_165_B1_G02_T7	g507910	BLASTN	591	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11048	GM_165_B1_H03_T7	g2583130	BLASTX	211	6e-15	37	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
11049	GM_165_B1_H08_T7	g18559	BLASTN	366	1e-09	71	G.max gene for catalase
11050	GM_165_B1_H10_T7	g100484	BLASTX	159	9e-10	43	hypothetical protein - garden snapdragon
11051	GM_165_B1_H12_T7	g3097320	BLASTN	969	7e-37	79	Glycine max gene for Bd 30K, complete cds
11052	GM_165_B2_A02_T7	g3650039	BLASTX	172	3e-11	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11053	GM_165_B2_A03_MR	g2995405	BLASTX	182	2e-15	47	(Y12432) polyprotein [Ananas comosus]
11054	GM_165_B2_A05_T7	g3319351	BLASTX	280	8e-33	45	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
11055	GM_165_B2_A10_T7	g18559	BLASTN	700	1e-24	83	G.max gene for catalase
11056	GM_165_B2_B01_MR	g1621467	BLASTX	369	3e-34	66	(U73106) laccase [Liriodendron tulipifera]
11057	GM_165_B2_B05_MR	g3142328	BLASTN	745	9e-38	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11058	GM_165_B2_B05_T7	g2129618	BLASTX	189	7e-13	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11059	GM_165_B2_B06_MR	g18559	BLASTN	757	3e-27	75	G.max gene for catalase
11060	GM_165_B2_B07_MR	g1769897	BLASTX	195	7e-14	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11061	GM_165_B2_B10_MR	g1666236	BLASTX	145	7e-09	28	(U76261) unknown [Hordeum vulgare]
11062	GM_165_B2_B10_T7	g507910	BLASTN	549	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11063	GM_165_B2_C04_MR	g4063760	BLASTX	371	4e-32	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11064	GM_165_B2_D02_MR	g3142328	BLASTN	872	2e-32	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11065	GM_165_B2_D03_MR	g3820976	BLASTN	436	1e-12	65	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
11066	GM_165_B2_D07_MR	g507910	BLASTN	523	5e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11067	GM_165_B2_D07_T7	g507910	BLASTN	597	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11068	GM_165_B2_D09_MR	g3193221	BLASTN	755	4e-27	81	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
11069	GM_165_B2_E01_MR	g1480927	BLASTN	537	2e-17	81	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
11070	GM_165_B2_E01_T7	g3097320	BLASTN	816	6e-30	75	Glycine max gene for Bd 30K, complete cds
11071	GM_165_B2_E05_T7	g3702341	BLASTX	343	6e-30	46	(AC005397) hypothetical protein [Arabidopsis thaliana]
11072	GM_165_B2_E06_MR	g507910	BLASTN	373	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11073	GM_165_B2_E08_MR	g2827711	BLASTX	304	4e-25	77	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]
11074	GM_165_B2_E08_T7	g3355474	BLASTX	396	4e-36	84	(AC004218) unknown protein [Arabidopsis thaliana]
11075	GM_165_B2_E11_T7	g4151321	BLASTX	218	1e-16	72	(AF089085) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11076	GM_165_B2_F01_T7	g2760832	BLASTX	185	1e-13	52	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
11077	GM_165_B2_F02_T7	g3695387	BLASTX	301	9e-25	65	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
11078	GM_165_B2_F07_T7	g3142379	BLASTX	220	8e-17	54	(AF053008) envelope-like [Glycine max]
11079	GM_165_B2_F08_T7	g421948	BLASTX	320	5e-28	55	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - garden petunia
11080	GM_165_B2_F09_MR	g2618704	BLASTX	163	1e-11	80	(AC002510) putative thioredoxin reductase [Arabidopsis thaliana]
11081	GM_165_B2_F09_T7	g2995405	BLASTX	249	3e-19	51	(Y12432) polyprotein [Ananas comosus]
11082	GM_165_B2_G01_T7	g18559	BLASTN	862	5e-32	75	G.max gene for catalase
11083	GM_165_B2_G02_MR	g4063760	BLASTX	254	1e-19	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11084	GM_165_B2_G04_MR	g3142328	BLASTN	698	1e-24	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11085	GM_165_B2_G04_T7	g3645899	BLASTX	160	9e-10	47	(U68408) 5' end not determined experimentally [Zea mays]
11086	GM_165_B2_G07_T7	g2522228	BLASTX	226	1e-17	41	(AB007466) reverse transcriptase-like protein [Vicia faba]
11087	GM_165_B2_G11_T7	g218179	BLASTX	171	6e-11	67	(D10207) H-ATPase [Oryza sativa] gi 444339 prf 1906387A H ATPase [Oryza sativa]
11088	GM_165_B2_H02_MR	g3142328	BLASTN	843	3e-31	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11089	GM_165_B2_H05_T7	g3142328	BLASTN	795	5e-29	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11090	GM_166_A2_E03_MR	g3097320	BLASTN	500	1e-15	77	Glycine max gene for Bd 30K, complete cds
11091	GM_166_A2_E05_MR	g1658457	BLASTX	272	6e-23	74	(U75248) reverse transcriptase [Gossypium barbadense]
11092	GM_166_A2_E06_T7	g629693	BLASTX	212	4e-16	49	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11093	GM_166_A2_F04_T7	g3142328	BLASTN	429	2e-12	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11094	GM_166_A2_F06_MR	g3935157	BLASTX	172	4e-11	66	(AC005106) T25N20.21 [Arabidopsis thaliana]
11095	GM_166_A2_G02_T7	g3176795	BLASTN	470	4e-15	65	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
11096	GM_166_B1_A08_MR	g905361	BLASTX	127	2e-12	33	(U22103) gag-protease polyprotein [Glycine max]
11097	GM_166_B1_A12_T7	g3777527	BLASTX	166	4e-10	36	(AF053008) gag-pol polyprotein [Glycine max]
11098	GM_166_B1_B04_MR	g1946355	BLASTX	288	1e-23	50	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11099	GM_166_B1_C06_T7	g3241935	BLASTN	395	8e-11	65	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
11100	GM_166_B1_C09_T7	g421955	BLASTX	185	4e-13	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
11101	GM_166_B1_C11_MR	g58340	BLASTN	443	4e-13	64	D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val
11102	GM_166_B1_D01_T7	g18559	BLASTN	678	1e-23	76	G.max gene for catalase
11103	GM_166_B1_D02_T7	g3142328	BLASTN	1073	1e-41	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11104	GM_166_B1_D03_MR	g1666236	BLASTX	224	7e-18	32	(U76261) unknown [Hordeum vulgare]
11105	GM_166_B1_D05_T7	g498931	BLASTX	141	5e-09	46	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
11106	GM_166_B1_D06_MR	g3142379	BLASTX	237	1e-18	67	(AF053008) envelope-like [Glycine max]
11107	GM_166_B1_E02_MR	g4063760	BLASTX	288	3e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11108	GM_166_B1_E04_MR	g3142328	BLASTN	784	2e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11109	GM_166_B1_E04_T7	g3142328	BLASTN	528	6e-17	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11110	GM_166_B1_E05_MR	g1673583	BLASTX	317	7e-27	71	(U76687) lipoxygenase [Phaseolus vulgaris]
11111	GM_166_B1_E07_MR	g4115365	BLASTX	197	2e-13	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
11112	GM_166_B1_E12_MR	g4063760	BLASTX	195	2e-13	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11113	GM_166_B1_F01_MR	g3142328	BLASTN	1275	7e-51	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11114	GM_166_B1_G01_T7	g99922	BLASTX	375	8e-34	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11115	GM_166_B1_G03_T7	g1091678	BLASTX	179	7e-12	44	activator-like transposable element [Pennisetum glaucum]
11116	GM_166_B1_G05_T7	g3142328	BLASTN	438	8e-13	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11117	GM_166_B1_G06_T7	g3097320	BLASTN	399	5e-11	80	Glycine max gene for Bd 30K, complete cds
11118	GM_166_B1_H01_T7	g3142328	BLASTN	1010	8e-39	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11119	GM_166_B1_H04_T7	g4050011	BLASTN	362	2e-09	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
11120	GM_166_B1_H06_T7	g4063760	BLASTX	297	3e-24	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11121	GM_167_A2_A01_MR	g1352078	BLASTX	168	3e-25	87	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (EXO-(1-->4)-BETA-D-GALACTANASE) gi 507278 (L29451) b-galactosidase-related protein; putative [Malus domestica]
11122	GM_167_A2_A02_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11123	GM_167_A2_A02_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11124	GM_167_A2_A03_T7	g2443320	BLASTX	122	5e-10	58	(D85597) polyprotein [Oryza australiensis]
11125	GM_167_A2_A04_T7	g18559	BLASTN	664	5e-23	71	G.max gene for catalase
11126	GM_167_A2_A08_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11127	GM_167_A2_A08_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11128	GM_167_A2_A10_MR	g3777527	BLASTX	312	1e-25	51	(AF053008) gag-pol polyprotein [Glycine max]
11129	GM_167_A2_B05_MR	g3873182	BLASTN	368	1e-09	61	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
11130	GM_167_A2_C03_T7	g1666236	BLASTX	183	5e-13	36	(U76261) unknown [Hordeum vulgare]
11131	GM_167_A2_C07_MR	g3763934	BLASTX	191	2e-13	73	(AC004450) hypothetical protein [Arabidopsis thaliana]
11132	GM_167_A2_C11_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11133	GM_167_A2_D03_MR	g3445210	BLASTX	100	2e-10	28	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
11134	GM_167_A2_D07_T7	g3142328	BLASTN	791	7e-29	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11135	GM_167_A2_D09_T7	g3142328	BLASTN	892	2e-33	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11136	GM_167_A2_D12_T7	g531389	BLASTX	228	3e-18	52	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
11137	GM_167_A2_E01_MR	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11138	GM_167_A2_E01_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11139	GM_167_A2_E05_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11140	GM_167_A2_E10_MR	g3930515	BLASTX	109	4e-09	43	(AF059674) putative gag protein [Nicotiana tabacum]
11141	GM_167_A2_F04_T7	g2522230	BLASTX	220	2e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11142	GM_167_A2_F10_MR	g4050011	BLASTN	384	2e-10	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
11143	GM_167_A2_F11_MR	g3033389	BLASTX	182	4e-12	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
11144	GM_167_A2_F11_T7	g3033389	BLASTX	169	9e-11	42	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
11145	GM_167_A2_G03_MR	g629722	BLASTX	167	7e-11	33	finger protein pcp1 - potato gi 563623 (X82328) putative DNA/RNA binding protein [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11146	GM_167_A2_G07_T7	g4038056	BLASTX	328	9e-28	56	(AC005897) putative transposon [Arabidopsis thaliana]
11147	GM_167_A2_G08_T7	g3869075	BLASTN	376	2e-12	75	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
11148	GM_167_A2_G12_MR	g3510538	BLASTX	415	4e-38	93	(U93167) expansin [Prunus armeniaca]
11149	GM_167_A2_H04_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11150	GM_167_A2_H04_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11151	GM_167_A2_H06_T7	g3097320	BLASTN	567	1e-18	79	Glycine max gene for Bd 30K, complete cds
11152	GM_167_A2_H11_T7	g18559	BLASTN	473	2e-14	78	G.max gene for catalase
11153	GM_167_B1_A11_T7	g2443320	BLASTX	158	2e-14	43	(D85597) polyprotein [Oryza australiensis]
11154	GM_167_B1_B01_MR	g3142328	BLASTN	668	6e-43	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11155	GM_167_B1_B01_T7	g2443320	BLASTX	340	1e-28	51	(D85597) polyprotein [Oryza australiensis]
11156	GM_167_B1_B08_MR	g1514643	BLASTX	205	3e-14	53	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11157	GM_167_B1_C03_T7	g3142328	BLASTN	960	2e-36	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11158	GM_167_B1_C04_MR	g3298551	BLASTX	169	6e-11	52	(AC004681) putative salt-inducible protein [Arabidopsis thaliana]
11159	GM_167_B1_C05_T7	g3142330	BLASTX	644	2e-62	98	(U96295) envelope-like [Glycine max]
11160	GM_167_B1_C06_T7	g4038056	BLASTX	321	5e-27	53	(AC005897) putative transposon [Arabidopsis thaliana]
11161	GM_167_B1_C09_MR	g2995405	BLASTX	339	6e-29	61	(Y12432) polyprotein [Ananas comosus]
11162	GM_167_B1_C09_T7	g1142700	BLASTN	357	8e-14	73	Glycine max satellite STR120-A.2.
11163	GM_167_B1_C12_T7	g3334667	BLASTX	158	6e-10	85	(Y10493) putative cytochrome P450 [Glycine max]
11164	GM_167_B1_D01_T7	g3097320	BLASTN	558	3e-18	78	Glycine max gene for Bd 30K, complete cds
11165	GM_167_B1_D04_MR	g1171591	BLASTN	359	3e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
11166	GM_167_B1_D06_T7	g3243214	BLASTN	465	6e-14	69	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
11167	GM_167_B1_E01_T7	g3777527	BLASTX	291	2e-23	46	(AF053008) gag-pol polyprotein [Glycine max]
11168	GM_167_B1_E02_T7	g1769898	BLASTX	370	9e-33	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11169	GM_167_B1_E04_MR	g507910	BLASTN	411	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11170	GM_167_B1_F01_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11171	GM_167_B1_F01_T7	g4063760	BLASTX	337	4e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11172	GM_167_B1_F03_MR	g130582	BLASTX	259	2e-25	57	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11173	GM_167_B1_F04_MR	g1167523	BLASTX	387	9e-34	62	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11174	GM_167_B1_F04_T7	g2462134	BLASTX	353	2e-31	50	(Y13368) reverse transcriptase [Beta vulgaris]
11175	GM_167_B1_F05_T7	g3810596	BLASTX	145	3e-14	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11176	GM_167_B1_F06_T7	g2522228	BLASTX	250	3e-20	42	(AB007466) reverse transcriptase-like protein [Vicia faba]
11177	GM_167_B1_G01_MR	g1167523	BLASTX	299	2e-24	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11178	GM_167_B1_G05_MR	g507910	BLASTN	526	4e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11179	GM_167_B1_G05_T7	g507910	BLASTN	566	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11180	GM_167_B1_G08_T7	g541936	BLASTX	198	4e-15	67	4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL14) - soybean (fragment)
11181	GM_167_B1_G12_T7	g336279	BLASTN	357	4e-09	62	Apis mellifera ligustica complete mitochondrial genome
11182	GM_167_B1_H06_T7	g3142328	BLASTN	1583	6e-65	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11183	GM_167_B1_H08_T7	g2244876	BLASTX	159	3e-19	71	(Z97338) hypothetical protein [Arabidopsis thaliana]
11184	GM_167_B1_H09_MR	g2522230	BLASTX	157	1e-10	36	(AB007467) retrotransposon-like gene, the first amino acid was determined to be leucine [Vicia faba]
11185	GM_168_A1_A09_MR	g507910	BLASTN	458	4e-14	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11186	GM_168_A1_D02_MR	g13767	BLASTN	483	1e-15	68	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
11187	GM_168_A1_H10_MR	g3152629	BLASTN	429	2e-12	66	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
11188	GM_168_A2_A01_T7	g1431738	BLASTN	392	8e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
11189	GM_168_A2_A03_T7	g1709918	BLASTX	420	1e-38	91	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) gi 438899 (L23833) glutamine phosphoribosylpyrophosphate amidotransferase [Glycine max]
11190	GM_168_A2_A05_MR	g1769898	BLASTX	444	3e-41	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11191	GM_168_A2_A08_MR	g1171583	BLASTN	349	1e-08	60	P.falciparum complete gene map of plastid-like DNA (IR-A)
11192	GM_168_A2_B01_MR	g1805254	BLASTX	195	4e-30	73	(U62622) monogalactosyldiacylglycerol synthase [Cucumis sativus]
11193	GM_168_A2_B04_MR	g3777527	BLASTX	200	9e-14	31	(AF053008) gag-pol polyprotein [Glycine max]
11194	GM_168_A2_B06_MR	g3319351	BLASTX	245	1e-18	44	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11195	GM_168_A2_B07_MR	g3097320	BLASTN	586	2e-19	75	Glycine max gene for Bd 30K, complete cds
11196	GM_168_A2_B09_MR	g905361	BLASTX	667	9e-65	96	(U22103) gag-protease polyprotein [Glycine max]
11197	GM_168_A2_B09_T7	g4038056	BLASTX	131	4e-15	44	(AC005897) putative transposon [Arabidopsis thaliana]
11198	GM_168_A2_C08_T7	g4063760	BLASTX	201	2e-21	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11199	GM_168_A2_C10_T7	g905361	BLASTX	420	2e-38	92	(U22103) gag-protease polyprotein [Glycine max]
11200	GM_168_A2_D01_MR	g2522230	BLASTX	263	6e-22	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11201	GM_168_A2_D02_T7	g1514643	BLASTX	173	6e-11	56	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11202	GM_168_A2_D03_T7	g2760832	BLASTX	262	7e-22	62	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
11203	GM_168_A2_D04_MR	g2145358	BLASTX	121	5e-12	56	(Y10922) HD-Zip protein [Arabidopsis thaliana]
11204	GM_168_A2_D07_MR	g178823	BLASTN	333	7e-09	61	Human apolipoprotein B gene hypervariable region, 3' flank.
11205	GM_168_A2_D10_MR	g2995405	BLASTX	434	3e-39	61	(Y12432) polyprotein [Ananas comosus]
11206	GM_168_A2_D12_MR	g3777527	BLASTX	639	2e-60	96	(AF053008) gag-pol polyprotein [Glycine max]
11207	GM_168_A2_E06_T7	g3023281	BLASTX	194	8e-14	50	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
11208	GM_168_A2_E09_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11209	GM_168_A2_E09_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11210	GM_168_A2_E12_MR	g99922	BLASTX	360	4e-58	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11211	GM_168_A2_F05_T7	g2702264	BLASTX	143	3e-09	41	(AC003033) similar to disease resistance protein (Cf-2.2) [Arabidopsis thaliana]
11212	GM_168_A2_F07_T7	g1167523	BLASTX	348	1e-29	69	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11213	GM_168_A2_F10_T7	g3777527	BLASTX	477	3e-43	94	(AF053008) gag-pol polyprotein [Glycine max]
11214	GM_168_A2_G01_MR	g2959767	BLASTX	150	4e-18	54	(AJ002584) AtMRP4 [Arabidopsis thaliana]
11215	GM_168_A2_G07_T7	g170080	BLASTN	737	2e-26	91	Soybean seed lectin gene transposable element tgm1.
11216	GM_168_A2_G08_MR	g2853072	BLASTX	311	4e-27	54	(AL021768) putative protein [Arabidopsis thaliana]
11217	GM_168_A2_G12_MR	g3860167	BLASTX	156	3e-09	40	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]
11218	GM_168_A2_H03_MR	g905361	BLASTX	185	1e-12	62	(U22103) gag-protease polyprotein [Glycine max]
11219	GM_168_A2_H04_T7	g2264309	BLASTN	582	3e-19	75	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
11220	GM_168_A2_H05_T7	g3063690	BLASTN	444	5e-13	77	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11221	GM_168_A2_H06_MR	g4159702	BLASTN	581	3e-19	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence [Arabidopsis thaliana]
11222	GM_168_A2_H12_MR	g2495155	BLASTX	92	2e-13	61	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) gi 1694926 gnl PID d1009544 (D50407) glutamyl-tRNA reductase [Cucumis sativus]
11223	GM_168_B1_A01_T7	g862479	BLASTN	434	1e-12	81	Glycine max valosin-containing protein mRNA, complete cds.
11224	GM_168_B1_A04_T7	g100484	BLASTX	121	5e-13	48	hypothetical protein - garden snapdragon
11225	GM_168_B1_A07_MR	g2894502	BLASTN	352	6e-09	65	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-102, complete sequence [Plasmodium falciparum]
11226	GM_168_B1_A09_MR	g18559	BLASTN	487	5e-15	73	G.max gene for catalase
11227	GM_168_B1_B01_T7	g4063770	BLASTX	185	2e-12	37	(AB004906) transposase [Ipomoea purpurea]
11228	GM_168_B1_B04_MR	g1171591	BLASTN	358	4e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
11229	GM_168_B1_B06_T7	g3777527	BLASTX	548	8e-51	96	(AF053008) gag-pol polyprotein [Glycine max]
11230	GM_168_B1_B07_T7	g2982444	BLASTX	184	2e-13	43	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]
11231	GM_168_B1_B08_T7	g3452136	BLASTN	339	4e-09	79	Glycine max mRNA for glucose-6-phosphate-dehydrogenase, partial
11232	GM_168_B1_B09_MR	g3738114	BLASTN	364	2e-09	62	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
11233	GM_168_B1_B09_T7	g282881	BLASTX	224	1e-16	49	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
11234	GM_168_B1_B10_MR	g1514643	BLASTX	128	5e-14	56	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11235	GM_168_B1_C03_T7	g1769898	BLASTX	225	5e-17	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11236	GM_168_B1_C09_MR	g2995405	BLASTX	394	7e-35	62	(Y12432) polyprotein [Ananas comosus]
11237	GM_168_B1_D03_T7	g3688600	BLASTX	266	1e-27	70	(AB009030) beta-Amyrin Synthase [Panax ginseng]
11238	GM_168_B1_D04_MR	g3142328	BLASTN	766	1e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11239	GM_168_B1_D11_MR	g2145358	BLASTX	196	1e-13	77	(Y10922) HD-Zip protein [Arabidopsis thaliana]
11240	GM_168_B1_E01_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11241	GM_168_B1_E02_T7	g3176686	BLASTX	320	5e-27	69	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
11242	GM_168_B1_E03_T7	g3283026	BLASTX	150	3e-11	62	putative transposase [Arabidopsis thaliana]
11243	GM_168_B1_E05_T7	g1236920	BLASTN	356	4e-09	65	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11244	GM_168_B1_E06_MR	g3097320	BLASTN	361	3e-09	78	Glycine max gene for Bd 30K, complete cds
11245	GM_168_B1_E11_MR	g3142328	BLASTN	554	4e-18	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11246	GM_168_B1_F02_MR	g1085621	BLASTX	179	2e-12	89	alcohol dehydrogenase (EC 1.1.1.1) 1CN - Phaseolus acutifolius gi 452767 (Z23171) alcohol dehydrogenase-1CN [Phaseolus acutifolius]
11247	GM_168_B1_F07_MR	g4063760	BLASTX	253	1e-19	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11248	GM_168_B1_F10_MR	g3810596	BLASTX	213	2e-15	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11249	GM_168_B1_G08_T7	g576754	BLASTN	347	5e-09	64	Myrmecia pilosula HI87-128 mitochondrion cytochrome b gene, partial cds.
11250	GM_168_B1_H02_MR	g507910	BLASTN	518	8e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11251	GM_168_B1_H06_MR	g2586083	BLASTX	254	1e-19	46	(U72725) receptor kinase-like protein [Oryza longistaminata]
11252	GM_168_B1_H06_T7	g3250688	BLASTX	210	2e-16	47	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
11253	GM_168_B1_H07_MR	g2522228	BLASTX	165	7e-11	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
11254	GM_168_B1_H09_MR	g18559	BLASTN	598	4e-20	74	G.max gene for catalase
11255	GM_168_B1_H09_T7	g3789709	BLASTN	402	4e-11	66	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
11256	GM_168_B1_H10_T7	g3142328	BLASTN	527	7e-17	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11257	GM_168_B2_B01_MR	g3549652	BLASTX	109	8e-09	83	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
11258	GM_168_B2_B02_MR	g505129	BLASTN	371	8e-10	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11259	GM_168_B2_B04_T7	g4063760	BLASTX	335	3e-28	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11260	GM_168_B2_B07_MR	g3777527	BLASTX	694	2e-66	94	(AF053008) gag-pol polyprotein [Glycine max]
11261	GM_168_B2_C07_MR	g2443320	BLASTX	342	6e-29	49	(D85597) polyprotein [Oryza australiensis]
11262	GM_168_B2_D03_MR	g2497486	BLASTX	114	8e-16	65	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]
11263	GM_168_B2_D04_T7	g3777527	BLASTX	619	2e-58	94	(AF053008) gag-pol polyprotein [Glycine max]
11264	GM_168_B2_D07_MR	g3142328	BLASTN	658	8e-23	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11265	GM_168_B2_D08_MR	g4006828	BLASTX	119	1e-12	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
11266	GM_168_B2_E04_MR	g3097320	BLASTN	363	2e-09	73	Glycine max gene for Bd 30K, complete cds
11267	GM_168_B2_G04_MR	g2995405	BLASTX	317	3e-31	62	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11268	GM_168_B2_G09_MR	g3283026	BLASTX	174	2e-11	30	putative transposase [Arabidopsis thaliana]
11269	GM_168_B2_G09_T7	g2522228	BLASTX	198	2e-14	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
11270	GM_168_B2_G10_MR	g2624372	BLASTN	365	2e-09	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence [Plasmodium falciparum]
11271	GM_168_B2_H05_MR	g2429543	BLASTX	237	8e-18	44	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
11272	GM_168_B2_H06_MR	g99922	BLASTX	365	8e-33	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11273	GM_168_B2_H10_T7	g2828183	BLASTN	404	3e-11	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]
11274	GM_168_B2_H11_MR	g100484	BLASTX	173	3e-11	45	hypothetical protein - garden snapdragon
11275	GM_169_A1_A04_MR	g2522230	BLASTX	265	3e-22	43	(AB007467) retrotransposon-like gene, the first amino acid was determined to be leucine [Vicia faba]
11276	GM_169_A1_A05_MR	g1167523	BLASTX	429	3e-38	68	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11277	GM_169_A1_A06_MR	g3097320	BLASTN	511	4e-16	73	Glycine max gene for Bd 30K, complete cds
11278	GM_169_A1_A07_MR	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
11279	GM_169_A1_B05_MR	g905361	BLASTX	178	7e-12	40	(U22103) gag-protease polyprotein [Glycine max]
11280	GM_169_A1_B06_MR	g4063756	BLASTN	447	4e-13	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11281	GM_169_A1_C07_MR	g1666236	BLASTX	174	4e-12	30	(U76261) unknown [Hordeum vulgare]
11282	GM_169_A1_C12_MR	g2398681	BLASTX	366	6e-33	93	(Y14798) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]
11283	GM_169_A1_D05_MR	g2129832	BLASTX	323	2e-28	78	heat shock transcription factor 5 - soybean gi 671868 (Z46956) heat shock transcription factor 5 [Glycine max]
11284	GM_169_A1_D06_MR	g1771160	BLASTX	389	2e-34	65	(X98929) SBT1 [Lycopersicon esculentum] gi 3687305 gnl PID e1299610 (AJ006378) subtilisin-like protease [Lycopersicon esculentum]
11285	GM_169_A1_D07_MR	g3777527	BLASTX	508	2e-46	92	(AF053008) gag-pol polyprotein [Glycine max]
11286	GM_169_A1_D08_MR	g1142701	BLASTN	1188	2e-47	85	Glycine max satellite STR120-A.3.
11287	GM_169_A1_D10_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11288	GM_169_A1_E06_MR	g18559	BLASTN	492	3e-15	71	G.max gene for catalase
11289	GM_169_A1_E07_MR	g4063760	BLASTX	407	6e-36	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11290	GM_169_A1_E08_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11291	GM_169_A1_E11_MR	g4063760	BLASTX	178	8e-16	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11292	GM_169_A1_F04_MR	g4063756	BLASTN	429	2e-12	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11293	GM_169_A1_G01_MR	g2760839	BLASTX	212	1e-15	42	(AC003105) putative receptor kinase [Arabidopsis thaliana]
11294	GM_169_A1_G09_MR	g3319366	BLASTX	185	1e-13	42	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
11295	GM_169_A1_H02_MR	g421955	BLASTX	321	4e-28	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
11296	GM_169_A1_H03_MR	g3097320	BLASTN	667	4e-23	81	Glycine max gene for Bd 30K, complete cds
11297	GM_169_A2_A04_T7	g1167523	BLASTX	181	8e-12	38	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11298	GM_169_A2_A06_T7	g2522230	BLASTX	160	4e-11	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11299	GM_169_A2_A07_MR	g4063760	BLASTX	154	6e-09	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11300	GM_169_A2_A08_T7	g3097320	BLASTN	990	8e-38	78	Glycine max gene for Bd 30K, complete cds
11301	GM_169_A2_B02_MR	g3319345	BLASTX	140	5e-11	42	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
11302	GM_169_A2_B03_MR	g3097320	BLASTN	1424	2e-57	81	Glycine max gene for Bd 30K, complete cds
11303	GM_169_A2_B04_MR	g905361	BLASTX	297	2e-29	70	(U22103) gag-protease polyprotein [Glycine max]
11304	GM_169_A2_B07_T7	g3097320	BLASTN	405	3e-11	68	Glycine max gene for Bd 30K, complete cds
11305	GM_169_A2_C04_MR	g3869176	BLASTX	215	6e-17	81	(AB019518) cyclophilin [Trichophyton mentagrophytes]
11306	GM_169_A2_C07_MR	g1769898	BLASTX	420	2e-38	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11307	GM_169_A2_C07_T7	g3097320	BLASTN	988	1e-37	77	Glycine max gene for Bd 30K, complete cds
11308	GM_169_A2_D02_MR	g1167523	BLASTX	153	7e-15	32	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11309	GM_169_A2_D09_MR	g3097320	BLASTN	368	1e-09	75	Glycine max gene for Bd 30K, complete cds
11310	GM_169_A2_D09_T7	g99922	BLASTX	374	1e-33	57	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11311	GM_169_A2_E01_MR	g130582	BLASTX	231	9e-23	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
11312	GM_169_A2_E04_MR	g18767	BLASTN	382	9e-17	70	Soybean Tgm6 transposable element 5' end
11313	GM_169_A2_E06_MR	g905361	BLASTX	199	4e-14	36	(U22103) gag-protease polyprotein [Glycine max]
11314	GM_169_A2_F01_MR	g530207	BLASTX	198	3e-26	68	(L35272) heat shock protein [Glycine max]
11315	GM_169_A2_F04_T7	g3980405	BLASTX	220	2e-17	75	(AC004561) putative tropinone reductase [Arabidopsis thaliana]
11316	GM_169_A2_F05_MR	g1813979	BLASTX	184	1e-13	49	(Y10860) hypothetical protein [Musa acuminata]
11317	GM_169_A2_F06_MR	g3746069	BLASTX	256	8e-20	41	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11318	GM_169_A2_F07_T7	g343789	BLASTN	359	3e-09	62	Yeast (S.cerevisiae) mitochondrial cytochrome oxi1 gene and flanks.
11319	GM_169_A2_F11_MR	g3367528	BLASTX	147	7e-09	30	(AC004392) Strong similarity to gi 2160138 F19K23.6 gene product from A. thaliana BAC gb AC000375. [Arabidopsis thaliana]
11320	GM_169_A2_G01_MR	g2462936	BLASTX	533	1e-50	55	(Y12321) open reading frame 2 [Brassica oleracea]
11321	GM_169_A2_G02_MR	g4063770	BLASTX	160	8e-20	37	(AB004906) transposase [Ipomoea purpurea]
11322	GM_169_A2_G03_MR	g505129	BLASTN	349	8e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11323	GM_169_A2_G05_MR	g992916	BLASTN	1210	1e-47	71	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
11324	GM_169_A2_G10_MR	g4063760	BLASTX	388	6e-34	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11325	GM_169_A2_G12_MR	g18559	BLASTN	879	8e-33	71	G.max gene for catalase
11326	GM_169_A2_H02_T7	g1167523	BLASTX	486	3e-44	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11327	GM_169_A2_H04_MR	g2160155	BLASTN	373	3e-21	69	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
11328	GM_169_A2_H05_MR	g1730796	BLASTX	210	5e-15	40	HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION gi 2132760 pir S60964 probable membrane protein YNL163c - yeast (Saccharomyces cerevisiae) gi 1050790 (X92517) N1718 gene product [Saccharomyces cerevisiae] gi 1302132 gnl PID e239817 (Z71439) ORF YNL163c [Saccharomyces cerevisiae]
11329	GM_169_A2_H06_T7	g130405	BLASTX	241	3e-18	35	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
11330	GM_169_A2_H09_MR	g507910	BLASTN	367	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11331	GM_169_B1_A02_MR	g100484	BLASTX	372	1e-32	53	hypothetical protein - garden snapdragon
11332	GM_169_B1_A02_T7	g576754	BLASTN	351	3e-09	63	Myrmecia pilosula HI87-128 mitochondrion cytochrome b gene, partial cds.
11333	GM_169_B1_A07_MR	g18559	BLASTN	351	7e-09	73	G.max gene for catalase
11334	GM_169_B1_A10_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11335	GM_169_B1_A10_T7	g507910	BLASTN	402	1e-11	84	Glycine max BSR-101 satellite SB92 genomic sequence.
11336	GM_169_B1_B07_T7	g1769899	BLASTX	286	2e-24	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11337	GM_169_B1_C08_MR	g3785980	BLASTX	283	3e-23	42	(AC005560) hypothetical protein [Arabidopsis thaliana]
11338	GM_169_B1_C09_MR	g2982169	BLASTN	358	4e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence [Homo sapiens]
11339	GM_169_B1_C09_T7	g340796	BLASTN	405	3e-12	64	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
11340	GM_169_B1_C12_MR	g2335097	BLASTX	269	2e-21	83	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
11341	GM_169_B1_D03_MR	g2522230	BLASTX	345	1e-30	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11342	GM_169_B1_D04_MR	g3334667	BLASTX	324	4e-28	43	(Y10493) putative cytochrome P450 [Glycine max]
11343	GM_169_B1_D04_T7	g3334667	BLASTX	177	4e-14	75	(Y10493) putative cytochrome P450 [Glycine max]
11344	GM_169_B1_D09_T7	g507910	BLASTN	346	5e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11345	GM_169_B1_D11_T7	g18559	BLASTN	452	2e-13	80	G.max gene for catalase
11346	GM_169_B1_E03_MR	g4063760	BLASTX	324	4e-27	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11347	GM_169_B1_E04_MR	g452593	BLASTX	162	1e-14	57	(D21814) ORF [Lilium longiflorum]
11348	GM_169_B1_E07_MR	g2492675	BLASTX	156	8e-10	76	ACTIN-LIKE PROTEIN 3 >gi 1718497 (U79737) actin-related protein 3 [Neurospora crassa]
11349	GM_169_B1_F01_MR	g3184285	BLASTX	208	3e-16	52	(AC004136) hypothetical protein [Arabidopsis thaliana]
11350	GM_169_B1_F03_MR	g1769898	BLASTX	428	1e-41	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11351	GM_169_B1_F04_MR	g3250687	BLASTX	264	1e-24	40	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
11352	GM_169_B1_F04_T7	g1769896	BLASTN	387	2e-10	66	A.thaliana lectin receptor kinase gene
11353	GM_169_B1_F08_MR	g507910	BLASTN	406	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11354	GM_169_B1_G09_MR	g992916	BLASTN	414	1e-11	63	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
11355	GM_169_B1_G10_MR	g1906369	BLASTX	400	7e-36	61	(Y11998) hypothetical protein [Pseudomonas fluorescens]
11356	GM_169_B1_G10_T7	g1906369	BLASTX	300	2e-38	50	(Y11998) hypothetical protein [Pseudomonas fluorescens]
11357	GM_169_B1_H02_MR	g3024387	BLASTX	297	1e-25	66	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) gi 668998 (U20431) polygalacturonase [Medicago sativa]
11358	GM_169_B1_H04_T7	g2244803	BLASTX	280	9e-24	44	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11359	GM_169_B1_H05_MR	g2501460	BLASTX	154	5e-19	66	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
11360	GM_169_B1_H08_MR	g2194117	BLASTX	439	3e-40	60	(AC002062) Strong similarity to Arabidopsis receptor protein kinase PR5K (gb ATU48698). [Arabidopsis thaliana]
11361	GM_169_B1_H12_T7	g18768	BLASTN	386	4e-11	76	Soybean Tgm6 transposable element 3' end
11362	GM_169_B2_A03_T7	g2462936	BLASTX	164	2e-11	44	(Y12321) open reading frame 2 [Brassica oleracea]
11363	GM_169_B2_A08_MR	g3142328	BLASTN	741	1e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11364	GM_169_B2_B02_MR	g507910	BLASTN	363	8e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11365	GM_169_B2_B03_MR	g4063756	BLASTN	542	2e-17	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11366	GM_169_B2_B06_T7	g18559	BLASTN	1112	2e-43	84	G.max gene for catalase
11367	GM_169_B2_B09_MR	g99922	BLASTX	205	4e-31	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11368	GM_169_B2_B10_MR	g4156182	BLASTN	432	2e-12	64	Homo sapiens clone DJ0815D20, complete sequence [Homo sapiens]
11369	GM_169_B2_B11_MR	g2264320	BLASTN	547	1e-17	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
11370	GM_169_B2_B11_T7	g3894387	BLASTX	151	9e-09	46	(AF053995) Hcr2-0B [Lycopersicon esculentum]
11371	GM_169_B2_C05_MR	g3650036	BLASTX	185	1e-12	30	(AC005396) putative transposase [Arabidopsis thaliana]
11372	GM_169_B2_C12_T7	g3599418	BLASTN	525	9e-17	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11373	GM_169_B2_D06_MR	g3377848	BLASTX	216	6e-23	56	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
11374	GM_169_B2_D12_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
11375	GM_169_B2_E07_MR	g1799782	BLASTX	238	4e-19	92	BILE ACID-INDUCIBLE OPERON PROTEIN F. [Escherichia coli]
11376	GM_169_B2_E07_T7	g1799782	BLASTX	196	3e-14	100	BILE ACID-INDUCIBLE OPERON PROTEIN F. [Escherichia coli]
11377	GM_169_B2_E09_T7	g99922	BLASTX	341	5e-42	80	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11378	GM_169_B2_E11_MR	g2522228	BLASTX	327	9e-29	74	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
11379	GM_169_B2_F01_MR	g3142328	BLASTN	681	1e-38	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11380	GM_169_B2_F01_T7	g3738337	BLASTX	214	2e-15	38	(AC005170) putative reverse transcriptase [Arabidopsis thaliana]
11381	GM_169_B2_F09_MR	g3645899	BLASTX	286	2e-24	47	(U68408) 5' end not determined experimentally [Zea mays]
11382	GM_169_B2_F10_MR	g1209754	BLASTN	375	6e-10	64	Trypanosoma cruzi kinetoplast maxicircle DNA, clone TRCKPMAX
11383	GM_169_B2_F12_MR	g3645899	BLASTX	285	5e-23	48	(U68408) 5' end not determined experimentally [Zea mays]
11384	GM_169_B2_G07_T7	g4063760	BLASTX	347	2e-29	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11385	GM_169_B2_G10_T7	g18559	BLASTN	887	3e-33	77	G.max gene for catalase
11386	GM_169_B2_G11_MR	g4063756	BLASTN	377	5e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11387	GM_169_B2_G11_T7	g507910	BLASTN	698	6e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
11388	GM_169_B2_G12_MR	g3097320	BLASTN	406	2e-11	70	Glycine max gene for Bd 30K, complete cds
11389	GM_169_B2_G12_T7	g3645899	BLASTX	197	1e-13	56	(U68408) 5' end not determined experimentally [Zea mays]
11390	GM_169_B2_H01_T7	g3319366	BLASTX	192	2e-14	43	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
11391	GM_170_A2_A01_T7	g3650039	BLASTX	144	2e-12	54	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11392	GM_170_A2_A03_MR	g2326264	BLASTN	429	2e-12	61	Arabidopsis thaliana DNA for CCT alpha/TCP-1, complete cds.
11393	GM_170_A2_A06_MR	g2654226	BLASTX	97	2e-09	58	(AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis thaliana]
11394	GM_170_A2_A06_T7	g1946355	BLASTX	153	4e-09	33	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
11395	GM_170_A2_A08_MR	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11396	GM_170_A2_A09_MR	g13774	BLASTN	347	6e-09	61	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
11397	GM_170_A2_A10_MR	g1871190	BLASTX	305	2e-29	52	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
11398	GM_170_A2_A10_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11399	GM_170_A2_B08_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11400	GM_170_A2_B08_T7	g4063760	BLASTX	389	5e-34	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11401	GM_170_A2_B09_MR	g3176726	BLASTX	164	3e-10	51	(AC002392) putative serine proteinase [Arabidopsis thaliana]
11402	GM_170_A2_B11_MR	g3779030	BLASTX	168	6e-12	32	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
11403	GM_170_A2_B12_MR	g4063760	BLASTX	194	4e-17	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11404	GM_170_A2_B12_T7	g507910	BLASTN	456	5e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11405	GM_170_A2_C01_T7	g18559	BLASTN	961	2e-36	94	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11406	GM_170_A2_C02_T7	g3142328	BLASTN	1448	9e-59	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11407	GM_170_A2_D11_MR	g18559	BLASTN	388	1e-10	76	G.max gene for catalase
11408	GM_170_A2_E01_T7	g3777526	BLASTN	675	2e-23	81	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
11409	GM_170_A2_E04_MR	g1666236	BLASTX	249	2e-20	33	(U76261) unknown [Hordeum vulgare]
11410	GM_170_A2_E05_T7	g100484	BLASTX	301	5e-25	58	hypothetical protein - garden snapdragon
11411	GM_170_A2_E08_MR	g421955	BLASTX	216	1e-16	37	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
11412	GM_170_A2_E11_MR	g905361	BLASTX	384	3e-34	95	(U22103) gag-protease polyprotein [Glycine max]
11413	GM_170_A2_F04_MR	g112609	BLASTX	193	1e-14	45	jacalin a' - jackfruit
11414	GM_170_A2_F05_MR	g3264544	BLASTN	403	4e-11	61	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
11415	GM_170_A2_G02_T7	g2129618	BLASTX	181	5e-12	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11416	GM_170_A2_G03_T7	g507910	BLASTN	534	2e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11417	GM_170_A2_G04_MR	g3142328	BLASTN	479	1e-14	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11418	GM_170_A2_G06_MR	g4038056	BLASTX	345	1e-29	48	(AC005897) putative transposon [Arabidopsis thaliana]
11419	GM_170_A2_G10_MR	g507910	BLASTN	432	6e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11420	GM_170_A2_H02_MR	g479357	BLASTX	174	2e-11	33	hypothetical protein 612 - maize transposon MuA2 gi 22375 (X62251) ORF [Zea mays]
11421	GM_170_A2_H04_MR	g3142328	BLASTN	483	7e-15	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11422	GM_170_A2_H07_MR	g3646936	BLASTN	410	2e-11	62	Caenorhabditis elegans cosmid Y47D3B, complete sequence [Caenorhabditis elegans]
11423	GM_170_B2_A09_T7	g2316016	BLASTX	282	2e-22	49	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
11424	GM_170_B2_B01_MR	g2443320	BLASTX	170	1e-10	34	(D85597) polyprotein [Oryza australiensis]
11425	GM_170_B2_B07_T7	g507910	BLASTN	592	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11426	GM_170_B2_B11_MR	g2832304	BLASTX	126	6e-14	57	(AF044489) receptor-like protein kinase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11427	GM_170_B2_C03_T7	g122106	BLASTX	235	4e-19	69	HISTONE H4 gi 70771 pir HSZM4 histone H4 - maize gi 81642 pir S06904 histone H4 - Arabidopsis thaliana gi 2119028 pir S60475 histone H4 - garden pea gi 21795 (X00043) histone H4 [Triticum aestivum] gi 166740 (M17132) histone H4 [Arabidopsis thaliana] gi 166742 (M17133) histone H4 [Arabidopsis thaliana] gi 168499 (M36659) histone H4 (H4C13) [Zea mays] gi 168501 (M13370) histone H4 [Zea mays] gi 168503 (M13377) histone H4 [Zea mays] gi 498898 (U10042) histone H4 homolog [Pisum sativum] gi 1806285 gnl PID e263432 (Z79638) histone H4 homologue [Sesbania rostrata] gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]
11428	GM_170_B2_C05_MR	g1514643	BLASTX	152	5e-24	75	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11429	GM_170_B2_C09_T7	g3645899	BLASTX	366	1e-31	49	(U68408) 5' end not determined experimentally [Zea mays]
11430	GM_170_B2_D03_MR	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
11431	GM_170_B2_D05_T7	g2522230	BLASTX	327	9e-29	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11432	GM_170_B2_D06_T7	g3056601	BLASTX	369	3e-33	80	(AC004255) T1F9.22 [Arabidopsis thaliana]
11433	GM_170_B2_D07_T7	g3319372	BLASTX	240	4e-18	40	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
11434	GM_170_B2_D10_MR	g18559	BLASTN	702	8e-25	76	G.max gene for catalase
11435	GM_170_B2_D10_T7	g100484	BLASTX	262	8e-21	44	hypothetical protein - garden snapdragon
11436	GM_170_B2_E05_MR	g2454214	BLASTN	382	2e-10	63	Glycine max nodule-specific phosphoribosylpyrophosphate amidotransferase (PRAT) gene, 5' upstream sequence and partial cds
11437	GM_170_B2_E07_T7	g905361	BLASTX	396	1e-35	89	(U22103) gag-protease polyprotein [Glycine max]
11438	GM_170_B2_E10_MR	g4063760	BLASTX	349	9e-30	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11439	GM_170_B2_F01_T7	g629693	BLASTX	148	4e-09	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11440	GM_170_B2_F04_T7	g2995405	BLASTX	564	2e-53	57	(Y12432) polyprotein [Ananas comosus]
11441	GM_170_B2_F05_T7	g1666236	BLASTX	200	5e-15	29	(U76261) unknown [Hordeum vulgare]
11442	GM_170_B2_G02_T7	g3021265	BLASTX	206	6e-18	59	(AL022347) protein kinase - like protein [Arabidopsis thaliana] gi 3292839 gnl PID e1310082 (AL031018) protein kinase - like protein [Arabidopsis thaliana]
11443	GM_170_B2_G03_T7	g2522227	BLASTX	163	1e-16	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
11444	GM_170_B2_G04_T7	g3097320	BLASTN	432	2e-12	70	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
11445	GM_170_B2_G06_T7	g3097320	BLASTN	1038	6e-40	81	Glycine max gene for Bd 30K, complete cds
11446	GM_170_B2_G09_T7	g3097320	BLASTN	402	4e-11	66	Glycine max gene for Bd 30K, complete cds
11447	GM_170_B2_G12_MR	g4063760	BLASTX	274	9e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11448	GM_170_B2_H01_MR	g3777527	BLASTX	183	9e-13	39	(AF053008) gag-pol polyprotein [Glycine max]
11449	GM_170_B2_H03_T7	g4038056	BLASTX	365	1e-31	47	(AC005897) putative transposon [Arabidopsis thaliana]
11450	GM_170_B2_H04_MR	g4063760	BLASTX	103	5e-10	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11451	GM_170_B2_H04_T7	g1402877	BLASTX	159	2e-10	60	(X98130) unknown [Arabidopsis thaliana] gi 1495257 gnl PID e242925 (X97485) orf03 [Arabidopsis thaliana]
11452	GM_170_B2_H06_MR	g507910	BLASTN	350	3e-09	87	Glycine max BSR-101 satellite SB92 genomic sequence.
11453	GM_170_B2_H09_T7	g3688172	BLASTX	162	1e-11	50	(AL031804) putative protein [Arabidopsis thaliana]
11454	GM_171_A1_A03_MR	g18559	BLASTN	626	2e-21	74	G.max gene for catalase
11455	GM_171_A1_A09_T7	g3097320	BLASTN	511	4e-16	76	Glycine max gene for Bd 30K, complete cds
11456	GM_171_A1_A10_MR	g3063460	BLASTX	145	4e-12	69	(AC003981) F22O13.22 [Arabidopsis thaliana]
11457	GM_171_A1_A10_T7	g3859610	BLASTN	427	3e-12	64	Arabidopsis thaliana BAC T9E19
11458	GM_171_A1_B06_MR	g3645899	BLASTX	207	1e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
11459	GM_171_A1_B08_T7	g2651303	BLASTX	215	4e-17	64	(AC002336) putative potassium transporter [Arabidopsis thaliana]
11460	GM_171_A1_C02_MR	g3142328	BLASTN	1274	8e-51	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11461	GM_171_A1_C11_T7	g3645899	BLASTX	154	5e-09	45	(U68408) 5' end not determined experimentally [Zea mays]
11462	GM_171_A1_C12_MR	g507910	BLASTN	461	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
11463	GM_171_A1_D03_MR	g507910	BLASTN	572	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11464	GM_171_A1_D04_T7	g2388577	BLASTX	274	6e-22	59	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
11465	GM_171_A1_D05_T7	g3142328	BLASTN	1382	9e-56	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11466	GM_171_A1_D08_MR	g2522230	BLASTX	167	8e-12	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11467	GM_171_A1_D11_MR	g507910	BLASTN	567	5e-19	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11468	GM_171_A1_E03_T7	g4063760	BLASTX	323	6e-27	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11469	GM_171_A1_E10_MR	g509768	BLASTN	455	1e-13	67	Glycine max seed-specific low molecular weight sulfur-rich protein.
11470	GM_171_A1_F06_T7	g18559	BLASTN	430	2e-12	67	G.max gene for catalase
11471	GM_171_A1_F09_T7	g342960	BLASTN	356	5e-10	64	paramecium mutant 4.51clm-cl mt dna dimer: repl. init. region, clone 2.
11472	GM_171_A1_F12_T7	g4063760	BLASTX	261	2e-20	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11473	GM_171_A1_G09_T7	g18559	BLASTN	728	6e-26	75	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11474	GM_171_A1_H01_MR	g342954	BLASTN	394	9e-12	60	paramecium species 4.51b mt dna dimer: replication init. region, clone-1.
11475	GM_171_A1_H05_T7	g4063770	BLASTX	164	3e-10	41	(AB004906) transposase [Ipomoea purpurea]
11476	GM_171_A1_H12_T7	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11477	GM_171_A2_A03_MR	g100488	BLASTX	175	2e-11	34	TNP2 protein - garden snapdragon
11478	GM_171_A2_A04_MR	g905361	BLASTX	109	2e-12	42	(U22103) gag-protease polyprotein [Glycine max]
11479	GM_171_A2_B10_MR	g3810596	BLASTX	334	2e-28	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11480	GM_171_A2_C10_MR	g1946279	BLASTX	278	1e-23	46	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
11481	GM_171_A2_D04_MR	g21098	BLASTN	426	6e-13	66	Tomato U1 small nuclear RNA gene U1.5
11482	GM_171_A2_D05_MR	g3063708	BLASTX	240	5e-18	46	(AL022537) putative protein [Arabidopsis thaliana]
11483	GM_171_A2_D10_MR	g1946279	BLASTX	303	3e-26	47	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
11484	GM_171_A2_E03_MR	g131026	BLASTX	170	4e-12	47	PATHOGENESIS-RELATED PROTEIN STH-2 gi 479691 pir S35161 STH-2 protein - potato gi 169551 (M25155) pSTH-2 protein [Solanum tuberosum] gi 169576 (M29041) STH-2 protein [Solanum tuberosum]
11485	GM_171_A2_E11_MR	g18559	BLASTN	562	1e-31	79	G.max gene for catalase
11486	GM_171_A2_F06_MR	g2522230	BLASTX	313	3e-27	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11487	GM_171_A2_G07_MR	g3142328	BLASTN	775	4e-28	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11488	GM_171_A2_G08_MR	g2961349	BLASTX	160	1e-09	40	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
11489	GM_171_A2_G09_MR	g13584	BLASTN	438	3e-13	62	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
11490	GM_171_A2_G12_MR	g2995405	BLASTX	218	2e-17	46	(Y12432) polyprotein [Ananas comosus]
11491	GM_171_A2_H03_MR	g100484	BLASTX	133	6e-16	41	hypothetical protein - garden snapdragon
11492	GM_171_A2_H04_MR	g1171591	BLASTN	350	9e-09	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
11493	GM_171_A2_H06_MR	g3193311	BLASTN	363	2e-09	76	Arabidopsis thaliana BAC F6N15
11494	GM_171_A2_H09_MR	g99922	BLASTX	519	4e-49	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11495	GM_171_A2_H11_MR	g3668083	BLASTX	158	4e-10	60	(AC004667) hypothetical protein [Arabidopsis thaliana]
11496	GM_171_B2_A08_MR	g507910	BLASTN	655	6e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11497	GM_171_B2_A09_MR	g2462936	BLASTX	211	1e-16	32	(Y12321) open reading frame 2 [Brassica oleracea]
11498	GM_171_B2_A12_MR	g507910	BLASTN	347	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11499	GM_171_B2_C06_MR	g3097320	BLASTN	373	7e-10	71	Glycine max gene for Bd 30K, complete cds
11500	GM_171_B2_D09_MR	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11501	GM_171_B2_E10_MR	g3377848	BLASTX	105	7e-16	66	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
11502	GM_171_B2_F01_MR	g1374720	BLASTN	381	2e-10	62	Neocallimastix patriciarum cellobiohydrolase precursor (celA) mRNA, complete cds
11503	GM_171_B2_F11_MR	g100484	BLASTX	348	4e-30	58	hypothetical protein - garden snapdragon
11504	GM_171_B2_G01_MR	g13769	BLASTN	241	2e-11	66	Torulopsis glabrata mitochondrial DNA for tRNA-Met and tRNA-Pro downstream of cytochrome b gene >gi 343952 gb M11873 YSLMTIG02 Yeast (T.glabrata) mitochondrial DNA between cytochrome b and cytochrome oxidase subunit 1 genes.
11505	GM_172_A1_A08_MR	g3142328	BLASTN	817	5e-30	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11506	GM_172_A1_B03_T7	g1769898	BLASTX	419	2e-38	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11507	GM_172_A1_B06_MR	g1769898	BLASTX	208	3e-19	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11508	GM_172_A1_B12_MR	g507910	BLASTN	361	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11509	GM_172_A1_C05_MR	g629693	BLASTX	398	3e-36	57	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11510	GM_172_A1_C05_T7	g3097320	BLASTN	454	2e-13	67	Glycine max gene for Bd 30K, complete cds
11511	GM_172_A1_C09_MR	g3413322	BLASTX	94	1e-10	56	(Y11118) polygalacturonase [Medicago sativa]
11512	GM_172_A1_D01_MR	g18559	BLASTN	421	5e-12	73	G.max gene for catalase
11513	GM_172_A1_E04_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11514	GM_172_A1_E10_T7	g2995405	BLASTX	240	2e-18	42	(Y12432) polyprotein [Ananas comosus]
11515	GM_172_A1_F07_MR	g1769897	BLASTX	187	5e-13	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11516	GM_172_A1_F09_T7	g3264565	BLASTN	372	9e-10	63	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
11517	GM_172_A1_G01_MR	g3176811	BLASTN	360	3e-10	61	Homo sapiens allele 18 fragile site locus (FRA10B) minisatellite, 3' sequence
11518	GM_172_A1_G03_MR	g2323254	BLASTN	383	3e-10	62	Human Chromosome X, complete sequence [Homo sapiens]
11519	GM_172_A1_G03_T7	g3860167	BLASTX	159	2e-09	41	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]
11520	GM_172_A1_G05_MR	g3142328	BLASTN	778	3e-51	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11521	GM_172_A1_G07_MR	g3063445	BLASTX	255	8e-20	61	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11522	GM_172_A1_H01_MR	g2522230	BLASTX	313	3e-27	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11523	GM_172_A1_H04_MR	g3075383	BLASTN	534	4e-17	69	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]
11524	GM_172_A1_H08_MR	g13584	BLASTN	381	2e-10	63	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
11525	GM_172_A1_H08_T7	g3688428	BLASTX	409	2e-37	72	(AJ011534) sucrose synthase [Lycopersicon esculentum]
11526	GM_172_A1_H11_T7	g1658457	BLASTX	212	1e-16	69	(U75248) reverse transcriptase [Gossypium barbadense]
11527	GM_172_A1_H12_MR	g2781345	BLASTX	170	7e-11	37	(AC003113) F24O1.2 [Arabidopsis thaliana]
11528	GM_172_A2_A03_T7	g4063760	BLASTX	305	4e-25	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11529	GM_172_A2_A04_T7	g905361	BLASTX	119	2e-10	33	(U22103) gag-protease polyprotein [Glycine max]
11530	GM_172_A2_A05_T7	g2996647	BLASTN	405	3e-11	64	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
11531	GM_172_A2_A08_T7	g392991	BLASTN	402	4e-11	71	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds.
11532	GM_172_A2_B02_MR	g4159699	BLASTN	381	4e-10	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence [Arabidopsis thaliana]
11533	GM_172_A2_B02_T7	g3928116	BLASTN	438	9e-13	62	, complete sequence [Homo sapiens]
11534	GM_172_A2_B03_T7	g3337395	BLASTN	436	1e-12	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
11535	GM_172_A2_B04_MR	g4115943	BLASTX	208	1e-20	80	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana]
11536	GM_172_A2_B11_MR	g4063760	BLASTX	357	1e-30	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11537	GM_172_A2_C01_MR	g2244901	BLASTN	510	5e-16	69	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 4
11538	GM_172_A2_C03_MR	g4063760	BLASTX	198	1e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11539	GM_172_A2_C04_T7	g18559	BLASTN	722	1e-25	73	G.max gene for catalase
11540	GM_172_A2_C12_T7	g507910	BLASTN	609	7e-21	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11541	GM_172_A2_D06_T7	g2995405	BLASTX	304	3e-25	61	(Y12432) polyprotein [Ananas comosus]
11542	GM_172_A2_D08_MR	g3599418	BLASTN	382	3e-10	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11543	GM_172_A2_D11_MR	g2443320	BLASTX	308	3e-25	52	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11544	GM_172_A2_E02_T7	g13767	BLASTN	365	2e-10	68	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
11545	GM_172_A2_E07_MR	g100484	BLASTX	304	2e-25	54	hypothetical protein - garden snapdragon
11546	GM_172_A2_F06_T7	g3142328	BLASTN	1609	4e-66	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11547	GM_172_A2_F11_MR	g18559	BLASTN	875	1e-32	76	G.max gene for catalase
11548	GM_172_A2_G04_T7	g1666236	BLASTX	207	7e-16	31	(U76261) unknown [Hordeum vulgare]
11549	GM_172_A2_G05_T7	g2618602	BLASTN	411	2e-11	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
11550	GM_172_A2_G07_MR	g3702339	BLASTX	212	3e-16	54	(AC005397) unknown protein [Arabidopsis thaliana]
11551	GM_172_A2_G11_MR	g2292907	BLASTX	165	4e-10	32	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
11552	GM_172_A2_H06_MR	g3777527	BLASTX	445	8e-40	94	(AF053008) gag-pol polyprotein [Glycine max]
11553	GM_172_A2_H09_T7	g4140712	BLASTX	218	3e-17	56	(AF110183) putative integrase [Oryza sativa]
11554	GM_172_B1_A07_T7	g1769898	BLASTX	118	1e-18	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11555	GM_172_B1_A08_MR	g4038056	BLASTX	99	1e-10	53	(AC005897) putative transposon [Arabidopsis thaliana]
11556	GM_172_B1_A08_T7	g507910	BLASTN	367	6e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11557	GM_172_B1_A09_MR	g342965	BLASTN	339	1e-08	61	paramecium species 7.227 mt dna dimer: replication init. region.
11558	GM_172_B1_B01_T7	g3153873	BLASTX	552	1e-52	79	(AF065393) putative G-binding protein [Homo sapiens]
11559	GM_172_B1_B02_T7	g3176686	BLASTX	334	2e-28	61	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
11560	GM_172_B1_B07_T7	g421954	BLASTX	128	2e-15	38	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
11561	GM_172_B1_B12_MR	g2522228	BLASTX	207	2e-15	46	(AB007466) reverse transcriptase-like protein [Vicia faba]
11562	GM_172_B1_C01_MR	g3924609	BLASTX	90	2e-09	62	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
11563	GM_172_B1_C04_MR	g1666236	BLASTX	106	8e-09	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11564	GM_172_B1_C04_T7	g125271	BLASTX	180	9e-13	84	CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA) gi 100860 pir S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize gi 3318993 pdb 1A6O Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays Transferase, SerineTHREONINE-Protein Kinase, Casein Kinase, SerTHR KINASE Mol_id: 1; Molecule: Protein Kinase Ck2ALPHA-Subunit; Chain: Null; Ec: 2.7.1.37; Engineered: Yes gi 22117 (X61387) casein kinase II alpha subunit [Zea mays]
11565	GM_172_B1_C08_MR	g2564050	BLASTN	527	9e-17	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]
11566	GM_172_B1_D03_MR	g3142328	BLASTN	705	6e-25	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11567	GM_172_B1_D09_T7	g3643611	BLASTX	129	2e-16	95	(AC005395) putative casein kinase [Arabidopsis thaliana]
11568	GM_172_B1_D10_MR	g3142328	BLASTN	571	7e-19	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11569	GM_172_B1_D12_T7	g3142330	BLASTX	353	8e-31	88	(U96295) envelope-like [Glycine max]
11570	GM_172_B1_E09_MR	g507910	BLASTN	611	5e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
11571	GM_172_B1_E09_T7	g507910	BLASTN	544	6e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
11572	GM_172_B1_F03_MR	g1167523	BLASTX	279	3e-22	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11573	GM_172_B1_F07_T7	g629693	BLASTX	299	7e-26	52	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11574	GM_172_B1_F12_MR	g3445210	BLASTX	189	2e-13	45	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
11575	GM_172_B1_G03_T7	g4159700	BLASTN	377	5e-10	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence [Arabidopsis thaliana]
11576	GM_172_B1_G04_MR	g905361	BLASTX	479	7e-45	85	(U22103) gag-protease polyprotein [Glycine max]
11577	GM_172_B1_G05_T7	g2982303	BLASTX	270	9e-23	79	(AF051236) hypothetical protein [Picea mariana]
11578	GM_172_B1_G07_MR	g2598589	BLASTX	191	1e-13	51	(Y15367) MtN19 [Medicago truncatula]
11579	GM_172_B1_H02_MR	g507910	BLASTN	565	6e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11580	GM_172_B1_H03_T7	g4063760	BLASTX	380	4e-33	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11581	GM_172_B2_A04_MR	g1076755	BLASTX	332	2e-43	75	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
11582	GM_172_B2_A08_MR	g2864613	BLASTX	171	5e-11	62	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana]
11583	GM_172_B2_A12_MR	g3953471	BLASTX	289	7e-41	64	(AC002328) F22O2.16 [Arabidopsis thaliana]
11584	GM_172_B2_A12_T7	g1769898	BLASTX	212	1e-15	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11585	GM_172_B2_B01_MR	g1346113	BLASTX	298	1e-25	67	GTP CYCLOHYDROLASE II gi 1084339 pir JC4209 GTP cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana gi 940383 gnl PID d1008704 (D45165) GTP cyclohydrolase II [Arabidopsis thaliana]
11586	GM_172_B2_B04_MR	g2827621	BLASTX	178	8e-12	44	(AL021636) putative protein [Arabidopsis thaliana]
11587	GM_172_B2_B04_T7	g3851529	BLASTN	558	1e-18	97	Glycine max nodulin mRNA, complete cds
11588	GM_172_B2_B09_T7	g2062167	BLASTX	98	5e-11	60	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
11589	GM_172_B2_B10_T7	g4115536	BLASTX	212	1e-16	48	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
11590	GM_172_B2_C02_MR	g1769898	BLASTX	131	3e-10	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11591	GM_172_B2_C03_T7	g4063756	BLASTN	373	8e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11592	GM_172_B2_C05_MR	g2443320	BLASTX	192	2e-14	40	(D85597) polyprotein [Oryza australiensis]
11593	GM_172_B2_C08_MR	g4063760	BLASTX	248	6e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11594	GM_172_B2_C12_MR	g1167523	BLASTX	181	9e-12	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11595	GM_172_B2_D07_MR	g4063756	BLASTN	518	2e-16	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11596	GM_172_B2_D07_T7	g3777527	BLASTX	588	5e-55	97	(AF053008) gag-pol polyprotein [Glycine max]
11597	GM_172_B2_E03_MR	g2129618	BLASTX	203	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11598	GM_172_B2_E08_T7	g170606	BLASTN	685	2e-24	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
11599	GM_172_B2_E10_T7	g1769899	BLASTX	242	8e-20	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11600	GM_172_B2_E12_T7	g4063760	BLASTX	237	7e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11601	GM_172_B2_F03_T7	g4063760	BLASTX	186	2e-12	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11602	GM_172_B2_F05_T7	g3513745	BLASTX	171	5e-14	40	(AF080118) contains similarity to reverse tranciptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
11603	GM_172_B2_F07_T7	g18664	BLASTN	298	1e-12	76	Soybean leghaemoglobin gene lba promoter region
11604	GM_172_B2_F12_T7	g3184283	BLASTX	129	1e-09	70	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
11605	GM_172_B2_G01_T7	g4115365	BLASTX	302	1e-24	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
11606	GM_172_B2_G09_MR	g3142328	BLASTN	564	1e-18	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11607	GM_172_B2_G11_T7	g507910	BLASTN	534	2e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11608	GM_172_B2_H01_T7	g3097320	BLASTN	638	7e-22	71	Glycine max gene for Bd 30K, complete cds
11609	GM_172_B2_H02_T7	g3777527	BLASTX	577	7e-54	93	(AF053008) gag-pol polyprotein [Glycine max]
11610	GM_173_A1_A05_T7	g1840106	BLASTN	498	1e-16	68	Human fragile site locus (FRA16B) minisatellite repeat

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
11611	GM_173_A1_A09_MR	g2665890	BLASTX	213	8e-16	71	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]
11612	GM_173_A1_A10_T7	g3047068	BLASTX	182	4e-12	36	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
11613	GM_173_A1_A11_T7	g3777527	BLASTX	350	9e-30	95	(AF053008) gag-pol polyprotein [Glycine max]
11614	GM_173_A1_B01_MR	g3319362	BLASTX	225	1e-16	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11615	GM_173_A1_B02_MR	g4063756	BLASTN	551	7e-18	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11616	GM_173_A1_B03_MR	g2739003	BLASTN	709	2e-25	82	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
11617	GM_173_A1_B05_MR	g3649752	BLASTN	352	7e-09	64	Plasmodium falciparum MAL3P3, complete sequence [Plasmodium falciparum]
11618	GM_173_A1_B08_MR	g507910	BLASTN	455	6e-14	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11619	GM_173_A1_B08_T7	g507910	BLASTN	534	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11620	GM_173_A1_B09_MR	g3426334	BLASTN	501	1e-15	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
11621	GM_173_A1_B11_T7	g3097320	BLASTN	387	2e-10	68	Glycine max gene for Bd 30K, complete cds
11622	GM_173_A1_B12_MR	g507910	BLASTN	342	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11623	GM_173_A1_B12_T7	g507910	BLASTN	365	7e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11624	GM_173_A1_C07_MR	g4165194	BLASTX	171	8e-11	35	(AJ009736) Pol protein [Drosophila melanogaster]
11625	GM_173_A1_D02_T7	g3319359	BLASTN	377	2e-14	62	Arabidopsis thaliana BAC T7M24
11626	GM_173_A1_D07_T7	g4160362	BLASTN	412	1e-11	60	Saccharomyces cerevisiae complete mitochondrial genome
11627	GM_173_A1_E01_T7	g505129	BLASTN	429	2e-12	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11628	GM_173_A1_E05_T7	g2443320	BLASTX	131	1e-14	48	(D85597) polyprotein [Oryza australiensis]
11629	GM_173_A1_E07_MR	g4063762	BLASTX	128	3e-10	27	(AC005561) putative retrotransposon [Arabidopsis thaliana]
11630	GM_173_A1_F01_MR	g1480927	BLASTN	1115	4e-44	85	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
11631	GM_173_A1_F04_T7	g2191150	BLASTX	209	6e-16	80	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]
11632	GM_173_A1_F05_MR	g1769898	BLASTX	178	9e-18	39	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11633	GM_173_A1_F07_MR	g4063760	BLASTX	371	4e-32	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11634	GM_173_A1_G03_MR	g3355463	BLASTN	671	3e-23	67	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]
11635	GM_173_A1_G04_MR	g3452273	BLASTX	157	2e-23	91	(AF043110) phosphatidylinositol 4-kinase alpha [Daucus carota]
11636	GM_173_A1_G04_T7	g4063770	BLASTX	122	4e-09	40	(AB004906) transposase [Ipomoea purpurea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11637	GM_173_A1_G06_MR	g2495365	BLASTX	250	1e-19	79	HEAT SHOCK PROTEIN 81-2 (HSP81-2) gi 445127 prf 1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]
11638	GM_173_A1_G10_T7	g505129	BLASTN	361	2e-09	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11639	GM_173_A1_G11_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11640	GM_173_A1_H01_T7	g2764526	BLASTN	443	6e-25	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
11641	GM_173_A1_H05_MR	g2194136	BLASTX	207	1e-14	48	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
11642	GM_173_A1_H06_MR	g3319351	BLASTX	263	1e-20	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
11643	GM_173_A1_H08_MR	g3142328	BLASTN	1131	3e-44	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11644	GM_173_A1_H09_T7	g336279	BLASTN	489	5e-15	63	Apis mellifera ligustica complete mitochondrial genome
11645	GM_173_A1_H10_MR	g1658457	BLASTX	216	5e-17	68	(U75248) reverse transcriptase [Gossypium barbadense]
11646	GM_173_B1_A05_MR	g1850550	BLASTX	97	3e-09	43	(U88030) reverse transcriptase [Secale cereale]
11647	GM_173_B1_B05_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11648	GM_173_B1_B05_T7	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11649	GM_173_B1_D05_MR	g507910	BLASTN	348	4e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11650	GM_173_B1_D05_T7	g4063760	BLASTX	352	4e-30	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11651	GM_173_B1_D07_MR	g507910	BLASTN	354	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11652	GM_173_B1_D10_MR	g158813	BLASTN	383	7e-11	67	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
11653	GM_173_B1_E10_T7	g114411	BLASTX	158	6e-10	73	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL gi 320126 pir S26979 H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - kidney bean mitochondrion gi 169318 (M64246) adenosine triphosphatase [Phaseolus vulgaris]
11654	GM_173_B1_G05_MR	g3645899	BLASTX	233	2e-17	50	(U68408) 5' end not determined experimentally [Zea mays]
11655	GM_173_B1_G08_MR	g3281853	BLASTX	173	5e-19	64	(AL031004) putative protein [Arabidopsis thaliana]
11656	GM_173_B1_G08_T7	g3281850	BLASTX	214	6e-16	68	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
11657	GM_173_B1_G10_T7	g3645899	BLASTX	205	2e-14	45	(U68408) 5' end not determined experimentally [Zea mays]
11658	GM_173_B1_H02_T7	g1769898	BLASTX	290	5e-24	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11659	GM_173_B1_H10_T7	g2244915	BLASTX	179	9e-12	39	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
11660	GM_173_B2_A07_MR	g3142328	BLASTN	737	2e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11661	GM_173_B2_A10_MR	g2827637	BLASTX	235	6e-18	41	(AL021636) putative protein [Arabidopsis thaliana]
11662	GM_173_B2_B10_T7	g2522230	BLASTX	141	6e-09	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11663	GM_173_B2_C03_T7	g2833380	BLASTX	143	1e-08	82	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2) (PRS II) gi 2146772 pir S71262 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) II - Arabidopsis thaliana (fragment) gi 1064885 (X92974) phosphoribosyl pyrophosphate synthetase II [Arabidopsis thaliana]
11664	GM_173_B2_C04_T7	g507910	BLASTN	900	5e-34	99	Glycine max BSR-101 satellite SB92 genomic sequence
11665	GM_173_B2_C09_MR	g4063760	BLASTX	188	1e-12	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11666	GM_173_B2_C09_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence
11667	GM_173_B2_C12_MR	g4063760	BLASTX	409	3e-36	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11668	GM_173_B2_D03_MR	g4063760	BLASTX	273	1e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11669	GM_173_B2_D03_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11670	GM_173_B2_D05_MR	g4063756	BLASTN	484	8e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11671	GM_173_B2_F02_T7	g531389	BLASTX	221	2e-23	45	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
11672	GM_173_B2_F04_T7	g422028	BLASTX	222	1e-17	71	transcription factor OBF3.1, ocs element-binding - maize gi 297020 (X69153) ocs-element binding factor 3.1 [Zea mays]
11673	GM_173_B2_F09_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11674	GM_173_B2_G02_T7	g1840106	BLASTN	412	2e-12	62	Human fragile site locus (FRA16B) minisatellite repeat
11675	GM_173_B2_G03_T7	g4063760	BLASTX	418	4e-37	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11676	GM_173_B2_G05_T7	g507910	BLASTN	573	3e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11677	GM_173_B2_G10_MR	g3513747	BLASTX	271	3e-21	54	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
11678	GM_173_B2_H05_T7	g3080421	BLASTX	327	1e-27	65	(AL022604) putative protein [Arabidopsis thaliana]
11679	GM_174_A1_A01_MR	g18559	BLASTN	816	6e-30	78	G.max gene for catalase
11680	GM_174_A1_A02_T7	g2865424	BLASTX	167	3e-10	33	(AF039371) polyprotein [Arabidopsis thaliana]
11681	GM_174_A1_A03_T7	g3142328	BLASTN	855	9e-32	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11682	GM_174_A1_A07_T7	g4063760	BLASTX	291	1e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11683	GM_174_A1_A10_T7	g1666236	BLASTX	198	8e-15	33	(U76261) unknown [Hordeum vulgare]
11684	GM_174_A1_B04_MR	g2522228	BLASTX	345	1e-30	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
11685	GM_174_A1_B05_MR	g2522228	BLASTX	324	2e-28	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
11686	GM_174_A1_B06_T7	g531389	BLASTX	214	3e-15	48	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
11687	GM_174_A1_B07_MR	g133872	BLASTX	209	9e-16	74	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) gi 282838 pir S26494 ribosomal protein S1, chloroplast - spinach gi 322404 pir A44121 small subunit ribosomal protein CS1, CS-S2 - spinach gi 18060 (X66135) ribosomal protein S1 [Spinacia oleracea] gi 170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]
11688	GM_174_A1_B08_MR	g1840106	BLASTN	522	1e-17	66	Human fragile site locus (FRA16B) minisatellite repeat
11689	GM_174_A1_B10_MR	g3269291	BLASTX	99	4e-10	73	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
11690	GM_174_A1_B11_MR	g3777527	BLASTX	159	3e-21	42	(AF053008) gag-pol polyprotein [Glycine max]
11691	GM_174_A1_C11_MR	g3097320	BLASTN	1257	7e-50	82	Glycine max gene for Bd 30K, complete cds
11692	GM_174_A1_D02_T7	g4063760	BLASTX	232	3e-17	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11693	GM_174_A1_D03_MR	g4063756	BLASTN	491	4e-15	67	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11694	GM_174_A1_D05_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11695	GM_174_A1_D08_T7	g2760839	BLASTX	159	7e-10	48	(AC003105) putative receptor kinase [Arabidopsis thaliana]
11696	GM_174_A1_E04_MR	g3319362	BLASTX	188	1e-12	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11697	GM_174_A1_E05_T7	g1769897	BLASTX	189	3e-13	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11698	GM_174_A1_E08_MR	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11699	GM_174_A1_E11_T7	g3319362	BLASTX	212	9e-20	48	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11700	GM_174_A1_F01_T7	g1167523	BLASTX	335	3e-28	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11701	GM_174_A1_F02_MR	g905361	BLASTX	398	7e-36	92	(U22103) gag-protease polyprotein [Glycine max]
11702	GM_174_A1_F02_T7	g18559	BLASTN	691	3e-24	73	G.max gene for catalase
11703	GM_174_A1_F04_T7	g13767	BLASTN	346	2e-09	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
11704	GM_174_A1_F07_T7	g169669	BLASTX	307	1e-26	69	(M96069) tyrosine decarboxylase [Petroselinum crispum]
11705	GM_174_A1_F11_T7	g4063760	BLASTX	202	2e-15	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
11706	GM_174_A1_G08_T7	g2586082	BLASTX	323	6e-27	48	(U72725) retrofit [Oryza longistaminata]
11707	GM_174_A1_H04_MR	g3142328	BLASTN	601	3e-20	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11708	GM_174_A1_H05_T7	g3777527	BLASTX	333	7e-28	47	(AF053008) gag-pol polyprotein [Glycine max]
11709	GM_174_A1_H07_T7	g3777527	BLASTX	326	5e-40	84	(AF053008) gag-pol polyprotein [Glycine max]
11710	GM_174_A2_A01_MR	g2244835	BLASTX	145	2e-11	57	(Z97337) protein kinase homolog [Arabidopsis thaliana]
11711	GM_174_A2_A04_T7	g1946279	BLASTX	249	2e-20	48	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
11712	GM_174_A2_A09_MR	g18559	BLASTN	682	7e-24	72	G max gene for catalase
11713	GM_174_A2_B09_MR	g4115536	BLASTX	251	8e-21	59	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
11714	GM_174_A2_B11_MR	g2921625	BLASTN	590	1e-19	68	Lupinus luteus leghemoglobin (LbI) gene, complete cds
11715	GM_174_A2_C03_MR	g4063760	BLASTX	523	2e-48	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11716	GM_174_A2_C05_MR	g507910	BLASTN	472	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11717	GM_174_A2_C07_MR	g507910	BLASTN	492	1e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11718	GM_174_A2_C08_MR	g1654140	BLASTX	424	5e-38	71	(U37840) lipoxygenase [Lycopersicon esculentum]
11719	GM_174_A2_D06_MR	g4063756	BLASTN	354	6e-09	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11720	GM_174_A2_D12_T7	g99755	BLASTX	265	2e-21	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
11721	GM_174_A2_F01_MR	g2961358	BLASTX	151	1e-09	38	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]
11722	GM_174_A2_F02_T7	g1256830	BLASTX	408	2e-37	82	(U52970) cysteine endopeptidase 1 [Phaseolus vulgaris] gi 2959418 gnl PID e1264083 (AJ224766) cysteine protease [Phaseolus vulgaris]
11723	GM_174_A2_F04_MR	g905361	BLASTX	176	1e-11	28	(U22103) gag-protease polyprotein [Glycine max]
11724	GM_174_A2_F10_MR	g3763969	BLASTN	561	3e-18	67	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
11725	GM_174_A2_G05_MR	g2522228	BLASTX	215	2e-28	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
11726	GM_174_A2_G05_T7	g1165321	BLASTN	527	7e-17	71	Glycine max extensin (SbHRGP3) gene, complete cds
11727	GM_174_A2_G10_MR	g3550983	BLASTX	127	3e-13	70	(AB010690) mutM homologue-2 [Arabidopsis thaliana]
11728	GM_174_B1_A02_MR	g3777527	BLASTX	359	1e-30	80	(AF053008) gag-pol polyprotein [Glycine max]
11729	GM_174_B1_A02_T7	g1666236	BLASTX	153	8e-10	30	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11730	GM_174_B1_A04_T7	g3492889	BLASTN	378	5e-10	62	Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence [Homo sapiens]
11731	GM_174_B1_A08_MR	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11732	GM_174_B1_A08_T7	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11733	GM_174_B1_A09_MR	g3142328	BLASTN	1302	4e-52	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11734	GM_174_B1_A11_MR	g3522943	BLASTX	380	5e-33	80	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
11735	GM_174_B1_B01_MR	g507910	BLASTN	556	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11736	GM_174_B1_B01_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11737	GM_174_B1_B02_T7	g4063756	BLASTN	364	2e-09	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11738	GM_174_B1_B06_MR	g422418	BLASTX	193	3e-13	39	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
11739	GM_174_B1_B06_T7	g3142328	BLASTN	1187	7e-47	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11740	GM_174_B1_B09_MR	g3046704	BLASTX	254	1e-19	44	(AL022223) putative protein [Arabidopsis thaliana]
11741	GM_174_B1_B10_MR	g1666229	BLASTN	454	1e-13	73	Pisum sativum actin (PEAc9) mRNA, complete cds gi 1724138 gb U81047 PSU81047 Pisum sativum actin (PEAc9) mRNA, complete cds
11742	GM_174_B1_B11_T7	g100484	BLASTX	400	9e-36	52	hypothetical protein - garden snapdragon
11743	GM_174_B1_C10_T7	g3097320	BLASTN	422	4e-12	71	Glycine max gene for Bd 30K, complete cds
11744	GM_174_B1_D01_MR	g3097320	BLASTN	493	3e-15	65	Glycine max gene for Bd 30K, complete cds
11745	GM_174_B1_D02_T7	g3687234	BLASTX	206	1e-14	41	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
11746	GM_174_B1_D03_MR	g3142328	BLASTN	712	2e-47	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11747	GM_174_B1_D08_T7	g3645899	BLASTX	182	4e-15	51	(U68408) 5' end not determined experimentally [Zea mays]
11748	GM_174_B1_D09_T7	g2443320	BLASTX	232	1e-20	50	(D85597) polyprotein [Oryza australiensis]
11749	GM_174_B1_D11_MR	g556421	BLASTN	754	3e-41	77	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds.
11750	GM_174_B1_D11_T7	g3600030	BLASTX	130	3e-10	35	(AF080119) contains similarity to ankyrin repeats (Pfam: ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis thaliana]
11751	GM_174_B1_E01_T7	g1752734	BLASTX	190	5e-23	72	(D78510) beta-glucan-elicitor receptor [Glycine max]
11752	GM_174_B1_E04_MR	g1769897	BLASTX	377	5e-34	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11753	GM_174_B1_E07_MR	g3097320	BLASTN	663	5e-23	73	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11754	GM_174_B1_E08_MR	g507910	BLASTN	379	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11755	GM_174_B1_E08_T7	g507910	BLASTN	363	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11756	GM_174_B1_E09_MR	g2462058	BLASTX	269	1e-22	53	(Y13389) reverse transcriptase [Antirrhinum majus]
11757	GM_174_B1_F01_MR	g1084334	BLASTX	233	4e-18	75	calcium-dependent protein kinase (EC 2.7.1.-) 1 - Arabidopsis thaliana gi 604880 gnl PID d1005364 (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]
11758	GM_174_B1_G03_MR	g2443320	BLASTX	203	8e-31	51	(D85597) polyprotein [Oryza australiensis]
11759	GM_174_B1_G04_T7	g3513747	BLASTX	229	7e-26	58	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
11760	GM_174_B1_H01_MR	g507910	BLASTN	357	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11761	GM_174_B1_H05_MR	g1167523	BLASTX	287	4e-23	42	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11762	GM_174_B1_H07_MR	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11763	GM_174_B1_H08_T7	g3097320	BLASTN	583	2e-19	76	Glycine max gene for Bd 30K, complete cds
11764	GM_174_B2_A05_MR	g2194136	BLASTX	264	1e-20	53	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
11765	GM_174_B2_C05_MR	g1142703	BLASTN	293	5e-14	75	Glycine max satellite STR120-B.1.
11766	GM_174_B2_D02_MR	g2191135	BLASTX	115	1e-12	61	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]
11767	GM_174_B2_D03_MR	g3513747	BLASTX	163	9e-10	42	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
11768	GM_174_B2_E01_MR	g2129618	BLASTX	184	3e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11769	GM_174_B2_E12_MR	g3548808	BLASTX	315	7e-27	80	(AC005313) unknown protein [Arabidopsis thaliana]
11770	GM_174_B2_F03_MR	g3650039	BLASTX	271	7e-22	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11771	GM_174_B2_F12_MR	g4038056	BLASTX	111	9e-15	40	(AC005897) putative transposon [Arabidopsis thaliana]
11772	GM_174_B2_G03_MR	g2522228	BLASTX	156	1e-15	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
11773	GM_174_B2_H04_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11774	GM_174_B2_H06_MR	g1666236	BLASTX	182	6e-13	33	(U76261) unknown [Hordeum vulgare]
11775	GM_174_B2_H07_MR	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11776	GM_174_B2_H11_MR	g100484	BLASTX	393	5e-35	55	hypothetical protein - garden snapdragon
11777	GM_175_A1_A03_T7	g99719	BLASTX	201	3e-23	65	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 16384 (X53976) orf 2 [Arabidopsis thaliana]
11778	GM_175_A1_A05_T7	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11779	GM_175_A1_A06_MR	g2522230	BLASTX	260	1e-21	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11780	GM_175_A1_A08_MR	g3548806	BLASTX	227	5e-17	55	(AC005313) unknown protein [Arabidopsis thaliana]
11781	GM_175_A1_A08_T7	g22491	BLASTX	165	8e-11	33	(X01380) ORF2 [Zea mays]
11782	GM_175_A1_A09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence
11783	GM_175_A1_A09_T7	g3777527	BLASTX	617	4e-58	96	(AF053008) gag-pol polyprotein [Glycine max]
11784	GM_175_A1_A10_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11785	GM_175_A1_A10_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11786	GM_175_A1_A11_MR	g2129618	BLASTX	203	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11787	GM_175_A1_B03_MR	g4063760	BLASTX	321	9e-27	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11788	GM_175_A1_B04_T7	g3953458	BLASTX	195	7e-14	82	(AC002328) F20N2.3 [Arabidopsis thaliana]
11789	GM_175_A1_B06_MR	g320565	BLASTX	166	1e-11	50	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
11790	GM_175_A1_B08_T7	g1666236	BLASTX	146	5e-09	27	(U76261) unknown [Hordeum vulgare]
11791	GM_175_A1_C01_T7	g4038056	BLASTX	190	6e-13	36	(AC005897) putative transposon [Arabidopsis thaliana]
11792	GM_175_A1_C04_T7	g4063760	BLASTX	139	1e-11	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11793	GM_175_A1_C05_MR	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11794	GM_175_A1_C05_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11795	GM_175_A1_C10_T7	g3845197	BLASTN	379	4e-10	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
11796	GM_175_A1_C11_MR	g1742959	BLASTX	192	5e-22	81	(Z71450) CLC-d chloride channel protein [Arabidopsis thaliana]
11797	GM_175_A1_C11_T7	g2244834	BLASTX	305	1e-25	91	(Z97337) hypothetical protein [Arabidopsis thaliana]
11798	GM_175_A1_D04_MR	g479178	BLASTX	227	1e-16	46	pol polyprotein - Volvox carteri f. nagariensis retrotransposon Osser gi 288597 (X69552) gag,protease,endonuclease, reverse transcriptase,RNaseH [Volvox carteri]
11799	GM_175_A1_D07_MR	g2522227	BLASTX	200	2e-15	48	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
11800	GM_175_A1_D07_T7	g2995405	BLASTX	370	3e-32	55	(Y12432) polyprotein [Ananas comosus]
11801	GM_175_A1_D08_T7	g2995405	BLASTX	181	2e-26	50	(Y12432) polyprotein [Ananas comosus]
11802	GM_175_A1_D09_MR	g3097320	BLASTN	621	4e-21	78	Glycine max gene for Bd 30K, complete cds
11803	GM_175_A1_E08_MR	g2191130	BLASTX	461	6e-43	76	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]
11804	GM_175_A1_E10_T7	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11805	GM_175_A1_F01_MR	g421954	BLASTX	152	8e-21	43	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
11806	GM_175_A1_F06_MR	g4038056	BLASTX	257	4e-20	45	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11807	GM_175_A1_F08_T7	g2801423	BLASTN	419	7e-12	64	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
11808	GM_175_A1_F09_MR	g3142328	BLASTN	663	5e-23	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11809	GM_175_A1_F09_T7	g3319362	BLASTX	331	5e-30	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11810	GM_175_A1_F10_MR	g3170525	BLASTX	234	5e-18	45	(AF054615) cellulase [Fragaria x ananassa]
11811	GM_175_A1_G05_T7	g1174498	BLASTX	156	1e-10	68	SYNAPTOBREVIN-RELATED PROTEIN gi 600710 (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]
11812	GM_175_A1_G06_T7	g2522228	BLASTX	396	4e-36	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
11813	GM_175_A1_G07_T7	g130582	BLASTX	237	9e-18	44	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
11814	GM_175_A1_G11_T7	g4063756	BLASTN	392	1e-10	68	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11815	GM_175_A1_G12_T7	g3738114	BLASTN	395	8e-11	65	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
11816	GM_175_A1_H02_T7	g3687234	BLASTX	196	2e-13	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
11817	GM_175_A1_H05_MR	g1666236	BLASTX	180	9e-13	29	(U76261) unknown [Hordeum vulgare]
11818	GM_175_A1_H07_MR	g1142700	BLASTN	400	1e-11	72	Glycine max satellite STR120-A 2
11819	GM_175_A1_H08_T7	g4063760	BLASTX	478	2e-43	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11820	GM_175_A1_H11_MR	g905361	BLASTX	420	3e-38	95	(U22103) gag-protease polyprotein [Glycine max]
11821	GM_175_A1_H12_T7	g1931641	BLASTX	164	3e-10	50	(U95973) unknown protein [Arabidopsis thaliana]
11822	GM_175_A2_A03_T7	g3097320	BLASTN	744	1e-26	73	Glycine max gene for Bd 30K, complete cds
11823	GM_175_A2_A04_MR	g22491	BLASTX	119	3e-13	36	(X01380) ORF2 [Zea mays]
11824	GM_175_A2_B01_MR	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11825	GM_175_A2_B02_T7	g3869069	BLASTN	543	2e-17	73	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
11826	GM_175_A2_B05_MR	g1326016	BLASTX	98	5e-11	47	TY3-2 orfB

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11827	GM_175_A2_B07_MR	g3059060	BLASTN	374	7e-10	62	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
11828	GM_175_A2_B07_T7	g1805654	BLASTX	154	5e-09	37	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]
11829	GM_175_A2_B09_T7	g3738114	BLASTN	354	6e-09	61	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
11830	GM_175_A2_B11_MR	g4063756	BLASTN	477	2e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11831	GM_175_A2_C03_MR	g2462058	BLASTX	170	4e-27	56	(Y13389) reverse transcriptase [Antirrhinum majus]
11832	GM_175_A2_C07_T7	g3212847	BLASTX	310	6e-27	61	(AC004005) putative polygalacturonase [Arabidopsis thaliana]
11833	GM_175_A2_C08_MR	g905361	BLASTX	566	4e-54	92	(U22103) gag-protease polyprotein [Glycine max]
11834	GM_175_A2_D04_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11835	GM_175_A2_D06_T7	g3650039	BLASTX	150	7e-09	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11836	GM_175_A2_E07_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
11837	GM_175_A2_E11_MR	g3915165	BLASTX	205	4e-15	78	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 2792520 (AF042320) tryptophan synthase beta subunit [Camptotheca acuminata] >gi 2801771 (AF042321) tryptophan synthase beta [Camptotheca acuminata]
11838	GM_175_A2_F06_MR	g507910	BLASTN	566	6e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11839	GM_175_A2_F10_T7	g2995405	BLASTX	256	5e-20	62	(Y12432) polyprotein [Ananas comosus]
11840	GM_175_A2_G02_T7	g4063760	BLASTX	177	2e-11	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11841	GM_175_A2_G03_MR	g507910	BLASTN	571	3e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11842	GM_175_A2_G03_T7	g4063760	BLASTX	279	3e-22	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11843	GM_175_A2_G04_T7	g3142328	BLASTN	859	6e-32	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11844	GM_175_A2_G06_MR	g1142703	BLASTN	293	8e-17	75	Glycine max satellite STR120-B.1.
11845	GM_175_A2_G06_T7	g2995405	BLASTX	161	7e-16	65	(Y12432) polyprotein [Ananas comosus]
11846	GM_175_A2_H04_MR	g975703	BLASTN	958	2e-36	74	P.sativum GR gene
11847	GM_175_A2_H05_MR	g99730	BLASTX	109	8e-11	48	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
11848	GM_175_A2_H10_MR	g3319362	BLASTX	292	8e-31	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11849	GM_175_A2_H11_MR	g507910	BLASTN	400	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11850	GM_175_B1_A02_MR	g4063760	BLASTX	162	8e-10	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11851	GM_175_B1_A05_T7	g2997591	BLASTX	409	2e-37	83	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]
11852	GM_175_B1_A09_T7	g3645899	BLASTX	222	3e-16	42	(U68408) 5' end not determined experimentally [Zea mays]
11853	GM_175_B1_A11_MR	g4063760	BLASTX	275	7e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11854	GM_175_B1_A11_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11855	GM_175_B1_B01_T7	g2224927	BLASTX	422	8e-39	80	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]
11856	GM_175_B1_B08_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11857	GM_175_B1_B12_MR	g3777527	BLASTX	178	2e-11	50	(AF053008) gag-pol polyprotein [Glycine max]
11858	GM_175_B1_C01_T7	g2522230	BLASTX	365	9e-33	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11859	GM_175_B1_C03_T7	g3142328	BLASTN	1175	3e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11860	GM_175_B1_C04_T7	g2335061	BLASTN	476	2e-14	65	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
11861	GM_175_B1_C06_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11862	GM_175_B1_C10_T7	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11863	GM_175_B1_C12_T7	g1666236	BLASTX	169	1e-11	32	(U76261) unknown [Hordeum vulgare]
11864	GM_175_B1_D01_T7	g3599418	BLASTN	1240	3e-49	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11865	GM_175_B1_D04_MR	g3142289	BLASTX	427	2e-39	68	(AC002411) Strong similarity to beta-keto-Coa synthase gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
11866	GM_175_B1_D05_T7	g3176774	BLASTN	371	1e-10	60	Homo sapiens allele 3 fragile site locus (FRA10B) minisatellite, 3' sequence
11867	GM_175_B1_D06_MR	g3810596	BLASTX	266	5e-21	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11868	GM_175_B1_E01_T7	g2735745	BLASTN	364	9e-10	60	Oncorhynchus kisutch growth hormone 1 gene, intron C, complete sequence
11869	GM_175_B1_E08_MR	g3269281	BLASTX	139	8e-11	50	(AL030978) putative protein [Arabidopsis thaliana]
11870	GM_175_B1_E11_MR	g3135962	BLASTN	490	4e-15	65	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
11871	GM_175_B1_E11_T7	g1785739	BLASTX	237	3e-19	45	(Y08502) orf240b [Arabidopsis thaliana]
11872	GM_175_B1_F01_MR	g3777527	BLASTX	239	7e-18	97	(AF053008) gag-pol polyprotein [Glycine max]
11873	GM_175_B1_F03_MR	g2995405	BLASTX	329	7e-28	55	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11874	GM_175_B1_F10_MR	g1171583	BLASTN	456	1e-13	62	P.falciparum complete gene map of plastid-like DNA (IR-A)
11875	GM_175_B1_F12_MR	g3287156	BLASTN	468	4e-14	65	Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence [Homo sapiens]
11876	GM_175_B1_G07_MR	g4063760	BLASTX	511	5e-47	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11877	GM_175_B1_G07_T7	g343537	BLASTN	416	9e-12	64	T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.
11878	GM_175_B1_G11_MR	g3322325	BLASTX	210	4e-15	60	(AE001191) ATP-dependent Clp protease subunit B (clpB) [Treponema pallidum]
11879	GM_175_B1_H06_MR	g3097320	BLASTN	1223	2e-48	84	Glycine max gene for Bd 30K, complete cds
11880	GM_175_B1_H10_MR	g3059060	BLASTN	399	6e-11	62	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
11881	GM_175_B2_A02_T7	g99729	BLASTX	138	2e-15	64	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
11882	GM_175_B2_A11_T7	g2642431	BLASTX	293	1e-23	67	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
11883	GM_175_B2_A12_T7	g507910	BLASTN	578	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11884	GM_175_B2_B02_T7	g2160694	BLASTX	209	2e-15	56	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
11885	GM_175_B2_C02_MR	g2558962	BLASTX	306	2e-26	98	(AF025667) histone H2B1 [Gossypium hirsutum]
11886	GM_175_B2_C08_T7	g3777527	BLASTX	359	1e-30	89	(AF053008) gag-pol polyprotein [Glycine max]
11887	GM_175_B2_D05_T7	g4063760	BLASTX	251	3e-19	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11888	GM_175_B2_D10_MR	g3142328	BLASTN	400	4e-11	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11889	GM_175_B2_E04_MR	g3193221	BLASTN	401	4e-11	82	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
11890	GM_175_B2_E07_T7	g507910	BLASTN	399	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11891	GM_175_B2_F06_MR	g3548808	BLASTX	285	1e-23	80	(AC005313) unknown protein [Arabidopsis thaliana]
11892	GM_175_B2_F07_T7	g3777527	BLASTX	409	6e-36	91	(AF053008) gag-pol polyprotein [Glycine max]
11893	GM_175_B2_F11_MR	g905361	BLASTX	417	6e-38	84	(U22103) gag-protease polyprotein [Glycine max]
11894	GM_175_B2_G09_MR	g3650039	BLASTX	206	7e-15	46	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11895	GM_175_B2_H06_T7	g100484	BLASTX	134	4e-14	57	hypothetical protein - garden snapdragon
11896	GM_175_B2_H11_MR	g3142328	BLASTN	452	2e-13	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11897	GM_176_A1_A04_T7	g18559	BLASTN	816	6e-30	79	G.max gene for catalase
11898	GM_176_A1_A09_MR	g18559	BLASTN	661	6e-25	72	G.max gene for catalase
11899	GM_176_A1_A11_T7	g4063760	BLASTX	310	1e-25	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11900	GM_176_A1_A12_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11901	GM_176_A1_B04_MR	g4063760	BLASTX	311	1e-25	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11902	GM_176_A1_B04_T7	g4063760	BLASTX	253	1e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11903	GM_176_A1_B06_T7	g507910	BLASTN	370	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence
11904	GM_176_A1_B07_T7	g2586082	BLASTX	205	3e-14	44	(U72725) retrofit [Oryza longistaminata]
11905	GM_176_A1_B08_T7	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11906	GM_176_A1_B09_T7	g1142702	BLASTN	256	3e-12	72	Glycine max satellite STR120-A.4.
11907	GM_176_A1_B11_T7	g3047073	BLASTX	180	4e-12	44	(AF058825) contains similarity to retrotransposon-like proteins [Arabidopsis thaliana]
11908	GM_176_A1_C02_T7	g1040717	BLASTN	360	4e-10	66	D.polychroa microsatellite sequence (clone Dp ch1 F3)
11909	GM_176_A1_C03_T7	g3097320	BLASTN	861	6e-32	78	Glycine max gene for Bd 30K, complete cds
11910	GM_176_A1_C06_T7	g3142328	BLASTN	793	6e-45	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11911	GM_176_A1_C10_T7	g905361	BLASTX	431	1e-39	93	(U22103) gag-protease polyprotein [Glycine max]
11912	GM_176_A1_C11_T7	g3645899	BLASTX	283	9e-23	53	(U68408) 5' end not determined experimentally [Zea mays]
11913	GM_176_A1_D01_T7	g2190548	BLASTX	153	3e-16	49	(AC001229) EST gb ATTS1121 comes from this gene. [Arabidopsis thaliana]
11914	GM_176_A1_D04_MR	g507910	BLASTN	354	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11915	GM_176_A1_D06_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11916	GM_176_A1_D12_T7	g2231046	BLASTX	181	2e-12	91	(Y12618) PPF-1 protein [Pisum sativum]
11917	GM_176_A1_E02_T7	g3142328	BLASTN	758	2e-27	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11918	GM_176_A1_E06_T7	g1769898	BLASTX	265	3e-21	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11919	GM_176_A1_E07_T7	g3650035	BLASTX	225	1e-16	43	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
11920	GM_176_A1_E11_T7	g2522228	BLASTX	158	3e-10	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
11921	GM_176_A1_F04_T7	g2522227	BLASTX	147	3e-09	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
11922	GM_176_A1_F05_T7	g1769899	BLASTX	146	1e-09	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11923	GM_176_A1_F06_T7	g2252828	BLASTX	142	4e-09	37	(AF013293) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11924	GM_176_A1_F10_MR	g2244878	BLASTX	284	3e-23	71	(Z97338) hypothetical protein [Arabidopsis thaliana]
11925	GM_176_A1_F11_T7	g3135269	BLASTX	214	2e-15	44	(AC003058) unknown protein [Arabidopsis thaliana]
11926	GM_176_A1_G01_T7	g507910	BLASTN	535	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11927	GM_176_A1_G10_T7	g1167523	BLASTX	234	2e-17	51	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11928	GM_176_A1_H02_MR	g2462749	BLASTX	220	2e-16	60	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
11929	GM_176_A1_H02_T7	g13581	BLASTN	390	2e-11	66	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
11930	GM_176_A1_H06_MR	g2462749	BLASTX	183	2e-12	55	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
11931	GM_176_A1_H07_T7	g2246449	BLASTN	486	6e-15	67	Lycopersicon esculentum copia-like retrotransposon ToRTL1, 3-hydroxy-3-methylglutaryl CoA reductase 2 (HMG2) gene, complete cds.
11932	GM_176_A2_A05_MR	g507910	BLASTN	498	7e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11933	GM_176_A2_A05_T7	g507910	BLASTN	591	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11934	GM_176_A2_A08_T7	g2914758	BLASTN	398	6e-11	58	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
11935	GM_176_A2_B05_MR	g18559	BLASTN	828	2e-30	68	G.max gene for catalase
11936	GM_176_A2_B05_T7	g2995405	BLASTX	497	5e-46	56	(Y12432) polyprotein [Ananas comosus]
11937	GM_176_A2_C04_T7	g3142328	BLASTN	742	4e-53	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11938	GM_176_A2_C08_T7	g2995405	BLASTX	282	6e-27	46	(Y12432) polyprotein [Ananas comosus]
11939	GM_176_A2_C09_MR	g3142328	BLASTN	1061	4e-41	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11940	GM_176_A2_D07_MR	g1666171	BLASTX	167	2e-11	85	(Y09105) unknown [Nicotiana plumbaginifolia]
11941	GM_176_A2_D08_MR	g1707642	BLASTX	216	1e-15	33	(Y07748) TMK [Oryza sativa]
11942	GM_176_A2_D09_MR	g2852447	BLASTX	174	2e-16	57	(D88206) protein kinase [Arabidopsis thaliana]
11943	GM_176_A2_E01_T7	g4063760	BLASTX	198	1e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11944	GM_176_A2_E03_T7	g4063760	BLASTX	273	1e-21	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11945	GM_176_A2_E05_T7	g421954	BLASTX	160	1e-18	43	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
11946	GM_176_A2_F02_T7	g1769897	BLASTX	169	5e-11	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11947	GM_176_A2_G02_T7	g4063760	BLASTX	175	3e-11	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
11948	GM_176_A2_G04_T7	g2979597	BLASTN	349	1e-08	67	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
11949	GM_176_A2_G07_MR	g2642431	BLASTX	224	3e-16	45	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
11950	GM_176_A2_G09_T7	g2522228	BLASTX	348	9e-44	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
11951	GM_176_A2_H03_MR	g3142328	BLASTN	796	4e-29	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11952	GM_176_A2_H10_T7	g3142328	BLASTN	657	9e-23	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11953	GM_176_B1_A03_MR	g3004480	BLASTX	96	5e-11	51	(AJ228333) reverse transcriptase [Pinus elliottii]
11954	GM_176_B1_A05_T7	g1418331	BLASTX	207	4e-15	39	(X95909) receptor like protein kinase [Arabidopsis thaliana]
11955	GM_176_B1_A09_MR	g4050011	BLASTN	411	1e-11	60	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
11956	GM_176_B1_B01_MR	g3860272	BLASTX	157	1e-13	96	(AC005824) putative suppressor protein [Arabidopsis thaliana]
11957	GM_176_B1_B04_T7	g4106406	BLASTN	405	4e-12	64	Sorghum bicolor centromere specific element pHind22, complete sequence
11958	GM_176_B1_B09_MR	g100484	BLASTX	298	1e-24	58	hypothetical protein - garden snapdragon
11959	GM_176_B1_C05_T7	g4063760	BLASTX	270	2e-21	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11960	GM_176_B1_C08_MR	g905361	BLASTX	591	1e-56	95	(U22103) gag-protease polyprotein [Glycine max]
11961	GM_176_B1_D02_T7	g4063760	BLASTX	215	5e-27	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11962	GM_176_B1_D10_T7	g3135962	BLASTN	355	5e-09	67	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
11963	GM_176_B1_E02_MR	g3282250	BLASTX	193	7e-14	67	(AF009337) CDPK-related protein kinase [Tradescantia virginiana]
11964	GM_176_B1_E03_T7	g2708331	BLASTX	228	5e-17	53	(AF038557) ligand gated channel-like protein [Arabidopsis thaliana]
11965	GM_176_B1_E10_MR	g2618683	BLASTN	380	4e-10	67	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]
11966	GM_176_B1_F04_MR	g3645899	BLASTX	212	3e-15	41	(U68408) 5' end not determined experimentally [Zea mays]
11967	GM_176_B1_F08_MR	g507910	BLASTN	571	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11968	GM_176_B1_F10_T7	g3097320	BLASTN	429	2e-12	67	Glycine max gene for Bd 30K, complete cds
11969	GM_176_B1_G01_T7	g13373	BLASTN	347	1e-09	63	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
11970	GM_176_B1_G02_T7	g4063760	BLASTX	265	7e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
11971	GM_176_B1_G05_MR	g2832608	BLASTX	167	2e-11	33	(AL021637) leucine rich repeat-like protein (fragment) [Arabidopsis thaliana]
11972	GM_176_B1_H03_MR	g2967687	BLASTX	250	7e-20	52	(AF035630) epidermal germacrene C synthase [Lycopersicon esculentum]
11973	GM_176_B1_H03_T7	g1769898	BLASTX	335	6e-29	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11974	GM_176_B1_H09_MR	g3319362	BLASTX	170	2e-14	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11975	GM_176_B2_A05_T7	g3461840	BLASTX	249	6e-19	48	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
11976	GM_176_B2_B06_T7	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11977	GM_176_B2_C09_T7	g507910	BLASTN	391	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11978	GM_176_B2_C11_T7	g507910	BLASTN	351	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11979	GM_176_B2_C12_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11980	GM_176_B2_D12_T7	g2809246	BLASTX	206	4e-15	51	(AC002560) F24O1.15 [Arabidopsis thaliana]
11981	GM_176_B2_F06_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11982	GM_176_B2_F08_T7	g18683	BLASTN	456	1e-13	75	G.max N-20t gene
11983	GM_176_B2_F11_T7	g3184283	BLASTX	160	4e-13	80	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
11984	GM_176_B2_G06_T7	g3142328	BLASTN	644	4e-22	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11985	GM_176_B2_G11_T7	g3142328	BLASTN	790	8e-29	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11986	GM_177_A2_A02_MR	g2792208	BLASTX	190	3e-14	38	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
11987	GM_177_A2_A11_MR	g116570	BLASTX	146	1e-09	30	CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) gi 105602 pir A32760 cellular nucleic acid-binding protein - human gi 1083628 pir JC2512 cellular nucleic acid binding protein - rat gi 643576 (M28372) SRE-binding protein [Homo sapiens] gi 790571 (U19765) nucleic acid binding protein [Homo sapiens] gi 809511 gnl PID d1008807 (D45254) Cellular Nucleic Acid Binding Protein [Rattus rattus]
11988	GM_177_A2_B05_MR	g2522228	BLASTX	252	1e-20	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
11989	GM_177_A2_B09_MR	g1742955	BLASTX	253	8e-20	68	(Z71446) CLC-b chloride channel protein [Arabidopsis thaliana]
11990	GM_177_A2_B10_MR	g2464905	BLASTX	210	2e-16	55	(Z99708) minor allergen [Arabidopsis thaliana]
11991	GM_177_A2_C04_MR	g4063760	BLASTX	486	2e-44	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11992	GM_177_A2_C05_MR	g2911054	BLASTX	215	1e-20	42	(AL021961) putative protein [Arabidopsis thaliana]
11993	GM_177_A2_C09_MR	g4033335	BLASTX	138	9e-15	70	(AJ012745) RH27 helicase [Arabidopsis thaliana]
11994	GM_177_A2_D04_MR	g507910	BLASTN	512	2e-16	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11995	GM_177_A2_D07_MR	g3287270	BLASTX	199	1e-13	51	(Y09533) involved in starch metabalism [Solanum tuberosum]
11996	GM_177_A2_D09_MR	g719276	BLASTN	735	3e-26	67	Arabidopsis thaliana SABRE gene, exon 1
11997	GM_177_A2_E02_MR	g3894211	BLASTN	428	3e-12	62	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
11998	GM_177_A2_E03_MR	g905360	BLASTN	763	9e-28	87	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
11999	GM_177_A2_F03_MR	g4038056	BLASTX	177	1e-11	43	(AC005897) putative transposon [Arabidopsis thaliana]
12000	GM_177_A2_F05_MR	g3645899	BLASTX	277	4e-25	57	(U68408) 5' end not determined experimentally [Zea mays]
12001	GM_177_A2_H09_MR	g1666236	BLASTX	186	2e-13	33	(U76261) unknown [Hordeum vulgare]
12002	GM_177_A2_H11_MR	g2522227	BLASTX	204	1e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12003	GM_177_B2_A01_T7	g1769898	BLASTX	149	8e-09	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12004	GM_177_B2_A02_T7	g3355478	BLASTX	146	4e-09	43	(AC004218) hypothetical protein [Arabidopsis thaliana]
12005	GM_177_B2_A03_T7	g3377848	BLASTX	165	7e-11	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
12006	GM_177_B2_A04_MR	g1934877	BLASTN	408	2e-11	63	Human DNA sequence from PAC 447N6 on chromosome X contains ESTs and STS
12007	GM_177_B2_A05_T7	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
12008	GM_177_B2_A06_T7	g905361	BLASTX	345	6e-30	95	(U22103) gag-protease polyprotein [Glycine max]
12009	GM_177_B2_A08_T7	g3047086	BLASTX	222	7e-18	42	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]
12010	GM_177_B2_A09_T7	g2760839	BLASTX	421	8e-41	63	(AC003105) putative receptor kinase [Arabidopsis thaliana]
12011	GM_177_B2_A12_T7	g3645899	BLASTX	282	1e-22	48	(U68408) 5' end not determined experimentally [Zea mays]
12012	GM_177_B2_B03_T7	g2995405	BLASTX	472	3e-43	56	(Y12432) polyprotein [Ananas comosus]
12013	GM_177_B2_B06_MR	g18559	BLASTN	354	5e-09	64	G.max gene for catalase
12014	GM_177_B2_B12_MR	g4150930	BLASTN	381	4e-10	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12015	GM_177_B2_C04_MR	g905361	BLASTX	422	2e-38	95	(U22103) gag-protease polyprotein [Glycine max]
12016	GM_177_B2_C04_T7	g3777527	BLASTX	592	2e-55	89	(AF053008) gag-pol polyprotein [Glycine max]
12017	GM_177_B2_C10_MR	g2501495	BLASTX	185	4e-13	36	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 6 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 6) gi 542016 pir S41952 UTP-glucose glucosyltransferase - cassava (fragment) gi 453251 (X77463) UTP-glucose glucosyltransferase [Manihot esculenta]
12018	GM_177_B2_C12_MR	g2522228	BLASTX	242	2e-19	61	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12019	GM_177_B2_D01_T7	g4063760	BLASTX	568	4e-53	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12020	GM_177_B2_D02_MR	g507910	BLASTN	477	6e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12021	GM_177_B2_D10_MR	g2708744	BLASTX	171	2e-11	76	(AC003952) putative Bop-like zinc-finger protein [Arabidopsis thaliana]
12022	GM_177_B2_E03_T7	g2995405	BLASTX	390	2e-34	57	(Y12432) polyprotein [Ananas comosus]
12023	GM_177_B2_E05_MR	g3142328	BLASTN	664	4e-23	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12024	GM_177_B2_E06_T7	g531389	BLASTX	166	4e-10	32	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
12025	GM_177_B2_E08_T7	g3650039	BLASTX	187	8e-13	51	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12026	GM_177_B2_E10_MR	g507910	BLASTN	520	7e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12027	GM_177_B2_E10_T7	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12028	GM_177_B2_E11_T7	g3873182	BLASTN	396	7e-11	64	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
12029	GM_177_B2_E12_T7	g1840106	BLASTN	470	3e-15	61	Human fragile site locus (FRA16B) minisatellite repeat
12030	GM_177_B2_F06_T7	g1236920	BLASTN	402	3e-11	59	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
12031	GM_177_B2_F12_MR	g3915037	BLASTX	329	6e-28	84	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 2570067 gnl PID e1154401 (AJ001071) second sucrose synthase [Pisum sativum]
12032	GM_177_B2_G05_T7	g507910	BLASTN	445	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12033	GM_177_B2_G08_T7	g4050011	BLASTN	639	7e-22	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12034	GM_177_B2_H06_T7	g3097320	BLASTN	1350	4e-54	79	Glycine max gene for Bd 30K, complete cds
12035	GM_177_B2_H09_T7	g507910	BLASTN	431	7e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12036	GM_178_A1_A03_MR	g1066856	BLASTN	698	2e-24	73	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
12037	GM_178_A1_A05_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12038	GM_178_A1_B01_T7	g1865677	BLASTX	156	3e-09	94	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
12039	GM_178_A1_B02_T7	g3645899	BLASTX	166	9e-19	46	(U68408) 5' end not determined experimentally [Zea mays]
12040	GM_178_A1_B03_MR	g2522228	BLASTX	341	3e-30	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
12041	GM_178_A1_B07_MR	g3695395	BLASTX	205	8e-15	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12042	GM_178_A1_B08_MR	g4063760	BLASTX	155	2e-18	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12043	GM_178_A1_B10_MR	g3860246	BLASTX	144	8e-09	33	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
12044	GM_178_A1_B10_T7	g413796	BLASTN	355	5e-09	65	Cloning vector pMAMneoBlue, complete sequence
12045	GM_178_A1_C06_MR	g81800	BLASTX	179	4e-13	66	nodulin-26 precursor - soybean
12046	GM_178_A1_C09_MR	g4063760	BLASTX	332	6e-28	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12047	GM_178_A1_C11_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12048	GM_178_A1_C11_T7	g4063760	BLASTX	367	1e-31	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12049	GM_178_A1_D01_T7	g2316016	BLASTX	174	6e-11	60	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
12050	GM_178_A1_D03_T7	g18559	BLASTN	1521	5e-62	90	G.max gene for catalase
12051	GM_178_A1_D11_MR	g3097320	BLASTN	814	8e-30	78	Glycine max gene for Bd 30K, complete cds
12052	GM_178_A1_D11_T7	g3930515	BLASTX	122	7e-10	42	(AF059674) putative gag protein [Nicotiana tabacum]
12053	GM_178_A1_E05_MR	g18559	BLASTN	842	4e-31	79	G.max gene for catalase
12054	GM_178_A1_E05_T7	g2522228	BLASTX	124	6e-15	41	(AB007466) reverse transcriptase-like protein [Vicia faba]
12055	GM_178_A1_E06_MR	g3377855	BLASTX	188	9e-14	40	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
12056	GM_178_A1_E09_MR	g4063760	BLASTX	294	6e-24	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12057	GM_178_A1_E09_T7	g507910	BLASTN	444	2e-13	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12058	GM_178_A1_E12_MR	g4063760	BLASTX	398	5e-35	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12059	GM_178_A1_G05_MR	g3241923	BLASTN	370	1e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]
12060	GM_178_A1_G12_MR	g3810596	BLASTX	182	4e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12061	GM_178_A1_H02_MR	g2129618	BLASTX	211	3e-15	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12062	GM_178_A1_H04_MR	g1236920	BLASTN	371	7e-10	60	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
12063	GM_178_A1_H08_MR	g4115365	BLASTX	155	2e-18	43	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12064	GM_178_A1_H09_MR	g3513747	BLASTX	315	6e-26	53	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
12065	GM_178_A1_H09_T7	g4160362	BLASTN	391	1e-10	65	Saccharomyces cerevisiae complete mitochondrial genome
12066	GM_178_A1_H10_T7	g3323609	BLASTX	181	8e-13	59	(AF064093) KE04p [Homo sapiens]
12067	GM_178_A1_H11_MR	g3941725	BLASTN	355	5e-09	66	Homo sapiens clone BAC 72m22 chromosome 8 map 8p21, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12068	GM_178_A1_H12_MR	g2181190	BLASTX	260	1e-21	70	(Y12531) serine/threonine kinase [Brassica oleracea]
12069	GM_178_A1_H12_T7	g1783312	BLASTX	150	6e-10	54	(X98520) receptor-like kinase [Brassica oleracea]
12070	GM_178_B1_A07_MR	g3097320	BLASTN	712	3e-25	78	Glycine max gene for Bd 30K, complete cds
12071	GM_178_B1_B01_MR	g2522228	BLASTX	173	1e-11	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
12072	GM_178_B1_B06_MR	g1769897	BLASTX	172	2e-11	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12073	GM_178_B1_C01_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
12074	GM_178_B1_C01_T7	g507910	BLASTN	363	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12075	GM_178_B1_C06_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12076	GM_178_B1_D05_T7	g1946279	BLASTX	224	2e-22	50	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
12077	GM_178_B1_D12_T7	g2497702	BLASTX	140	5e-09	47	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR gi 2121019 pir I40710 outer membrane lipoprotein - Citrobacter freundii gi 717136 (U21727) lipocalin precursor [Citrobacter freundii]
12078	GM_178_B1_E02_T7	g4063760	BLASTX	251	2e-19	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12079	GM_178_B1_E03_T7	g99922	BLASTX	346	9e-31	75	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12080	GM_178_B1_E05_MR	g4092470	BLASTN	559	3e-18	70	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
12081	GM_178_B1_F04_T7	g4092471	BLASTN	429	2e-12	67	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
12082	GM_178_B1_G04_MR	g1480927	BLASTN	376	4e-10	98	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
12083	GM_178_B1_G06_MR	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12084	GM_178_B1_G06_T7	g3142328	BLASTN	739	2e-26	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12085	GM_178_B1_H02_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12086	GM_178_B1_H05_T7	g1350680	BLASTX	324	2e-28	77	60S RIBOSOMAL PROTEIN L1
12087	GM_178_B1_H11_T7	g2522230	BLASTX	167	8e-12	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12088	GM_178_B2_F05_MR	g2429543	BLASTX	190	8e-13	42	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
12089	GM_179_A1_A04_T7	g4006831	BLASTX	203	3e-14	42	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
12090	GM_179_A1_A05_T7	g3402709	BLASTX	252	6e-20	43	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12091	GM_179_A1_A09_MR	g3777527	BLASTX	561	3e-52	89	(AF053008) gag-pol polyprotein [Glycine max]
12092	GM_179_A1_B07_T7	g2914758	BLASTN	361	3e-09	63	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
12093	GM_179_A1_C09_T7	g3645899	BLASTX	155	3e-09	38	(U68408) 5' end not determined experimentally [Zea mays]
12094	GM_179_A1_D04_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12095	GM_179_A1_D10_MR	g99726	BLASTX	199	9e-25	49	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
12096	GM_179_A1_E05_MR	g4063760	BLASTX	278	4e-22	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12097	GM_179_A1_E05_T7	g3687234	BLASTX	191	6e-13	50	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
12098	GM_179_A1_E07_T7	g4038056	BLASTX	271	1e-21	47	(AC005897) putative transposon [Arabidopsis thaliana]
12099	GM_179_A1_E09_T7	g3142328	BLASTN	653	3e-33	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12100	GM_179_A1_E10_MR	g1666236	BLASTX	108	7e-10	33	(U76261) unknown [Hordeum vulgare]
12101	GM_179_A1_F04_MR	g3650039	BLASTX	224	8e-17	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12102	GM_179_A1_F05_MR	g2073447	BLASTN	487	6e-15	66	L.japonicus gln1, pge1 & krm genes
12103	GM_179_A1_F06_T7	g2443320	BLASTX	334	4e-28	54	(D85597) polyprotein [Oryza australiensis]
12104	GM_179_A1_F10_MR	g1769899	BLASTX	183	1e-13	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12105	GM_179_A1_G01_T7	g4063756	BLASTN	403	4e-11	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12106	GM_179_A1_G06_MR	g2522226	BLASTN	568	9e-19	70	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
12107	GM_179_A1_G07_MR	g4038056	BLASTX	241	2e-18	46	(AC005897) putative transposon [Arabidopsis thaliana]
12108	GM_179_A1_H01_MR	g505129	BLASTN	351	7e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12109	GM_179_A1_H02_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12110	GM_179_A2_A03_MR	g3063444	BLASTX	247	3e-20	70	(AC003981) F22O13.5 [Arabidopsis thaliana]
12111	GM_179_A2_A09_MR	g99922	BLASTX	426	3e-39	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12112	GM_179_A2_B03_MR	g629693	BLASTX	304	2e-26	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12113	GM_179_A2_B09_MR	g3650039	BLASTX	227	4e-17	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12114	GM_179_A2_C01_MR	g1045530	BLASTN	375	4e-10	63	Magnaporthe grisea host-species specificity (Pwl1) gene, complete cds.
12115	GM_179_A2_C04_MR	g4150930	BLASTN	349	1e-08	60	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12116	GM_179_A2_C11_MR	g12212	BLASTN	982	1e-42	92	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
12117	GM_179_A2_D05_MR	g18695	BLASTN	394	6e-11	69	Soybean nodulin 22 gene
12118	GM_179_A2_D08_MR	g2462058	BLASTX	150	1e-13	45	(Y13389) reverse transcriptase [Antirrhinum majus]
12119	GM_179_A2_E03_MR	g1167523	BLASTX	246	1e-18	39	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12120	GM_179_A2_E07_MR	g2055374	BLASTX	145	1e-20	63	(U29095) serine-threonine protein kinase [Triticum aestivum]
12121	GM_179_A2_E09_MR	g99755	BLASTX	359	1e-31	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12122	GM_179_A2_F03_MR	g3097320	BLASTN	632	1e-21	80	Glycine max gene for Bd 30K, complete cds
12123	GM_179_A2_F11_MR	g2522228	BLASTX	392	1e-35	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
12124	GM_179_A2_G05_MR	g3097320	BLASTN	445	4e-13	71	Glycine max gene for Bd 30K, complete cds
12125	GM_179_A2_H01_MR	g1769898	BLASTX	318	5e-27	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12126	GM_179_A2_H02_MR	g1040717	BLASTN	338	4e-09	64	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12127	GM_179_A2_H10_MR	g3810596	BLASTX	98	5e-09	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12128	GM_179_B1_A02_MR	g3461834	BLASTN	364	2e-09	68	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]
12129	GM_179_B1_A04_T7	g507910	BLASTN	372	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12130	GM_179_B1_A05_T7	g2924729	BLASTN	875	2e-32	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
12131	GM_179_B1_A06_MR	g507910	BLASTN	580	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12132	GM_179_B1_A06_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12133	GM_179_B1_A09_T7	g2522228	BLASTX	401	1e-36	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
12134	GM_179_B1_B02_T7	g505129	BLASTN	379	4e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12135	GM_179_B1_B03_T7	g1666236	BLASTX	101	2e-10	31	(U76261) unknown [Hordeum vulgare]
12136	GM_179_B1_B04_MR	g3845197	BLASTN	349	1e-08	67	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12137	GM_179_B1_B04_T7	g3947733	BLASTX	237	2e-18	42	(AJ009719) NL25 [Solanum tuberosum]
12138	GM_179_B1_B05_MR	g3777527	BLASTX	480	2e-43	96	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12139	GM_179_B1_B11_T7	g3142328	BLASTN	1808	3e-75	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12140	GM_179_B1_C02_T7	g3142328	BLASTN	580	3e-41	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12141	GM_179_B1_C03_MR	g4063760	BLASTX	198	1e-13	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12142	GM_179_B1_C03_T7	g507910	BLASTN	585	8e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12143	GM_179_B1_C08_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12144	GM_179_B1_C11_T7	g2160165	BLASTX	274	6e-22	44	(AC000132) F21M12.11 gene product [Arabidopsis thaliana]
12145	GM_179_B1_C12_MR	g4063760	BLASTX	186	2e-12	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12146	GM_179_B1_C12_T7	g507910	BLASTN	621	2e-21	86	Glycine max BSR-101 satellite SB92 genomic sequence.
12147	GM_179_B1_D01_MR	g2832404	BLASTX	200	1e-17	60	(Y14207) R2R3-MYB transcription factor [Arabidopsis thaliana]
12148	GM_179_B1_D03_T7	g4156188	BLASTN	597	6e-20	67	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
12149	GM_179_B1_D04_T7	g2801536	BLASTX	99	1e-09	80	(AF039531) lysophospholipase homolog [Oryza sativa]
12150	GM_179_B1_D07_T7	g3885328	BLASTX	105	1e-12	71	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]
12151	GM_179_B1_E02_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12152	GM_179_B1_E02_T7	g3777527	BLASTX	378	1e-32	53	(AF053008) gag-pol polyprotein [Glycine max]
12153	GM_179_B1_E04_T7	g1236920	BLASTN	366	1e-09	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
12154	GM_179_B1_E07_T7	g3142328	BLASTN	890	2e-33	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12155	GM_179_B1_E10_MR	g2342686	BLASTX	143	7e-09	45	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
12156	GM_179_B1_E10_T7	g3650039	BLASTX	190	4e-13	36	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12157	GM_179_B1_F02_T7	g2245003	BLASTX	278	3e-23	44	(Z97341) similarity to a membrane-associated salt-inducible protein - Nicotiana tabacum [Arabidopsis thaliana]
12158	GM_179_B1_F04_T7	g421955	BLASTX	232	2e-18	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
12159	GM_179_B1_F09_MR	g3645899	BLASTX	279	2e-22	55	(U68408) 5' end not determined experimentally [Zea mays]
12160	GM_179_B1_F11_MR	g507910	BLASTN	353	2e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12161	GM_179_B1_G02_MR	g2995405	BLASTX	298	1e-24	62	(Y12432) polyprotein [Ananas comosus]
12162	GM_179_B1_G03_T7	g2191181	BLASTN	708	6e-25	69	Arabidopsis thaliana BAC TM021B04

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12163	GM_179_B1_G05_T7	g4056428	BLASTX	159	7e-10	82	(AC005322) Similar to gb U43629 integral membrane protein from Beta vulgaris and a member of sugar transporter family PF 00083. [Arabidopsis thaliana]
12164	GM_179_B1_G07_T7	g905361	BLASTX	188	6e-13	29	(U22103) gag-protease polyprotein [Glycine max]
12165	GM_179_B1_G08_MR	g984307	BLASTN	426	3e-12	82	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso...
12166	GM_179_B1_G10_MR	g905361	BLASTX	154	3e-09	40	(U22103) gag-protease polyprotein [Glycine max]
12167	GM_179_B1_H02_T7	g4063756	BLASTN	487	6e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12168	GM_179_B1_H09_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12169	GM_179_B2_A03_MR	g3133272	BLASTN	386	2e-10	62	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence.
12170	GM_179_B2_A03_T7	g226407	BLASTX	111	8e-12	48	retrotransposon del1-46 [Lilium henryi]
12171	GM_179_B2_A06_MR	g3319362	BLASTX	194	2e-13	32	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12172	GM_179_B2_A06_T7	g1755162	BLASTX	332	6e-42	72	(U75192) germin-like protein [Arabidopsis thaliana]
12173	GM_179_B2_A07_T7	g3142328	BLASTN	1494	7e-61	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12174	GM_179_B2_A11_MR	g2980770	BLASTX	362	1e-32	64	(AL022198) putative protein kinase [Arabidopsis thaliana]
12175	GM_179_B2_A11_T7	g4063760	BLASTX	186	1e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12176	GM_179_B2_B04_T7	g3810596	BLASTX	266	4e-21	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12177	GM_179_B2_B06_T7	g18559	BLASTN	435	2e-20	73	G.max gene for catalase
12178	GM_179_B2_B07_T7	g3510505	BLASTX	115	5e-14	48	(AF030881) pol polyprotein [Fugu rubripes]
12179	GM_179_B2_B09_T7	g507910	BLASTN	446	1e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12180	GM_179_B2_B10_T7	g905361	BLASTX	330	3e-28	75	(U22103) gag-protease polyprotein [Glycine max]
12181	GM_179_B2_B12_T7	g18559	BLASTN	984	1e-37	77	G.max gene for catalase
12182	GM_179_B2_C01_T7	g3513747	BLASTX	234	5e-24	48	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
12183	GM_179_B2_C03_MR	g2129618	BLASTX	190	6e-13	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12184	GM_179_B2_C04_MR	g3021283	BLASTX	312	4e-26	70	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12185	GM_179_B2_C04_T7	g3142328	BLASTN	701	9e-25	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12186	GM_179_B2_C06_MR	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12187	GM_179_B2_C10_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12188	GM_179_B2_D01_T7	g1666236	BLASTX	157	3e-10	30	(U76261) unknown [Hordeum vulgare]
12189	GM_179_B2_D02_T7	g3097320	BLASTN	439	8e-13	70	Glycine max gene for Bd 30K, complete cds
12190	GM_179_B2_D05_MR	g2792161	BLASTX	170	4e-12	51	(AJ223558) reverse transcriptase [Alstroemeria ligtu]
12191	GM_179_B2_D06_MR	g3758836	BLASTN	358	4e-09	72	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
12192	GM_179_B2_D06_T7	g3142379	BLASTX	210	5e-30	91	(AF053008) envelope-like [Glycine max]
12193	GM_179_B2_D08_MR	g320565	BLASTX	215	7e-17	48	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
12194	GM_179_B2_D08_T7	g1431738	BLASTN	395	6e-11	83	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
12195	GM_179_B2_D11_T7	g2522227	BLASTX	201	2e-15	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12196	GM_179_B2_D12_MR	g3777527	BLASTX	720	3e-69	95	(AF053008) gag-pol polyprotein [Glycine max]
12197	GM_179_B2_D12_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12198	GM_179_B2_E05_MR	g18559	BLASTN	1030	1e-39	76	G.max gene for catalase
12199	GM_179_B2_E12_MR	g2801681	BLASTN	921	3e-35	86	Glycine max telomere-associated sequence STAS10
12200	GM_179_B2_F02_T7	g2864613	BLASTX	260	1e-20	61	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana]
12201	GM_179_B2_F03_MR	g1769898	BLASTX	366	2e-32	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12202	GM_179_B2_F04_MR	g3047066	BLASTX	97	8e-09	31	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
12203	GM_179_B2_G01_T7	g342959	BLASTN	361	7e-10	60	paramecium species 4.51er mt dna dimer: replication init. region, clone 3.
12204	GM_179_B2_G03_MR	g480618	BLASTX	168	6e-12	49	ATAF1 protein - Arabidopsis thaliana (fragment) gi 1345506 gnl PID e85756 (X74755) ATAF1 gene product [Arabidopsis thaliana]
12205	GM_179_B2_G03_T7	g343788	BLASTN	337	4e-09	65	Yeast (S.cerevisiae) mitochondrial cytochrome oxi1 gene, 5' flank.
12206	GM_179_B2_G06_T7	g2760322	BLASTX	256	3e-21	50	(AC002130) F1N21.7 [Arabidopsis thaliana]
12207	GM_179_B2_G07_MR	g505129	BLASTN	394	7e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12208	GM_179_B2_G09_T7	g3142328	BLASTN	548	8e-18	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12209	GM_179_B2_G10_T7	g2522228	BLASTX	256	6e-21	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
12210	GM_179_B2_H01_MR	g1769898	BLASTX	470	6e-44	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12211	GM_179_B2_H02_T7	g18559	BLASTN	459	9e-14	66	G.max gene for catalase
12212	GM_179_B2_H06_MR	g3378650	BLASTX	300	6e-26	81	(X97606) abscisic acid activated [Medicago sativa]
12213	GM_179_B2_H06_T7	g905361	BLASTX	373	5e-33	85	(U22103) gag-protease polyprotein [Glycine max]
12214	GM_179_B2_H08_T7	g2337888	BLASTN	331	6e-11	70	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]
12215	GM_179_B2_H09_T7	g3142328	BLASTN	622	4e-21	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12216	GM_179_B2_H12_MR	g130582	BLASTX	220	6e-16	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12217	GM_180_A1_A04_MR	g4063760	BLASTX	156	4e-09	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12218	GM_180_A1_A04_T7	g507910	BLASTN	473	9e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12219	GM_180_A1_A05_T7	g4106408	BLASTN	384	1e-10	78	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1
12220	GM_180_A1_A07_MR	g1732513	BLASTX	171	3e-12	67	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
12221	GM_180_A1_A12_T7	g3094014	BLASTX	167	8e-12	57	(AF060862) unknown [Homo sapiens]
12222	GM_180_A1_B01_T7	g170606	BLASTN	558	2e-18	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
12223	GM_180_A1_B05_MR	g507910	BLASTN	525	4e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12224	GM_180_A1_B07_MR	g4063756	BLASTN	448	3e-13	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12225	GM_180_A1_B07_T7	g507910	BLASTN	424	2e-12	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12226	GM_180_A1_B10_MR	g1076570	BLASTX	211	1e-16	78	homeotic protein CHB6 - carrot
12227	GM_180_A1_B12_T7	g4063760	BLASTX	100	1e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12228	GM_180_A1_C01_MR	g2801423	BLASTN	450	3e-13	63	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
12229	GM_180_A1_C07_MR	g130405	BLASTX	128	8e-11	50	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12230	GM_180_A1_C08_T7	g99922	BLASTX	187	1e-28	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12231	GM_180_A1_D01_T7	g3273387	BLASTN	368	1e-09	61	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
12232	GM_180_A1_D02_T7	g4063760	BLASTX	104	2e-11	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12233	GM_180_A1_D03_MR	g3645899	BLASTX	369	5e-32	51	(U68408) 5' end not determined experimentally [Zea mays]
12234	GM_180_A1_D04_MR	g1045614	BLASTX	285	6e-28	57	(U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]
12235	GM_180_A1_D05_MR	g3142302	BLASTX	236	1e-17	89	(AC002411) Strong similarity to myosin heavy chain gb Z34293 from A. thaliana. [Arabidopsis thaliana]
12236	GM_180_A1_E09_T7	g507910	BLASTN	479	5e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12237	GM_180_A1_E10_MR	g1666236	BLASTX	172	7e-12	32	(U76261) unknown [Hordeum vulgare]
12238	GM_180_A1_F01_T7	g2618605	BLASTN	417	8e-12	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]
12239	GM_180_A1_F02_MR	g2522228	BLASTX	416	4e-38	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
12240	GM_180_A1_F02_T7	g18559	BLASTN	755	3e-27	76	G.max gene for catalase
12241	GM_180_A1_F05_MR	g3511285	BLASTX	284	7e-24	87	(AF081534) cellulose synthase [Populus alba x Populus tremula]
12242	GM_180_A1_F05_T7	g1840106	BLASTN	388	4e-11	61	Human fragile site locus (FRA16B) minisatellite repeat
12243	GM_180_A1_F07_MR	g905360	BLASTN	640	4e-22	78	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
12244	GM_180_A1_F08_T7	g507910	BLASTN	566	6e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12245	GM_180_A1_G01_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12246	GM_180_A1_G04_MR	g2662469	BLASTX	142	1e-13	75	(AF034217) ribosomal protein S6 [Arabidopsis thaliana]
12247	GM_180_A1_G06_T7	g1040717	BLASTN	440	9e-14	62	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12248	GM_180_A1_G08_MR	g861155	BLASTX	202	1e-14	67	(Z35162) beta-fructofuranosidase; cell wall invertase I; fructosidase [Vicia faba]
12249	GM_180_A1_H02_T7	g170080	BLASTN	399	4e-11	80	Soybean seed lectin gene transposable element tgm1.
12250	GM_180_A1_H05_MR	g3777527	BLASTX	170	1e-10	31	(AF053008) gag-pol polyprotein [Glycine max]
12251	GM_180_A1_H10_MR	g1769898	BLASTX	279	8e-23	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12252	GM_180_A1_H11_MR	g18695	BLASTN	435	8e-13	74	Soybean nodulin 22 gene
12253	GM_180_A2_A01_T7	g2982283	BLASTX	165	2e-11	63	(AF051226) PREG-like protein [Picea mariana]
12254	GM_180_A2_A08_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12255	GM_180_A2_B01_T7	g4092470	BLASTN	394	9e-11	59	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
12256	GM_180_A2_B05_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12257	GM_180_A2_B06_T7	g3777527	BLASTX	301	2e-24	45	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12258	GM_180_A2_B07_T7	g13541	BLASTN	402	1e-11	62	Yeast mitochondrial HpaII-fragment 2.
12259	GM_180_A2_B08_T7	g3645899	BLASTX	228	6e-17	44	(U68408) 5' end not determined experimentally [Zea mays]
12260	GM_180_A2_B10_T7	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12261	GM_180_A2_C08_T7	g3004563	BLASTX	230	2e-18	56	(AC003673) similar to APG (non proline-rich region) [Arabidopsis thaliana] gi 3176703 (AC002392) putative proline-rich protein APG [Arabidopsis thaliana]
12262	GM_180_A2_C09_T7	g3135969	BLASTN	386	2e-10	63	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
12263	GM_180_A2_D02_T7	g4006831	BLASTX	147	1e-18	46	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
12264	GM_180_A2_D03_T7	g507910	BLASTN	624	1e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12265	GM_180_A2_D07_T7	g2522228	BLASTX	278	1e-23	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
12266	GM_180_A2_E01_T7	g170605	BLASTN	648	7e-23	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
12267	GM_180_A2_E04_T7	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12268	GM_180_A2_E05_T7	g2879886	BLASTN	270	5e-11	71	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
12269	GM_180_A2_E10_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12270	GM_180_A2_F03_T7	g2190544	BLASTX	137	3e-13	96	(AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb U40828). [Arabidopsis thaliana]
12271	GM_180_A2_F09_T7	g1666236	BLASTX	214	1e-16	31	(U76261) unknown [Hordeum vulgare]
12272	GM_180_A2_F10_T7	g4063760	BLASTX	153	7e-09	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12273	GM_180_A2_G01_T7	g100484	BLASTX	332	2e-28	41	hypothetical protein - garden snapdragon
12274	GM_180_A2_H04_T7	g3377855	BLASTX	240	2e-49	73	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
12275	GM_180_A2_H12_T7	g18683	BLASTN	659	6e-23	78	G.max N-20t gene
12276	GM_180_B1_A10_T7	g2522228	BLASTX	280	8e-24	40	(AB007466) reverse transcriptase-like protein [Vicia faba]
12277	GM_180_B1_B08_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12278	GM_180_B1_B08_T7	g3777527	BLASTX	689	7e-66	95	(AF053008) gag-pol polyprotein [Glycine max]
12279	GM_180_B1_B11_MR	g2982540	BLASTN	358	4e-09	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]
12280	GM_180_B1_C08_MR	g1363051	BLASTX	206	4e-15	52	P58 protein - bovine gi 468012 (U04631) PKR inhibitor P58 [Bos taurus]
12281	GM_180_B1_C09_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12282	GM_180_B1_D11_MR	g3283026	BLASTX	152	5e-09	42	putative transposase [Arabidopsis thaliana]
12283	GM_180_B1_D12_MR	g3461846	BLASTX	486	3e-44	59	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
12284	GM_180_B1_E07_T7	g629693	BLASTX	195	3e-14	79	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12285	GM_180_B1_E10_MR	g3097320	BLASTN	666	4e-23	76	Glycine max gene for Bd 30K, complete cds
12286	GM_180_B1_E10_T7	g1351239	BLASTX	119	2e-12	75	THIOREDOXIN M-TYPE PRECURSOR (TRX-M) gi 481594 pir S38909 thioredoxin m precursor - garden pea gi 431957 (X76269) thioredoxin m [Pisum sativum]
12287	GM_180_B1_F03_MR	g3142328	BLASTN	1691	7e-70	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12288	GM_180_B1_F04_MR	g3142328	BLASTN	842	4e-31	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12289	GM_180_B1_F08_MR	g3142328	BLASTN	1788	3e-74	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12290	GM_180_B1_F10_T7	g3142328	BLASTN	930	4e-35	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12291	GM_180_B1_F11_T7	g3777527	BLASTX	651	8e-62	92	(AF053008) gag-pol polyprotein [Glycine max]
12292	GM_180_B1_F12_MR	g507910	BLASTN	362	9e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12293	GM_180_B1_G09_T7	g3930515	BLASTX	117	1e-11	45	(AF059674) putative gag protein [Nicotiana tabacum]
12294	GM_180_B1_G10_MR	g3758836	BLASTN	351	8e-09	62	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
12295	GM_180_B1_H07_MR	g3845336	BLASTN	376	6e-10	63	Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence
12296	GM_180_B1_H08_T7	g4126312	BLASTN	364	2e-09	60	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
12297	GM_180_B2_A10_T7	g2995405	BLASTX	283	5e-23	52	(Y12432) polyprotein [Ananas comosus]
12298	GM_180_B2_B01_MR	g3097320	BLASTN	751	6e-27	77	Glycine max gene for Bd 30K, complete cds
12299	GM_180_B2_B04_T7	g3810595	BLASTX	204	3e-14	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
12300	GM_180_B2_C02_MR	g2982452	BLASTX	331	6e-28	58	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
12301	GM_180_B2_C03_T7	g3450889	BLASTX	496	1e-46	73	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
12302	GM_180_B2_C08_MR	g4038056	BLASTX	214	1e-15	40	(AC005897) putative transposon [Arabidopsis thaliana]
12303	GM_180_B2_C08_T7	g3645899	BLASTX	225	1e-16	46	(U68408) 5' end not determined experimentally [Zea mays]
12304	GM_180_B2_C12_T7	g2462056	BLASTX	188	5e-14	44	(Y13388) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12305	GM_180_B2_D05_T7	g2462935	BLASTX	255	9e-20	40	(Y12321) open reading frame 1 [Brassica oleracea]
12306	GM_180_B2_D06_MR	g1769898	BLASTX	248	3e-22	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12307	GM_180_B2_E03_T7	g18559	BLASTN	445	4e-13	65	G.max gene for catalase
12308	GM_180_B2_E07_MR	g3142328	BLASTN	859	6e-32	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12309	GM_180_B2_F01_MR	g507910	BLASTN	603	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12310	GM_180_B2_F04_T7	g1805619	BLASTX	140	5e-09	76	(D49704) OSH42 transcript [Oryza sativa]
12311	GM_180_B2_F05_MR	g3845197	BLASTN	497	2e-15	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12312	GM_180_B2_F05_T7	g2462134	BLASTX	218	2e-16	41	(Y13368) reverse transcriptase [Beta vulgaris]
12313	GM_180_B2_F06_MR	g4038056	BLASTX	302	6e-25	49	(AC005897) putative transposon [Arabidopsis thaliana]
12314	GM_180_B2_F06_T7	g13767	BLASTN	409	2e-12	66	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
12315	GM_180_B2_F07_MR	g4063760	BLASTX	464	5e-42	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12316	GM_180_B2_F07_T7	g4115365	BLASTX	170	1e-10	33	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12317	GM_180_B2_F10_T7	g3142328	BLASTN	981	2e-37	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12318	GM_180_B2_G01_T7	g2292907	BLASTX	197	1e-13	35	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
12319	GM_180_B2_H03_MR	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12320	GM_180_B2_H03_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12321	GM_180_B2_H04_T7	g100484	BLASTX	276	2e-22	53	hypothetical protein - garden snapdragon
12322	GM_180_B2_H07_MR	g3142328	BLASTN	580	3e-19	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12323	GM_180_B2_H09_MR	g2522228	BLASTX	292	4e-25	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
12324	GM_181_A1_A07_T7	g3264565	BLASTN	450	3e-13	64	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
12325	GM_181_A1_A08_MR	g4126312	BLASTN	356	5e-09	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
12326	GM_181_A1_B02_T7	g1326016	BLASTX	265	7e-21	47	TY3-2 orfB
12327	GM_181_A1_B05_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12328	GM_181_A1_B08_MR	g507910	BLASTN	472	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12329	GM_181_A1_B08_T7	g4063760	BLASTX	312	8e-26	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12330	GM_181_A1_B09_T7	g3873182	BLASTN	514	4e-16	64	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
12331	GM_181_A1_B11_MR	g3176783	BLASTN	349	2e-09	64	Homo sapiens allele 7 fragile site locus (FRA10B) minisatellite, 5' sequence
12332	GM_181_A1_C05_T7	g131289	BLASTX	703	1e-68	96	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum]
12333	GM_181_A1_C10_MR	g3176795	BLASTN	418	2e-12	65	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
12334	GM_181_A1_D05_T7	g4063760	BLASTX	572	1e-53	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12335	GM_181_A1_D06_T7	g18730	BLASTN	2017	6e-85	96	Soybean 4.5 - 5S rRNA intergenic region
12336	GM_181_A1_D08_T7	g4063760	BLASTX	334	2e-33	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12337	GM_181_A1_E05_T7	g422418	BLASTX	241	3e-18	42	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
12338	GM_181_A1_E07_T7	g3645899	BLASTX	185	3e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
12339	GM_181_A1_F02_T7	g507910	BLASTN	533	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12340	GM_181_A1_F03_T7	g2245073	BLASTN	477	2e-14	65	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
12341	GM_181_A1_F07_T7	g1633547	BLASTN	398	6e-11	69	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
12342	GM_181_A1_F08_T7	g3097320	BLASTN	401	4e-11	77	Glycine max gene for Bd 30K, complete cds
12343	GM_181_A1_F09_MR	g2462134	BLASTX	136	8e-09	40	(Y13368) reverse transcriptase [Beta vulgaris]
12344	GM_181_A1_G02_T7	g3510505	BLASTX	240	1e-25	49	(AF030881) pol polyprotein [Fugu rubripes]
12345	GM_181_A1_G04_MR	g3023281	BLASTX	315	4e-29	64	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
12346	GM_181_A1_G09_MR	g665934	BLASTX	186	9e-13	40	(U20341) ORF III [Cassava vein mosaic virus] gi 1399884 (U59751) ORF 3 [Cassava vein mosaic virus]
12347	GM_181_A1_G10_MR	g507910	BLASTN	611	5e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12348	GM_181_A1_G10_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12349	GM_181_A1_H06_T7	g170080	BLASTN	390	1e-10	68	Soybean seed lectin gene transposable element tgm1.
12350	GM_181_A2_A01_MR	g3142328	BLASTN	899	9e-34	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12351	GM_181_A2_A04_T7	g4063760	BLASTX	372	3e-32	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12352	GM_181_A2_A09_MR	g3810596	BLASTX	274	6e-22	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12353	GM_181_A2_A11_T7	g100484	BLASTX	369	4e-38	60	hypothetical protein - garden snapdragon
12354	GM_181_A2_B01_MR	g169363	BLASTX	266	2e-22	56	(M75856) PVPR3 [Phaseolus vulgaris]
12355	GM_181_A2_B01_T7	g3287696	BLASTX	390	1e-34	62	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
12356	GM_181_A2_B02_MR	g18559	BLASTN	695	2e-24	77	G.max gene for catalase
12357	GM_181_A2_C04_MR	g2865424	BLASTX	143	1e-09	38	(AF039371) polyprotein [Arabidopsis thaliana]
12358	GM_181_A2_C06_T7	g2522228	BLASTX	629	9e-61	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
12359	GM_181_A2_C08_T7	g300517	BLASTN	453	2e-14	62	Apo(B) (HVE36)=Apolipoprotein B {3' region, AT rich minisatellite, VNTR} [human, caucasian, Genomic, 802 nt]
12360	GM_181_A2_C12_T7	g507910	BLASTN	619	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12361	GM_181_A2_D06_T7	g1495804	BLASTX	592	2e-58	76	(X96406) 13-lipoxygenase [Solanum tuberosum]
12362	GM_181_A2_D08_T7	g18559	BLASTN	529	6e-17	77	G.max gene for catalase
12363	GM_181_A2_D10_T7	g453514	BLASTN	402	4e-11	61	Tetrahymena pyriformis ribosomal RNA; tRNA-Trp; ORF 1-4; tRNA-Glu; cytochrome oxidase subunit 1; NADH dehydrogenase; ribosomal protein L14.
12364	GM_181_A2_E01_T7	g1769898	BLASTX	600	9e-58	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12365	GM_181_A2_E06_T7	g2245390	BLASTX	239	1e-18	53	(U89296) auxin response transcription factor 3; ARF3 [Arabidopsis thaliana]
12366	GM_181_A2_E08_T7	g3599418	BLASTN	354	5e-09	74	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12367	GM_181_A2_E12_MR	g2642165	BLASTX	156	7e-10	61	(AC003000) hypothetical protein [Arabidopsis thaliana]
12368	GM_181_A2_F01_MR	g4063760	BLASTX	189	1e-26	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12369	GM_181_A2_F04_MR	g507910	BLASTN	371	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12370	GM_181_A2_F05_MR	g3193284	BLASTX	246	3e-28	67	(AF069298) No definition line found [Arabidopsis thaliana]
12371	GM_181_A2_F07_MR	g3777527	BLASTX	376	2e-32	93	(AF053008) gag-pol polyprotein [Glycine max]
12372	GM_181_A2_F07_T7	g3176777	BLASTN	462	7e-15	65	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence
12373	GM_181_A2_F09_MR	g3097320	BLASTN	435	1e-12	68	Glycine max gene for Bd 30K, complete cds
12374	GM_181_A2_F12_MR	g3777527	BLASTX	396	1e-34	91	(AF053008) gag-pol polyprotein [Glycine max]
12375	GM_181_A2_F12_T7	g3142328	BLASTN	2487	4e-107	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12376	GM_181_A2_G03_MR	g1785744	BLASTX	99	4e-11	38	(Y08502) orf158 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12377	GM_181_A2_G08_MR	g2245044	BLASTX	185	2e-18	55	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
12378	GM_181_A2_G09_T7	g3142328	BLASTN	1828	4e-76	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12379	GM_181_A2_H08_MR	g4038056	BLASTX	149	1e-20	44	(AC005897) putative transposon [Arabidopsis thaliana]
12380	GM_181_A2_H12_T7	g1167523	BLASTX	455	5e-41	56	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12381	GM_181_B1_A05_T7	g1619300	BLASTX	163	2e-11	33	(X95269) LRR protein [Lycopersicon esculentum]
12382	GM_181_B1_A06_T7	g1142701	BLASTN	1352	9e-55	90	Glycine max satellite STR120-A.3.
12383	GM_181_B1_A09_MR	g905361	BLASTX	191	3e-13	31	(U22103) gag-protease polyprotein [Glycine max]
12384	GM_181_B1_B08_MR	g3142328	BLASTN	1069	2e-41	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12385	GM_181_B1_C01_MR	g507910	BLASTN	348	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence
12386	GM_181_B1_C01_T7	g507910	BLASTN	409	7e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12387	GM_181_B1_C03_MR	g2245104	BLASTX	320	2e-26	50	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
12388	GM_181_B1_C03_T7	g2088647	BLASTX	398	4e-36	66	(AF002109) hypothetical protein [Arabidopsis thaliana] gi 3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]
12389	GM_181_B1_C06_MR	g4063760	BLASTX	213	3e-15	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12390	GM_181_B1_C07_MR	g3142328	BLASTN	1088	2e-42	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12391	GM_181_B1_C09_MR	g3550435	BLASTN	532	5e-17	62	Hordeum vulgare Hotr1 gene
12392	GM_181_B1_C09_T7	g2213599	BLASTX	315	6e-26	51	(AC000348) T7N9.19 [Arabidopsis thaliana]
12393	GM_181_B1_D04_T7	g3046704	BLASTX	285	6e-23	46	(AL022223) putative protein [Arabidopsis thaliana]
12394	GM_181_B1_D05_T7	g2429512	BLASTN	534	4e-17	64	Caenorhabditis elegans cosmid T27A1
12395	GM_181_B1_D07_MR	g3599418	BLASTN	381	3e-10	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12396	GM_181_B1_D08_MR	g1167523	BLASTX	182	7e-12	33	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12397	GM_181_B1_D09_T7	g1402881	BLASTX	216	1e-15	43	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
12398	GM_181_B1_E03_T7	g3287679	BLASTX	157	2e-09	54	(AC003979) T22J18.6 [Arabidopsis thaliana]
12399	GM_181_B1_F08_T7	g18559	BLASTN	449	2e-13	68	G max gene for catalase
12400	GM_181_B1_E10_T7	g905361	BLASTX	586	3e-56	96	(U22103) gag-protease polyprotein [Glycine max]
12401	GM_181_B1_F02_T7	g905361	BLASTX	586	3e-56	95	(U22103) gag-protease polyprotein [Glycine max]
12402	GM_181_B1_F04_T7	g4063756	BLASTN	461	9e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12403	GM_181_B1_F06_T7	g1732362	BLASTN	406	8e-12	82	Malus domestica pAFD103 mRNA, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12404	GM_181_B1_F08_T7	g992916	BLASTN	422	5e-12	69	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
12405	GM_181_B1_F09_MR	g441205	BLASTN	485	6e-15	74	Soybean lox1gm4 gene encoding lipxygenase L-4
12406	GM_181_B1_F11_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12407	GM_181_B1_G02_T7	g3319362	BLASTX	226	9e-17	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12408	GM_181_B1_G07_T7	g3695395	BLASTX	169	2e-13	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
12409	GM_181_B1_H05_T7	g4063760	BLASTX	252	2e-19	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12410	GM_181_B1_H06_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12411	GM_181_B1_H07_MR	g3142328	BLASTN	796	2e-53	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12412	GM_181_B1_H09_T7	g3142328	BLASTN	887	3e-33	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12413	GM_181_B2_A02_MR	g2498731	BLASTX	310	6e-27	58	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 gi 1362013 pir S57611 zeta-crystallin homolog - Arabidopsis thaliana gi 886428 (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
12414	GM_181_B2_A08_MR	g507910	BLASTN	636	4e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12415	GM_181_B2_A08_T7	g3930515	BLASTX	105	2e-11	44	(AF059674) putative gag protein [Nicotiana tabacum]
12416	GM_181_B2_A09_MR	g134646	BLASTX	291	7e-37	91	SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) gi 169955 (M64267) Fe-superoxide dismutase [Glycine max] gi 228415 prf 1803527A Fe superoxide dismutase [Glycine max]
12417	GM_181_B2_A09_T7	g3786004	BLASTX	180	3e-13	59	(AC005499) hypothetical protein [Arabidopsis thaliana]
12418	GM_181_B2_A10_T7	g4063756	BLASTN	469	4e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12419	GM_181_B2_A11_MR	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12420	GM_181_B2_B01_T7	g905361	BLASTX	118	4e-10	25	(U22103) gag-protease polyprotein [Glycine max]
12421	GM_181_B2_B02_T7	g3492857	BLASTN	356	5e-09	69	Homo sapiens 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
12422	GM_181_B2_B03_MR	g507910	BLASTN	577	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12423	GM_181_B2_B03_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12424	GM_181_B2_B09_MR	g1040717	BLASTN	372	1e-10	63	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12425	GM_181_B2_C02_T7	g4063760	BLASTX	291	1e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12426	GM_181_B2_C09_T7	g1040717	BLASTN	333	6e-09	62	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12427	GM_181_B2_D01_MR	g1769898	BLASTX	422	1e-38	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12428	GM_181_B2_D02_MR	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12429	GM_181_B2_D02_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12430	GM_181_B2_D08_MR	g3482974	BLASTX	342	3e-29	76	(AL031369) ATP-dependent Clp proteinase - like protein [Arabidopsis thaliana]
12431	GM_181_B2_D11_MR	g3777527	BLASTX	701	4e-67	93	(AF053008) gag-pol polyprotein [Glycine max]
12432	GM_181_B2_D12_T7	g2443320	BLASTX	348	1e-29	52	(D85597) polyprotein [Oryza australiensis]
12433	GM_181_B2_E05_MR	g2462058	BLASTX	360	3e-32	52	(Y13389) reverse transcriptase [Antirrhinum majus]
12434	GM_181_B2_F03_MR	g505129	BLASTN	369	1e-09	74	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12435	GM_181_B2_F04_MR	g3845197	BLASTN	410	2e-11	60	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12436	GM_181_B2_F09_MR	g2522230	BLASTX	311	5e-27	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12437	GM_181_B2_F12_MR	g507910	BLASTN	604	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12438	GM_181_B2_F12_T7	g507910	BLASTN	635	4e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12439	GM_181_B2_G02_MR	g3142379	BLASTX	119	7e-10	86	(AF053008) envelope-like [Glycine max]
12440	GM_181_B2_G09_MR	g2979574	BLASTN	357	4e-09	58	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
12441	GM_181_B2_H01_T7	g4150930	BLASTN	407	2e-11	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12442	GM_182_A1_A01_MR	g3777527	BLASTX	167	3e-11	41	(AF053008) gag-pol polyprotein [Glycine max]
12443	GM_182_A1_A05_MR	g2522228	BLASTX	318	8e-28	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
12444	GM_182_A1_A06_MR	g4063760	BLASTX	478	2e-43	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12445	GM_182_A1_A06_T7	g3243214	BLASTN	490	4e-15	67	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
12446	GM_182_A1_A10_MR	g3688172	BLASTX	162	1e-11	50	(AL031804) putative protein [Arabidopsis thaliana]
12447	GM_182_A1_A12_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
12448	GM_182_A1_B01_MR	g4104931	BLASTX	120	9e-10	78	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
12449	GM_182_A1_B07_T7	g170606	BLASTN	554	3e-18	70	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
12450	GM_182_A1_B09_MR	g3142328	BLASTN	1112	2e-43	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12451	GM_182_A1_B10_T7	g905361	BLASTX	346	4e-30	96	(U22103) gag-protease polyprotein [Glycine max]
12452	GM_182_A1_B11_T7	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12453	GM_182_A1_B12_MR	g99922	BLASTX	381	4e-53	77	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12454	GM_182_A1_C02_MR	g4063760	BLASTX	551	2e-51	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12455	GM_182_A1_C03_MR	g905361	BLASTX	204	1e-14	35	(U22103) gag-protease polyprotein [Glycine max]
12456	GM_182_A1_C06_MR	g2995405	BLASTX	454	2e-41	66	(Y12432) polyprotein [Ananas comosus]
12457	GM_182_A1_C07_MR	g507910	BLASTN	361	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12458	GM_182_A1_C07_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12459	GM_182_A1_C10_MR	g100484	BLASTX	137	1e-12	36	hypothetical protein - garden snapdragon
12460	GM_182_A1_D07_T7	g2244802	BLASTX	324	5e-27	50	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
12461	GM_182_A1_D08_MR	g3097320	BLASTN	896	2e-33	75	Glycine max gene for Bd 30K, complete cds
12462	GM_182_A1_D10_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12463	GM_182_A1_D10_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12464	GM_182_A1_E02_T7	g3142328	BLASTN	1340	8e-54	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12465	GM_182_A1_E12_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12466	GM_182_A1_F04_MR	g3777526	BLASTN	355	5e-09	64	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
12467	GM_182_A1_F09_MR	g505129	BLASTN	352	6e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12468	GM_182_A1_F09_T7	g4063760	BLASTX	153	7e-09	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12469	GM_182_A1_F10_MR	g170606	BLASTN	785	5e-29	71	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
12470	GM_182_A1_F12_MR	g4063760	BLASTX	520	5e-48	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12471	GM_182_A1_G03_T7	g18559	BLASTN	437	9e-13	73	G.max gene for catalase
12472	GM_182_A1_G07_T7	g18559	BLASTN	628	2e-21	78	G.max gene for catalase
12473	GM_182_A1_G12_T7	g3319362	BLASTX	209	6e-15	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12474	GM_182_A1_H02_T7	g3097320	BLASTN	354	5e-09	72	Glycine max gene for Bd 30K, complete cds
12475	GM_182_A1_H04_MR	g3142328	BLASTN	763	1e-27	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12476	GM_182_A1_H04_T7	g1000971	BLASTN	406	3e-11	63	Hansenula wingei mitochondrial DNA, complete sequence
12477	GM_182_A1_H05_T7	g507910	BLASTN	438	4e-13	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12478	GM_182_A1_H06_MR	g4063760	BLASTX	178	2e-11	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12479	GM_182_A1_H06_T7	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12480	GM_182_A1_H07_T7	g18559	BLASTN	911	3e-34	77	G.max gene for catalase
12481	GM_182_A1_H09_T7	g4038056	BLASTX	290	1e-23	55	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12482	GM_182_A2_A03_MR	g505129	BLASTN	361	2e-09	73	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12483	GM_182_A2_A05_T7	g505129	BLASTN	383	2e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12484	GM_182_A2_B07_T7	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12485	GM_182_A2_B10_T7	g387902	BLASTX	191	8e-21	56	(L23524) ORF [Hordeum vulgare]
12486	GM_182_A2_C01_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12487	GM_182_A2_C03_T7	g3142328	BLASTN	426	3e-12	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12488	GM_182_A2_C10_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12489	GM_182_A2_C11_MR	g4092471	BLASTN	432	2e-12	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
12490	GM_182_A2_D03_T7	g3142328	BLASTN	2030	2e-85	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12491	GM_182_A2_D09_T7	g2586082	BLASTX	203	4e-14	54	(U72725) retrofit [Oryza longistaminata]
12492	GM_182_A2_D10_T7	g3395432	BLASTX	151	2e-20	93	(AC004683) unknown protein [Arabidopsis thaliana]
12493	GM_182_A2_E03_MR	g3097320	BLASTN	480	1e-14	72	Glycine max gene for Bd 30K, complete cds
12494	GM_182_A2_E05_T7	g3319362	BLASTX	310	9e-26	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12495	GM_182_A2_E06_T7	g3097320	BLASTN	480	1e-14	72	Glycine max gene for Bd 30K, complete cds
12496	GM_182_A2_E09_T7	g4160362	BLASTN	432	2e-12	63	Saccharomyces cerevisiae complete mitochondrial genome
12497	GM_182_A2_F02_T7	g100484	BLASTX	379	2e-33	53	hypothetical protein - garden snapdragon
12498	GM_182_A2_F04_MR	g1769899	BLASTX	170	4e-12	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12499	GM_182_A2_F04_T7	g93559	BLASTX	177	3e-11	34	ORF3 protein - rice tungro bacilliform virus gi 333967 (M65026) ORF3 [Rice tungro bacilliform virus]
12500	GM_182_A2_F08_T7	g2522230	BLASTX	303	3e-26	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12501	GM_182_A2_F11_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12502	GM_182_A2_G06_MR	g507910	BLASTN	508	2e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12503	GM_182_A2_G07_MR	g4063760	BLASTX	186	2e-12	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12504	GM_182_A2_H02_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12505	GM_182_A2_H04_T7	g18702	BLASTN	410	2e-12	65	Soybean nodulin-24 gene 5' end
12506	GM_182_B1_A10_MR	g3142379	BLASTX	232	4e-18	58	(AF053008) envelope-like [Glycine max]
12507	GM_182_B1_A11_T7	g170603	BLASTN	387	6e-11	62	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
12508	GM_182_B1_B05_MR	g4063760	BLASTX	260	3e-20	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12509	GM_182_B1_B05_T7	g3319362	BLASTX	197	1e-13	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12510	GM_182_B1_B07_MR	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12511	GM_182_B1_B10_T7	g3319362	BLASTX	407	4e-36	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12512	GM_182_B1_C07_MR	g3834324	BLASTX	166	2e-11	81	(AC005679) Similar to gb X92762 tafazzins protein from Homo sapiens. [Arabidopsis thaliana]
12513	GM_182_B1_C08_MR	g3297823	BLASTX	223	7e-20	51	(AL031032) putative protein [Arabidopsis thaliana]
12514	GM_182_B1_C09_T7	g4063760	BLASTX	195	3e-14	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12515	GM_182_B1_C10_T7	g4063760	BLASTX	497	1e-45	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12516	GM_182_B1_D04_MR	g3695395	BLASTX	236	4e-18	47	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
12517	GM_182_B1_D04_T7	g2961349	BLASTX	181	6e-12	40	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
12518	GM_182_B1_D08_T7	g2961349	BLASTX	166	3e-10	35	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
12519	GM_182_B1_D09_T7	g1684913	BLASTX	311	9e-26	47	(U77888) receptor-like protein kinase [Ipomoea nil]
12520	GM_182_B1_D12_T7	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12521	GM_182_B1_E08_T7	g170065	BLASTN	451	2e-13	73	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
12522	GM_182_B1_E10_T7	g99922	BLASTX	227	6e-38	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12523	GM_182_B1_E12_T7	g505129	BLASTN	365	1e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12524	GM_182_B1_F03_MR	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
12525	GM_182_B1_F05_T7	g99922	BLASTX	171	1e-26	68	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12526	GM_182_B1_F12_MR	g2522228	BLASTX	315	2e-27	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
12527	GM_182_B1_G07_MR	g4038056	BLASTX	170	9e-22	53	(AC005897) putative transposon [Arabidopsis thaliana]
12528	GM_182_B1_G07_T7	g4038056	BLASTX	288	2e-23	45	(AC005897) putative transposon [Arabidopsis thaliana]
12529	GM_182_B1_G08_MR	g3097320	BLASTN	457	1e-13	68	Glycine max gene for Bd 30K, complete cds
12530	GM_182_B1_G10_T7	g3540184	BLASTX	288	2e-23	56	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]
12531	GM_182_B1_G12_T7	g905361	BLASTX	197	6e-14	31	(U22103) gag-protease polyprotein [Glycine max]
12532	GM_182_B1_H04_MR	g3283026	BLASTX	197	7e-14	42	putative transposase [Arabidopsis thaliana]
12533	GM_182_B1_H05_T7	g2522230	BLASTX	139	1e-08	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12534	GM_182_B1_H08_T7	g2522226	BLASTN	562	2e-18	70	Vicia faba mRNA for reverse transcriptase-like protein, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12535	GM_182_B1_H12_MR	g3834307	BLASTX	233	4e-18	80	(AC005679) Strong similarity to gene T10I14.120 gi 2832679 putative protein from Arabidopsis thaliana BAC gb AL021712. ESTs gb N65887 and gb N65627 come from this gene. [Arabidopsis thaliana]
12536	GM_182_B2_A03_MR	g3548810	BLASTX	279	1e-27	48	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
12537	GM_182_B2_A05_T7	g3645899	BLASTX	225	5e-29	50	(U68408) 5' end not determined experimentally [Zea mays]
12538	GM_182_B2_A10_T7	g3928116	BLASTN	399	6e-11	61	, complete sequence [Homo sapiens]
12539	GM_182_B2_B05_T7	g3777527	BLASTX	173	7e-11	37	(AF053008) gag-pol polyprotein [Glycine max]
12540	GM_182_B2_B09_T7	g2129618	BLASTX	175	2e-11	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12541	GM_182_B2_C02_T7	g2346988	BLASTX	230	8e-18	54	(AB006606) ZPT4-4 [Petunia x hybrida]
12542	GM_182_B2_C04_MR	g2462058	BLASTX	192	2e-14	61	(Y13389) reverse transcriptase [Antirrhinum majus]
12543	GM_182_B2_C05_T7	g3810596	BLASTX	203	3e-14	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12544	GM_182_B2_C08_MR	g2995405	BLASTX	306	2e-25	55	(Y12432) polyprotein [Ananas comosus]
12545	GM_182_B2_D03_T7	g3097320	BLASTN	488	5e-15	70	Glycine max gene for Bd 30K, complete cds
12546	GM_182_B2_D06_T7	g4063770	BLASTX	203	2e-14	38	(AB004906) transposase [Ipomoea purpurea]
12547	GM_182_B2_D08_T7	g2979574	BLASTN	373	8e-10	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
12548	GM_182_B2_E03_T7	g2085783	BLASTN	445	8e-14	68	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
12549	GM_182_B2_E06_T7	g2129618	BLASTX	211	3e-15	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12550	GM_182_B2_F05_T7	g3097320	BLASTN	470	3e-14	73	Glycine max gene for Bd 30K, complete cds
12551	GM_182_B2_F06_MR	g2500724	BLASTX	142	4e-10	62	PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR gi 2129894 pir S72453 secA protein precursor - garden pea gi 1122325 (X82404) chloroplast SecA protein [Pisum sativum]
12552	GM_182_B2_F08_T7	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12553	GM_182_B2_F09_T7	g507910	BLASTN	598	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12554	GM_182_B2_G03_MR	g3650039	BLASTX	142	7e-14	50	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12555	GM_182_B2_G10_T7	g3777527	BLASTX	211	3e-20	44	(AF053008) gag-pol polyprotein [Glycine max]
12556	GM_182_B2_H02_MR	g507910	BLASTN	551	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
12557	GM_182_B2_H04_MR	g2129618	BLASTX	161	7e-10	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12558	GM_182_B2_H09_MR	g507910	BLASTN	358	1e-09	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12559	GM_183_A1_A03_MR	g4038056	BLASTX	265	5e-21	46	(AC005897) putative transposon [Arabidopsis thaliana]
12560	GM_183_A1_A07_MR	g18559	BLASTN	388	1e-10	68	G.max gene for catalase
12561	GM_183_A1_A12_T7	g3777527	BLASTX	633	7e-60	97	(AF053008) gag-pol polyprotein [Glycine max]
12562	GM_183_A1_B01_T7	g4063760	BLASTX	516	1e-47	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12563	GM_183_A1_B02_T7	g507910	BLASTN	641	2e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12564	GM_183_A1_B06_MR	g2258469	BLASTX	126	8e-12	70	(AF009179) replication protein A1 [Oryza sativa]
12565	GM_183_A1_B06_T7	g530207	BLASTX	517	4e-48	85	(L35272) heat shock protein [Glycine max]
12566	GM_183_A1_B08_T7	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12567	GM_183_A1_B11_T7	g3337361	BLASTX	286	4e-33	81	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
12568	GM_183_A1_C01_MR	g1769899	BLASTX	213	4e-20	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12569	GM_183_A1_C02_MR	g4063760	BLASTX	485	3e-44	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12570	GM_183_A1_C04_MR	g3142328	BLASTN	768	8e-28	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12571	GM_183_A1_C08_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12572	GM_183_A1_C11_MR	g3142328	BLASTN	706	5e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12573	GM_183_A1_C12_MR	g2564112	BLASTX	149	5e-09	45	(AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]
12574	GM_183_A1_D01_T7	g320564	BLASTX	173	2e-12	44	transposon copia - Arabidopsis thaliana (fragment)
12575	GM_183_A1_D04_T7	g3097320	BLASTN	1212	7e-48	83	Glycine max gene for Bd 30K, complete cds
12576	GM_183_A1_D08_T7	g2781351	BLASTX	246	3e-20	70	(AC003113) F24O1.7 [Arabidopsis thaliana]
12577	GM_183_A1_E01_MR	g18559	BLASTN	896	1e-33	75	G.max gene for catalase
12578	GM_183_A1_E05_T7	g3695395	BLASTX	178	7e-12	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
12579	GM_183_A1_E06_MR	g2245104	BLASTX	189	1e-12	46	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
12580	GM_183_A1_E07_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12581	GM_183_A1_E07_T7	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12582	GM_183_A1_E08_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12583	GM_183_A1_E09_MR	g3097320	BLASTN	381	3e-10	72	Glycine max gene for Bd 30K, complete cds
12584	GM_183_A1_E10_MR	g100484	BLASTX	266	3e-21	41	hypothetical protein - garden snapdragon
12585	GM_183_A1_E12_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12586	GM_183_A1_F02_T7	g905361	BLASTX	133	2e-14	36	(U22103) gag-protease polyprotein [Glycine max]
12587	GM_183_A1_F03_T7	g840618	BLASTN	345	9e-09	62	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
12588	GM_183_A1_F10_MR	g1769903	BLASTX	308	9e-27	74	(X95738) proline transporter 2 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12589	GM_183_A1_F11_MR	g4038056	BLASTX	185	2e-12	43	(AC005897) putative transposon [Arabidopsis thaliana]
12590	GM_183_A1_F12_T7	g1769898	BLASTX	329	3e-28	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12591	GM_183_A1_G04_T7	g18559	BLASTN	662	6e-23	73	G.max gene for catalase
12592	GM_183_A1_G05_T7	g2462058	BLASTX	269	1e-22	50	(Y13389) reverse transcriptase [Antirrhinum majus]
12593	GM_183_A1_G09_T7	g4038056	BLASTX	229	1e-27	52	(AC005897) putative transposon [Arabidopsis thaliana]
12594	GM_183_A1_G10_MR	g2642431	BLASTX	237	1e-17	56	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
12595	GM_183_A1_H02_MR	g3142328	BLASTN	1551	2e-63	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12596	GM_183_A1_H02_T7	g130582	BLASTX	166	3e-10	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12597	GM_183_A1_H04_MR	g3702121	BLASTX	136	1e-16	68	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]
12598	GM_183_A1_H07_MR	g1167523	BLASTX	321	1e-26	55	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12599	GM_183_A1_H09_MR	g100484	BLASTX	292	4e-24	50	hypothetical protein - garden snapdragon
12600	GM_183_A2_A01_MR	g2995405	BLASTX	444	3e-40	57	(Y12432) polyprotein [Ananas comosus]
12601	GM_183_A2_A06_MR	g4063760	BLASTX	385	1e-33	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12602	GM_183_A2_A09_MR	g3777527	BLASTX	614	7e-58	95	(AF053008) gag-pol polyprotein [Glycine max]
12603	GM_183_A2_A10_T7	g3337361	BLASTX	135	2e-12	73	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
12604	GM_183_A2_B01_MR	g3142328	BLASTN	862	4e-32	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12605	GM_183_A2_B05_T7	g905361	BLASTX	752	8e-74	87	(U22103) gag-protease polyprotein [Glycine max]
12606	GM_183_A2_B07_MR	g2160128	BLASTN	380	4e-10	61	Genomic sequence from Human 17, complete sequence [Homo sapiens]
12607	GM_183_A2_B09_MR	g4063760	BLASTX	332	6e-28	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12608	GM_183_A2_B12_MR	g3426334	BLASTN	537	3e-17	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
12609	GM_183_A2_C01_T7	g3142328	BLASTN	949	5e-36	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12610	GM_183_A2_C04_MR	g4063760	BLASTX	359	7e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12611	GM_183_A2_C04_T7	g905361	BLASTX	200	3e-14	31	(U22103) gag-protease polyprotein [Glycine max]
12612	GM_183_A2_C05_MR	g507910	BLASTN	485	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12613	GM_183_A2_C06_T7	g2454214	BLASTN	445	3e-13	71	Glycine max nodule-specific phosphoribosylpyrophosphate amidotransferase (PRAT) gene, 5' upstream sequence and partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12614	GM_183_A2_C08_MR	g4092470	BLASTN	477	2e-14	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
12615	GM_183_A2_C12_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12616	GM_183_A2_D01_MR	g1769897	BLASTX	220	1e-16	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12617	GM_183_A2_D02_MR	g18559	BLASTN	315	2e-10	70	G.max gene for catalase
12618	GM_183_A2_D03_MR	g1743251	BLASTN	406	3e-11	61	Human DNA sequence from PAC 293L6 on chromosome 22 Contains ESTs and STS, complete sequence [Homo sapiens]
12619	GM_183_A2_D03_T7	g99730	BLASTX	220	1e-16	34	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
12620	GM_183_A2_D09_MR	g3777527	BLASTX	591	2e-55	95	(AF053008) gag-pol polyprotein [Glycine max]
12621	GM_183_A2_E06_T7	g2980770	BLASTX	191	1e-13	48	(AL022198) putative protein kinase [Arabidopsis thaliana]
12622	GM_183_A2_E08_MR	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12623	GM_183_A2_E08_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12624	GM_183_A2_E10_MR	g4092471	BLASTN	508	7e-16	73	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
12625	GM_183_A2_E12_MR	g3046704	BLASTX	196	2e-13	41	(AL022223) putative protein [Arabidopsis thaliana]
12626	GM_183_A2_F07_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12627	GM_183_A2_F09_T7	g3241925	BLASTN	833	1e-30	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]
12628	GM_183_A2_G01_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12629	GM_183_A2_G02_MR	g507910	BLASTN	521	6e-17	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12630	GM_183_A2_G02_T7	g4063756	BLASTN	405	3e-11	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12631	GM_183_A2_G04_MR	g995751	BLASTN	396	5e-11	61	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
12632	GM_183_A2_G04_T7	g2462058	BLASTX	131	1e-17	52	(Y13389) reverse transcriptase [Antirrhinum majus]
12633	GM_183_A2_G06_MR	g4050011	BLASTN	486	6e-15	67	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12634	GM_183_A2_G08_T7	g2462058	BLASTX	310	6e-27	52	(Y13389) reverse transcriptase [Antirrhinum majus]
12635	GM_183_A2_G10_T7	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12636	GM_183_A2_G12_T7	g4063760	BLASTX	556	1e-52	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12637	GM_183_A2_H05_MR	g3319362	BLASTX	204	4e-27	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12638	GM_183_A2_H10_T7	g2129618	BLASTX	223	2e-16	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12639	GM_183_A2_H11_MR	g2564051	BLASTN	450	3e-13	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]
12640	GM_183_B1_A05_T7	g3142328	BLASTN	862	3e-47	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12641	GM_183_B1_A07_T7	g3452139	BLASTN	351	1e-09	69	Glycine max mRNA for resistance protein, partial
12642	GM_183_B1_B04_T7	g4063760	BLASTX	387	8e-34	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12643	GM_183_B1_B05_T7	g3080426	BLASTX	198	7e-14	54	(AL022604) putative protein [Arabidopsis thaliana]
12644	GM_183_B1_B06_MR	g3193298	BLASTX	162	3e-11	43	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]
12645	GM_183_B1_B06_T7	g3193287	BLASTX	449	1e-41	66	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]
12646	GM_183_B1_B07_MR	g3135251	BLASTX	351	3e-30	49	(AC003058) putative receptor protein kinase [Arabidopsis thaliana] gi 3176719 (AC002392) putative protein kinase [Arabidopsis thaliana]
12647	GM_183_B1_B09_MR	g18559	BLASTN	997	3e-38	74	G max gene for catalase
12648	GM_183_B1_B09_T7	g3097320	BLASTN	444	5e-13	68	Glycine max gene for Bd 30K, complete cds
12649	GM_183_B1_B11_T7	g2911063	BLASTN	364	2e-09	74	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSAII project)
12650	GM_183_B1_B12_MR	g3142328	BLASTN	729	5e-26	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12651	GM_183_B1_C01_MR	g18559	BLASTN	938	2e-35	73	G.max gene for catalase
12652	GM_183_B1_C02_MR	g2827718	BLASTX	313	5e-26	48	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
12653	GM_183_B1_C02_T7	g3845321	BLASTN	365	2e-09	65	Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence
12654	GM_183_B1_C07_MR	g3860320	BLASTN	396	6e-11	88	Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-5
12655	GM_183_B1_C09_MR	g2462134	BLASTX	346	1e-30	46	(Y13368) reverse transcriptase [Beta vulgaris]
12656	GM_183_B1_C10_T7	g1142703	BLASTN	301	4e-17	77	Glycine max satellite STR120-B.1.
12657	GM_183_B1_C12_T7	g3426334	BLASTN	361	3e-09	59	Pisum sativum pectin methylesterase (repme1) gene, complete cds
12658	GM_183_B1_D01_T7	g3142330	BLASTX	674	2e-65	94	(U96295) envelope-like [Glycine max]
12659	GM_183_B1_D02_T7	g3947735	BLASTX	374	9e-33	52	(AJ009720) NL27 [Solanum tuberosum]
12660	GM_183_B1_D07_MR	g18559	BLASTN	469	3e-14	69	G.max gene for catalase
12661	GM_183_B1_D08_T7	g3126935	BLASTN	361	1e-09	64	Neochanna diversus strain Kaimaumau14 mitochondrial D-loop, complete sequence
12662	GM_183_B1_D09_T7	g1769898	BLASTX	261	7e-21	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12663	GM_183_B1_D12_MR	g18768	BLASTN	525	2e-17	72	Soybean Tgm6 transposable element 3' end
12664	GM_183_B1_E03_T7	g3777527	BLASTX	110	5e-12	37	(AF053008) gag-pol polyprotein [Glycine max]
12665	GM_183_B1_E05_MR	g2522227	BLASTX	206	6e-16	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12666	GM_183_B1_E06_MR	g99755	BLASTX	321	2e-27	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12667	GM_183_B1_E07_MR	g2995405	BLASTX	323	3e-27	50	(Y12432) polyprotein [Ananas comosus]
12668	GM_183_B1_F01_MR	g3645899	BLASTX	277	7e-29	59	(U68408) 5' end not determined experimentally [Zea mays]
12669	GM_183_B1_F07_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12670	GM_183_B1_F07_T7	g4063756	BLASTN	541	2e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12671	GM_183_B1_F10_MR	g1666236	BLASTX	153	9e-10	31	(U76261) unknown [Hordeum vulgare]
12672	GM_183_B1_F11_T7	g2244837	BLASTX	134	8e-19	80	(Z97337) proteasome chain protein [Arabidopsis thaliana] gi 2511572 gnl PID e1179970 (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] gi 3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
12673	GM_183_B1_G01_MR	g1184075	BLASTX	159	1e-09	37	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
12674	GM_183_B1_G04_T7	g2462134	BLASTX	153	2e-09	37	(Y13368) reverse transcriptase [Beta vulgaris]
12675	GM_183_B1_G05_T7	g4063756	BLASTN	387	2e-10	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12676	GM_183_B1_G06_MR	g3777527	BLASTX	146	3e-20	42	(AF053008) gag-pol polyprotein [Glycine max]
12677	GM_183_B1_G08_T7	g1769897	BLASTX	458	1e-42	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12678	GM_183_B1_G12_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12679	GM_183_B1_G12_T7	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12680	GM_183_B1_H02_T7	g2462134	BLASTX	355	1e-31	50	(Y13368) reverse transcriptase [Beta vulgaris]
12681	GM_183_B1_H05_T7	g3643604	BLASTX	186	2e-12	43	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
12682	GM_183_B1_H09_T7	g3097320	BLASTN	448	3e-13	71	Glycine max gene for Bd 30K, complete cds
12683	GM_183_B1_H10_MR	g13533	BLASTN	299	4e-12	66	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala.
12684	GM_183_B1_H10_T7	g4056476	BLASTN	330	3e-09	64	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
12685	GM_183_B2_A05_MR	g1321822	BLASTX	271	7e-23	66	(X96865) phosphoribosylglycinamide formyltransferase [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12686	GM_183_B2_A05_T7	g1588265	BLASTX	178	9e-12	82	100RNP protein [Spinacia oleracea]
12687	GM_183_B2_A08_MR	g1769898	BLASTX	176	1e-11	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12688	GM_183_B2_B03_T7	g1091678	BLASTX	179	3e-16	42	activator-like transposable element [Pennisetum glaucum]
12689	GM_183_B2_B05_MR	g4063756	BLASTN	365	2e-09	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12690	GM_183_B2_B10_MR	g3021268	BLASTX	298	3e-24	43	(AL022347) putative protein [Arabidopsis thaliana]
12691	GM_183_B2_C02_MR	g3097320	BLASTN	507	6e-16	84	Glycine max gene for Bd 30K, complete cds
12692	GM_183_B2_C03_MR	g99755	BLASTX	425	3e-39	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12693	GM_183_B2_C04_MR	g3097320	BLASTN	636	9e-22	72	Glycine max gene for Bd 30K, complete cds
12694	GM_183_B2_C05_T7	g2522228	BLASTX	302	4e-26	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
12695	GM_183_B2_C10_T7	g2522228	BLASTX	206	2e-15	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
12696	GM_183_B2_C12_T7	g3097320	BLASTN	989	9e-38	74	Glycine max gene for Bd 30K, complete cds
12697	GM_183_B2_D01_MR	g3550044	BLASTN	392	1e-10	63	Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) ...
12698	GM_183_B2_D01_T7	g3142328	BLASTN	534	3e-17	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12699	GM_183_B2_D02_MR	g3738114	BLASTN	399	6e-11	61	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
12700	GM_183_B2_D02_T7	g4006828	BLASTX	183	3e-12	30	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
12701	GM_183_B2_D04_MR	g3319362	BLASTX	323	4e-27	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12702	GM_183_B2_D05_MR	g1142701	BLASTN	1253	3e-50	85	Glycine max satellite STR120-A.3.
12703	GM_183_B2_D07_T7	g862479	BLASTN	360	2e-17	92	Glycine max valosin-containing protein mRNA, complete cds.
12704	GM_183_B2_D11_MR	g3894391	BLASTX	192	5e-15	41	(AF053997) Hcr2-5B [Lycopersicon esculentum]
12705	GM_183_B2_E05_MR	g531389	BLASTX	134	7e-18	49	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
12706	GM_183_B2_E11_MR	g3142328	BLASTN	859	6e-32	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12707	GM_183_B2_F02_T7	g629693	BLASTX	405	5e-37	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12708	GM_183_B2_F06_MR	g3176798	BLASTN	351	4e-16	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
12709	GM_183_B2_F07_MR	g2462134	BLASTX	295	6e-25	39	(Y13368) reverse transcriptase [Beta vulgaris]
12710	GM_183_B2_F09_T7	g4150930	BLASTN	559	3e-18	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12711	GM_183_B2_G01_MR	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12712	GM_183_B2_G01_T7	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12713	GM_183_B2_G02_MR	g2583130	BLASTX	177	2e-11	35	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
12714	GM_183_B2_G02_T7	g3810596	BLASTX	271	1e-21	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12715	GM_183_B2_G03_MR	g454847	BLASTN	449	2e-13	72	Glycine max ribosomal protein S11 gene, complete cds
12716	GM_183_B2_G06_MR	g3142328	BLASTN	608	7e-34	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12717	GM_183_B2_G06_T7	g2995405	BLASTX	183	3e-12	41	(Y12432) polyprotein [Ananas comosus]
12718	GM_183_B2_G10_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12719	GM_183_B2_G10_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12720	GM_183_B2_H01_MR	g3482979	BLASTX	392	1e-35	71	(AL031369) putative protein [Arabidopsis thaliana]
12721	GM_183_B2_H04_T7	g2244915	BLASTX	233	3e-19	46	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
12722	GM_183_B2_H08_MR	g3126783	BLASTN	395	8e-11	60	Homo sapiens chromosome 17, clone hCIT529I10, complete sequence [Homo sapiens]
12723	GM_183_B2_H09_MR	g4063760	BLASTX	451	1e-40	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12724	GM_183_B2_H10_MR	g3142328	BLASTN	676	1e-23	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12725	GM_183_B2_H12_MR	g3097320	BLASTN	529	6e-17	67	Glycine max gene for Bd 30K, complete cds
12726	GM_184_A1_A01_MR	g3097320	BLASTN	467	4e-14	77	Glycine max gene for Bd 30K, complete cds
12727	GM_184_A1_A02_T7	g3142328	BLASTN	431	2e-12	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12728	GM_184_A1_A05_T7	g3645899	BLASTX	284	2e-24	52	(U68408) 5' end not determined experimentally [Zea mays]
12729	GM_184_A1_A06_MR	g2760330	BLASTX	153	3e-10	75	(AC002130) F1N21.15 [Arabidopsis thaliana]
12730	GM_184_A1_A11_MR	g507910	BLASTN	461	3e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12731	GM_184_A1_A11_T7	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12732	GM_184_A1_B01_T7	g3142330	BLASTX	616	2e-59	92	(U96295) envelope-like [Glycine max]
12733	GM_184_A1_B07_T7	g4006885	BLASTN	351	8e-09	71	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2
12734	GM_184_A1_B09_MR	g3885339	BLASTX	258	2e-20	46	(AC005623) putative bzip protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12735	GM_184_A1_B11_MR	g4140712	BLASTX	208	4e-16	42	(AF110183) putative integrase [Oryza sativa]
12736	GM_184_A1_B12_T7	g587603	BLASTN	375	5e-10	64	P.falciparum gene for beta subunit RNA polymerase
12737	GM_184_A1_C04_MR	g3599418	BLASTN	953	3e-36	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12738	GM_184_A1_C05_MR	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12739	GM_184_A1_C08_MR	g99711	BLASTX	211	2e-16	61	hypothetical protein H1.2flk - Arabidopsis thaliana (fragment) gi 16322 (X62460) H1-2flk [Arabidopsis thaliana]
12740	GM_184_A1_C10_MR	g3033398	BLASTX	165	7e-25	85	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]
12741	GM_184_A1_D03_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12742	GM_184_A1_D03_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12743	GM_184_A1_D04_MR	g84801	BLASTX	245	1e-18	37	hypothetical protein 2 - silkworm transposon mag
12744	GM_184_A1_D06_T7	g2995405	BLASTX	223	2e-16	51	(Y12432) polyprotein [Ananas comosus]
12745	GM_184_A1_D09_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12746	GM_184_A1_D10_MR	g1142701	BLASTN	1355	6e-55	87	Glycine max satellite STR120-A.3.
12747	GM_184_A1_E03_T7	g18559	BLASTN	390	1e-10	70	G.max gene for catalase
12748	GM_184_A1_E04_MR	g3769670	BLASTN	575	9e-20	72	Pisum sativum Tic22 mRNA, nuclear mRNA encoding chloroplast protein, complete cds
12749	GM_184_A1_F06_MR	g1142703	BLASTN	295	3e-17	77	Glycine max satellite STR120-B.1.
12750	GM_184_A1_F07_MR	g1769898	BLASTX	277	1e-32	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12751	GM_184_A1_F11_T7	g3947433	BLASTN	447	4e-13	66	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
12752	GM_184_A1_G02_MR	g3135965	BLASTN	363	2e-09	62	Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence [Homo sapiens]
12753	GM_184_A1_G06_T7	g4063760	BLASTX	179	1e-12	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12754	GM_184_A1_G07_T7	g4063760	BLASTX	186	2e-12	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12755	GM_184_A1_G09_T7	g3142330	BLASTX	645	2e-62	90	(U96295) envelope-like [Glycine max]
12756	GM_184_A1_H02_MR	g507910	BLASTN	602	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12757	GM_184_A1_H02_T7	g18559	BLASTN	453	2e-13	66	G.max gene for catalase
12758	GM_184_A1_H03_MR	g3319362	BLASTX	162	5e-10	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12759	GM_184_A1_H07_T7	g3599418	BLASTN	612	2e-28	77	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12760	GM_184_A1_H10_T7	g3777527	BLASTX	582	2e-54	94	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12761	GM_184_A2_A09_MR	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
12762	GM_184_A2_A11_MR	g3142328	BLASTN	856	8e-32	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12763	GM_184_A2_A12_MR	g3152938	BLASTX	130	3e-09	37	(AF065482) sorting nexin 2 [Homo sapiens]
12764	GM_184_A2_B07_MR	g12708	BLASTN	357	4e-09	59	Aspergillus nidlans mitochondrial DNA for L-rRNA
12765	GM_184_A2_C01_MR	g2196878	BLASTX	298	2e-28	80	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
12766	GM_184_A2_C03_MR	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12767	GM_184_A2_C04_MR	g4038056	BLASTX	247	2e-33	56	(AC005897) putative transposon [Arabidopsis thaliana]
12768	GM_184_A2_C08_MR	g3777527	BLASTX	927	2e-91	96	(AF053008) gag-pol polyprotein [Glycine max]
12769	GM_184_A2_D07_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12770	GM_184_A2_D09_MR	g3097320	BLASTN	529	6e-17	79	Glycine max gene for Bd 30K, complete cds
12771	GM_184_A2_E10_MR	g3377831	BLASTX	183	3e-12	29	(AF075598) similar to maize transposon MuDR mudrA (GB:M76978) [Arabidopsis thaliana]
12772	GM_184_A2_F01_MR	g4160362	BLASTN	410	5e-15	66	Saccharomyces cerevisiae complete mitochondrial genome
12773	GM_184_A2_F06_MR	g3645899	BLASTX	192	9e-25	39	(U68408) 5' end not determined experimentally [Zea mays]
12774	GM_184_A2_F09_MR	g3319362	BLASTX	287	3e-23	39	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12775	GM_184_A2_F11_MR	g2194124	BLASTX	194	4e-14	62	(AC002062) Similar to Glycine metalloendoproteinase (gb U63725). [Arabidopsis thaliana]
12776	GM_184_A2_G04_MR	g1045614	BLASTX	335	3e-29	51	(U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]
12777	GM_184_A2_G06_MR	g4098244	BLASTX	241	3e-37	97	(U76409) homeobox 1 protein [Lycopersicon esculentum]
12778	GM_184_A2_G08_MR	g3264544	BLASTN	700	1e-24	64	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
12779	GM_184_A2_G09_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12780	GM_184_A2_G12_MR	g2129618	BLASTX	179	8e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12781	GM_184_A2_H01_MR	g3645899	BLASTX	449	1e-42	59	(U68408) 5' end not determined experimentally [Zea mays]
12782	GM_184_A2_H04_MR	g3097320	BLASTN	1116	2e-43	75	Glycine max gene for Bd 30K, complete cds
12783	GM_184_A2_H12_MR	g170080	BLASTN	474	2e-14	67	Soybean seed lectin gene transposable element tgm1.
12784	GM_184_B1_A02_MR	g905361	BLASTX	334	9e-29	80	(U22103) gag-protease polyprotein [Glycine max]
12785	GM_184_B1_A03_MR	g1769898	BLASTX	326	7e-42	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12786	GM_184_B1_A10_T7	g2244959	BLASTX	154	1e-08	41	(Z97340) similar to B.vulgaris CMS-associated mitochondrial ... (reverse transcriptase) [Arabidopsis thaliana]
12787	GM_184_B1_A12_T7	g3097320	BLASTN	388	2e-10	73	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12788	GM_184_B1_B03_MR	g905361	BLASTX	329	3e-28	77	(U22103) gag-protease polyprotein [Glycine max]
12789	GM_184_B1_B05_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12790	GM_184_B1_B06_MR	g4063760	BLASTX	232	2e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12791	GM_184_B1_B07_MR	g3645899	BLASTX	235	6e-23	45	(U68408) 5' end not determined experimentally [Zea mays]
12792	GM_184_B1_B10_T7	g343799	BLASTN	411	4e-12	62	S.cerevisiae mitochondrial cytochrome c oxidase subunit 2 (COX2) gene, 5' end.
12793	GM_184_B1_C02_T7	g629693	BLASTX	442	6e-41	59	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12794	GM_184_B1_C07_T7	g4063760	BLASTX	352	8e-45	76	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12795	GM_184_B1_C10_T7	g507910	BLASTN	500	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12796	GM_184_B1_D01_MR	g3021278	BLASTX	134	2e-14	54	(AL022347) putative protein [Arabidopsis thaliana]
12797	GM_184_B1_D05_MR	g3810596	BLASTX	198	8e-14	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12798	GM_184_B1_D05_T7	g2586082	BLASTX	286	6e-23	45	(U72725) retrofit [Oryza longistaminata]
12799	GM_184_B1_D06_T7	g3894385	BLASTX	240	2e-18	50	(AF053994) Hcr2-0A [Lycopersicon esculentum]
12800	GM_184_B1_D09_MR	g4063760	BLASTX	296	4e-24	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12801	GM_184_B1_D10_T7	g3513745	BLASTX	249	7e-19	39	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
12802	GM_184_B1_D12_MR	g507910	BLASTN	388	6e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12803	GM_184_B1_E01_MR	g4150930	BLASTN	407	2e-11	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12804	GM_184_B1_E04_MR	g99922	BLASTX	188	4e-20	43	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12805	GM_184_B1_E04_T7	g507910	BLASTN	546	5e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12806	GM_184_B1_E05_T7	g507910	BLASTN	415	4e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12807	GM_184_B1_E06_T7	g3777527	BLASTX	623	8e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
12808	GM_184_B1_E08_MR	g3882356	BLASTX	217	9e-17	67	(U92460) pdr2 [Arabidopsis thaliana]
12809	GM_184_B1_E08_T7	g3097320	BLASTN	513	3e-16	83	Glycine max gene for Bd 30K, complete cds
12810	GM_184_B1_E09_T7	g2462936	BLASTX	329	5e-29	54	(Y12321) open reading frame 2 [Brassica oleracea]
12811	GM_184_B1_F02_MR	g3493214	BLASTX	217	1e-15	35	(AF056940) pol polyprotein [Drosophila virilis]
12812	GM_184_B1_F02_T7	g18559	BLASTN	1120	9e-44	77	G.max gene for catalase
12813	GM_184_B1_F03_MR	g4063760	BLASTX	387	7e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12814	GM_184_B1_G02_MR	g1431738	BLASTN	412	1e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
12815	GM_184_B1_G07_MR	g3152618	BLASTX	218	5e-23	53	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12816	GM_184_B1_G07_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12817	GM_184_B1_G08_T7	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12818	GM_184_B1_H02_MR	g99922	BLASTX	453	2e-54	84	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12819	GM_184_B2_A02_T7	g2462134	BLASTX	259	7e-21	50	(Y13368) reverse transcriptase [Beta vulgaris]
12820	GM_184_B2_A04_MR	g3176795	BLASTN	400	1e-11	61	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
12821	GM_184_B2_A05_MR	g4126312	BLASTN	390	1e-10	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
12822	GM_184_B2_A07_T7	g1769901	BLASTX	213	5e-16	78	(X95737) proline transporter 1 [Arabidopsis thaliana] gi 2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]
12823	GM_184_B2_A09_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12824	GM_184_B2_B01_T7	g507910	BLASTN	417	3e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12825	GM_184_B2_B03_T7	g4063760	BLASTX	165	1e-11	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12826	GM_184_B2_B05_T7	g507910	BLASTN	357	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12827	GM_184_B2_B09_T7	g3928116	BLASTN	442	6e-13	65	, complete sequence [Homo sapiens]
12828	GM_184_B2_B10_T7	g2522230	BLASTX	163	2e-11	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12829	GM_184_B2_B12_MR	g3097320	BLASTN	441	6e-13	74	Glycine max gene for Bd 30K, complete cds
12830	GM_184_B2_B12_T7	g2462134	BLASTX	149	6e-09	36	(Y13368) reverse transcriptase [Beta vulgaris]
12831	GM_184_B2_C01_T7	g2522228	BLASTX	175	6e-12	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
12832	GM_184_B2_C02_T7	g1091678	BLASTX	171	5e-11	44	activator-like transposable element [Pennisetum glaucum]
12833	GM_184_B2_C05_MR	g2522227	BLASTX	191	2e-14	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12834	GM_184_B2_C09_T7	g99721	BLASTX	173	2e-17	53	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
12835	GM_184_B2_D02_T7	g1435021	BLASTX	144	5e-09	56	(D26575) DNA-binding protein [Daucus carota]
12836	GM_184_B2_D04_T7	g1680686	BLASTX	369	1e-32	55	(U51330) rust resistance kinase Lr10 [Triticum aestivum]
12837	GM_184_B2_D10_MR	g4063760	BLASTX	280	2e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12838	GM_184_B2_D10_T7	g507910	BLASTN	661	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12839	GM_184_B2_E01_T7	g3645899	BLASTX	347	1e-29	48	(U68408) 5' end not determined experimentally [Zea mays]
12840	GM_184_B2_E04_T7	g3947433	BLASTN	364	2e-09	65	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
12841	GM_184_B2_E09_T7	g1769898	BLASTX	208	4e-15	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12842	GM_184_B2_F03_MR	g4063756	BLASTN	389	1e-10	74	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12843	GM_184_B2_F12_MR	g1142701	BLASTN	1285	9e-52	85	Glycine max satellite STR120-A.3.
12844	GM_184_B2_G01_MR	g905361	BLASTX	153	3e-09	83	(U22103) gag-protease polyprotein [Glycine max]
12845	GM_184_B2_G04_MR	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12846	GM_184_B2_G04_T7	g507910	BLASTN	414	4e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12847	GM_184_B2_G08_T7	g3097320	BLASTN	553	5e-18	79	Glycine max gene for Bd 30K, complete cds
12848	GM_184_B2_H01_T7	g130582	BLASTX	172	9e-12	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12849	GM_184_B2_H03_MR	g507910	BLASTN	484	3e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12850	GM_184_B2_H03_T7	g507910	BLASTN	480	4e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12851	GM_184_B2_H10_MR	g1769898	BLASTX	401	3e-36	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12852	GM_185_A1_A01_MR	g629693	BLASTX	278	1e-23	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12853	GM_185_A1_A01_T7	g1946279	BLASTX	242	8e-20	47	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
12854	GM_185_A1_A02_T7	g136125	BLASTX	194	2e-13	42	PUTATIVE AC TRANSPOSASE (ORFA) gi 22113 (X05424) ORFa [Zea mays]
12855	GM_185_A1_A04_T7	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12856	GM_185_A1_A05_MR	g507910	BLASTN	434	5e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12857	GM_185_A1_A05_T7	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12858	GM_185_A1_A08_T7	g343950	BLASTN	347	1e-09	63	S.cerevisiae mitochondrion Tyr-tRNA gene.
12859	GM_185_A1_B01_T7	g1785729	BLASTN	400	5e-11	66	A.thaliana mitochondrial genome, part B
12860	GM_185_A1_B07_T7	g3097322	BLASTN	1638	3e-67	99	Glycine max pseudogene for Bd 30K
12861	GM_185_A1_B08_MR	g99755	BLASTX	290	4e-24	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12862	GM_185_A1_B11_MR	g3402758	BLASTX	288	1e-24	73	(AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]
12863	GM_185_A1_B11_T7	g18559	BLASTN	948	6e-36	83	G.max gene for catalase
12864	GM_185_A1_C06_MR	g4092470	BLASTN	351	8e-09	63	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12865	GM_185_A1_C08_T7	g507910	BLASTN	367	6e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
12866	GM_185_A1_C10_T7	g2995405	BLASTX	241	5e-20	52	(Y12432) polyprotein [Ananas comosus]
12867	GM_185_A1_D03_MR	g3935157	BLASTX	147	7e-13	66	(AC005106) T25N20.21 [Arabidopsis thaliana]
12868	GM_185_A1_E04_MR	g3142328	BLASTN	1563	5e-64	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12869	GM_185_A1_E05_MR	g2367675	BLASTX	202	3e-14	34	(AF017040) Pol [Dictyostelium discoideum]
12870	GM_185_A1_E06_MR	g3097320	BLASTN	874	2e-32	79	Glycine max gene for Bd 30K, complete cds
12871	GM_185_A1_E10_MR	g2522228	BLASTX	266	3e-22	54	(AB007466) reverse transcriptase-like protein [Vicia faba]
12872	GM_185_A1_F09_T7	g1326016	BLASTX	205	2e-14	44	TY3-2 orfB
12873	GM_185_A1_G01_T7	g1045530	BLASTN	358	3e-09	63	Magnaporthe grisea host-species specificity (Pwl1) gene, complete cds.
12874	GM_185_A1_G04_MR	g4063760	BLASTX	181	7e-12	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12875	GM_185_A1_G06_MR	g3097320	BLASTN	363	2e-09	74	Glycine max gene for Bd 30K, complete cds
12876	GM_185_A1_G06_T7	g3142328	BLASTN	1258	4e-50	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12877	GM_185_A1_G08_MR	g4063760	BLASTX	243	2e-18	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12878	GM_185_A1_G09_MR	g1431738	BLASTN	357	3e-09	74	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
12879	GM_185_A1_H01_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence
12880	GM_185_A1_H03_T7	g130582	BLASTX	121	3e-14	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12881	GM_185_A1_H06_T7	g4050011	BLASTN	359	3e-09	62	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12882	GM_185_A2_A03_MR	g2995405	BLASTX	244	9e-19	37	(Y12432) polyprotein [Ananas comosus]
12883	GM_185_A2_A04_MR	g4115365	BLASTX	290	2e-23	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12884	GM_185_A2_A05_MR	g2583106	BLASTN	388	2e-10	68	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]
12885	GM_185_A2_A12_MR	g3935200	BLASTN	523	1e-16	71	Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence [Homo sapiens]
12886	GM_185_A2_B02_T7	g2981494	BLASTX	116	7e-09	62	(AF053473) kinesin heavy chain [Mus musculus]
12887	GM_185_A2_B04_T7	g2462134	BLASTX	172	7e-13	39	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
12888	GM_185_A2_B05_MR	g4049609	BLASTN	358	4e-09	61	Oryzias latipes gene for membrane guanylyl cyclase OlGC1, complete cds
12889	GM_185_A2_B05_T7	g3645899	BLASTX	222	3e-35	60	(U68408) 5' end not determined experimentally [Zea mays]
12890	GM_185_A2_B07_MR	g3845197	BLASTN	448	3e-13	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12891	GM_185_A2_B08_T7	g3650378	BLASTX	125	1e-14	52	(AL031740) putative rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein [Schizosaccharomyces pombe]
12892	GM_185_A2_B09_T7	g4063760	BLASTX	389	5e-34	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12893	GM_185_A2_B12_T7	g2443320	BLASTX	301	1e-24	44	(D85597) polyprotein [Oryza australiensis]
12894	GM_185_A2_C03_MR	g4115365	BLASTX	154	6e-09	30	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12895	GM_185_A2_C04_T7	g1666236	BLASTX	209	4e-16	34	(U76261) unknown [Hordeum vulgare]
12896	GM_185_A2_C06_T7	g2995405	BLASTX	324	2e-54	60	(Y12432) polyprotein [Ananas comosus]
12897	GM_185_A2_C08_MR	g100484	BLASTX	430	5e-39	49	hypothetical protein - garden snapdragon
12898	GM_185_A2_C10_MR	g2995405	BLASTX	558	1e-52	53	(Y12432) polyprotein [Ananas comosus]
12899	GM_185_A2_C11_T7	g3142328	BLASTN	1240	3e-49	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12900	GM_185_A2_D03_MR	g4115365	BLASTX	137	3e-13	28	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12901	GM_185_A2_D03_T7	g18559	BLASTN	1256	6e-50	76	G max gene for catalase
12902	GM_185_A2_D06_MR	g3097320	BLASTN	442	6e-13	79	Glycine max gene for Bd 30K, complete cds
12903	GM_185_A2_D07_MR	g1666236	BLASTX	288	1e-24	34	(U76261) unknown [Hordeum vulgare]
12904	GM_185_A2_D08_T7	g3283026	BLASTX	210	3e-15	33	putative transposase [Arabidopsis thaliana]
12905	GM_185_A2_D09_MR	g4063760	BLASTX	130	2e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12906	GM_185_A2_D09_T7	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12907	GM_185_A2_D11_MR	g2462134	BLASTX	237	3e-26	52	(Y13368) reverse transcriptase [Beta vulgaris]
12908	GM_185_A2_D11_T7	g4050011	BLASTN	565	1e-18	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12909	GM_185_A2_E01_T7	g4050011	BLASTN	395	8e-11	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12910	GM_185_A2_E04_T7	g535454	BLASTX	146	6e-09	50	(U13940) cysteine proteinase [Alnus glutinosa]
12911	GM_185_A2_E08_T7	g3599418	BLASTN	652	1e-22	75	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12912	GM_185_A2_E09_MR	g1769897	BLASTX	200	8e-20	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12913	GM_185_A2_E10_MR	g4038056	BLASTX	425	4e-38	55	(AC005897) putative transposon [Arabidopsis thaliana]
12914	GM_185_A2_E10_T7	g535454	BLASTX	179	2e-29	55	(U13940) cysteine proteinase [Alnus glutinosa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12915	GM_185_A2_E12_MR	g3142328	BLASTN	797	4e-29	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12916	GM_185_A2_F02_MR	g3810596	BLASTX	206	1e-14	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12917	GM_185_A2_F02_T7	g345511	BLASTX	193	2e-18	33	retrovirus-related copia polyprotein - fruit fly (Drosophila simulans) (fragments)
12918	GM_185_A2_F04_MR	g1666236	BLASTX	174	4e-12	30	(U76261) unknown [Hordeum vulgare]
12919	GM_185_A2_F07_T7	g2565011	BLASTX	235	7e-18	34	(AC002983) putative mudrA-like retrotransposon-associated protein [Arabidopsis thaliana]
12920	GM_185_A2_F11_T7	g728905	BLASTX	180	1e-11	45	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
12921	GM_185_A2_F12_MR	g3599418	BLASTN	315	2e-17	80	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12922	GM_185_A2_G10_T7	g3097320	BLASTN	552	6e-18	74	Glycine max gene for Bd 30K, complete cds
12923	GM_185_A2_H03_T7	g3153101	BLASTN	384	3e-10	64	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
12924	GM_185_A2_H05_MR	g2522230	BLASTX	361	2e-32	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12925	GM_185_A2_H08_T7	g3097322	BLASTN	2448	3e-104	94	Glycine max pseudogene for Bd 30K
12926	GM_185_A2_H10_MR	g99755	BLASTX	339	2e-42	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12927	GM_185_B2_A07_T7	g3080376	BLASTX	170	6e-11	70	(AL022580) putative protein [Arabidopsis thaliana]
12928	GM_185_B2_A09_MR	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12929	GM_185_B2_A11_MR	g342964	BLASTN	386	2e-11	63	paramecium species 5,311 mt dna dimer: replication init. region.
12930	GM_185_B2_A12_T7	g3319351	BLASTX	341	8e-29	52	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
12931	GM_185_B2_B04_MR	g3777527	BLASTX	629	2e-59	94	(AF053008) gag-pol polyprotein [Glycine max]
12932	GM_185_B2_B04_T7	g507910	BLASTN	357	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12933	GM_185_B2_B07_MR	g4063760	BLASTX	105	1e-09	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12934	GM_185_B2_B09_T7	g2522230	BLASTX	193	1e-14	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12935	GM_185_B2_B10_T7	g507910	BLASTN	356	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12936	GM_185_B2_B11_MR	g4038056	BLASTX	200	5e-14	44	(AC005897) putative transposon [Arabidopsis thaliana]
12937	GM_185_B2_B11_T7	g3413522	BLASTX	71	5e-09	33	(AB016585) unnamed protein product [Tricholoma matsutake]
12938	GM_185_B2_B12_T7	g3645899	BLASTX	319	1e-26	51	(U68408) 5' end not determined experimentally [Zea mays]
12939	GM_185_B2_C02_MR	g3122784	BLASTX	110	2e-09	50	PROBABLE 40S RIBOSOMAL PROTEIN S12 gi 2370511 gnl PID e339198 (Z98887) putative 40s ribosomal protein [Schizosaccharomyces pombe] gi 3451319 gnl PID e1316718 (AL031323) 40s ribosomal protein s12 [Schizosaccharomyces pombe]
12940	GM_185_B2_C10_T7	g3184283	BLASTX	323	4e-29	79	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
12941	GM_185_B2_C11_T7	g22490	BLASTX	174	1e-12	40	(X01380) ORF1 [Zea mays]
12942	GM_185_B2_D01_MR	g2264309	BLASTN	452	2e-13	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
12943	GM_185_B2_D04_T7	g3930515	BLASTX	115	7e-10	46	(AF059674) putative gag protein [Nicotiana tabacum]
12944	GM_185_B2_D08_T7	g3777527	BLASTX	529	9e-49	89	(AF053008) gag-pol polyprotein [Glycine max]
12945	GM_185_B2_D09_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12946	GM_185_B2_D10_T7	g507910	BLASTN	622	2e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12947	GM_185_B2_E03_T7	g2245104	BLASTX	155	5e-09	33	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
12948	GM_185_B2_E08_MR	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12949	GM_185_B2_E08_T7	g3142328	BLASTN	956	2e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12950	GM_185_B2_E10_T7	g4063760	BLASTX	211	5e-15	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12951	GM_185_B2_F03_MR	g3645899	BLASTX	195	2e-13	37	(U68408) 5' end not determined experimentally [Zea mays]
12952	GM_185_B2_F08_MR	g3135969	BLASTN	418	8e-12	61	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
12953	GM_185_B2_F09_MR	g130582	BLASTX	168	2e-10	35	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12954	GM_185_B2_F12_MR	g3645899	BLASTX	348	9e-30	60	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12955	GM_185_B2_G04_MR	g3550044	BLASTN	369	1e-09	62	Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) ...
12956	GM_185_B2_G05_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence
12957	GM_185_B2_G06_MR	g1666236	BLASTX	187	1e-13	34	(U76261) unknown [Hordeum vulgare]
12958	GM_185_B2_H07_T7	g3599418	BLASTN	469	3e-14	77	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12959	GM_185_B2_H08_T7	g322663	BLASTX	275	3e-23	58	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884) S-receptor kinase related protein [Brassica oleracea]
12960	GM_186_A2_A01_MR	g507910	BLASTN	444	2e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12961	GM_186_A2_A04_MR	g99755	BLASTX	383	2e-34	53	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12962	GM_186_A2_A10_MR	g3645899	BLASTX	239	4e-18	44	(U68408) 5' end not determined experimentally [Zea mays]
12963	GM_186_A2_B01_T7	g3935164	BLASTX	97	8e-10	38	(AC004557) F17L21.7 [Arabidopsis thaliana]
12964	GM_186_A2_B09_MR	g4063756	BLASTN	535	4e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12965	GM_186_A2_C11_MR	g3142328	BLASTN	405	3e-11	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12966	GM_186_A2_C12_MR	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
12967	GM_186_A2_C12_T7	g507910	BLASTN	343	7e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12968	GM_186_A2_D01_MR	g3142328	BLASTN	694	2e-24	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12969	GM_186_A2_D03_MR	g421954	BLASTX	199	4e-14	37	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
12970	GM_186_A2_D07_MR	g2982291	BLASTX	142	3e-09	59	(AF051230) heat shock protein [Picea mariana]
12971	GM_186_A2_D09_MR	g421955	BLASTX	388	2e-39	63	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
12972	GM_186_A2_F01_T7	g3645899	BLASTX	322	1e-29	65	(U68408) 5' end not determined experimentally [Zea mays]
12973	GM_186_A2_E08_MR	g3142328	BLASTN	667	3e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12974	GM_186_A2_E11_MR	g18559	BLASTN	715	2e-25	78	G.max gene for catalase
12975	GM_186_A2_F04_MR	g3142328	BLASTN	841	4e-31	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12976	GM_186_A2_F12_MR	g3097320	BLASTN	445	4e-13	70	Glycine max gene for Bd 30K, complete cds
12977	GM_186_A2_G01_T7	g507910	BLASTN	582	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12978	GM_186_A2_G04_MR	g267055	BLASTX	146	1e-09	65	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) gi 66572 pir YUMU sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana gi 16526 (X60987) sucrose synthase [Arabidopsis thaliana]
12979	GM_186_A2_G04_T7	g1769899	BLASTX	177	7e-13	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12980	GM_186_A2_G05_MR	g1666236	BLASTX	149	3e-09	29	(U76261) unknown [Hordeum vulgare]
12981	GM_186_A2_G07_MR	g3135252	BLASTX	159	4e-10	29	(AC003058) hypothetical protein [Arabidopsis thaliana] gi 3176720 (AC002392) hypothetical protein [Arabidopsis thaliana]
12982	GM_186_A2_G11_T7	g1346113	BLASTX	334	2e-29	92	GTP CYCLOHYDROLASE II gi 1084339 pir JC4209 GTP cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana gi 940383 gnl PID d1008704 (D45165) GTP cyclohydrolase II [Arabidopsis thaliana]
12983	GM_186_A2_H05_MR	g3142330	BLASTX	720	2e-70	98	(U96295) envelope-like [Glycine max]
12984	GM_186_A2_H10_T7	g2642431	BLASTX	188	2e-12	60	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
12985	GM_186_A2_H12_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12986	GM_186_B2_A08_T7	g3142328	BLASTN	834	8e-31	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12987	GM_186_B2_A10_T7	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12988	GM_186_B2_B03_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12989	GM_186_B2_B09_T7	g3777527	BLASTX	265	1e-20	52	(AF053008) gag-pol polyprotein [Glycine max]
12990	GM_186_B2_B11_MR	g507910	BLASTN	503	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12991	GM_186_B2_B12_T7	g2642431	BLASTX	145	1e-10	46	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
12992	GM_186_B2_C01_MR	g4063760	BLASTX	268	4e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12993	GM_186_B2_C03_T7	g3513747	BLASTX	364	4e-31	52	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
12994	GM_186_B2_C04_MR	g3510251	BLASTX	150	6e-09	46	(AC005310) unknown protein [Arabidopsis thaliana]
12995	GM_186_B2_C04_T7	g3979928	BLASTN	430	2e-12	63	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
12996	GM_186_B2_C10_MR	g4063760	BLASTX	209	8e-15	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12997	GM_186_B2_D01_T7	g3645899	BLASTX	276	5e-22	38	(U68408) 5' end not determined experimentally [Zea mays]
12998	GM_186_B2_D03_MR	g3928083	BLASTX	141	6e-10	87	(AC005770) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12999	GM_186_B2_E02_MR	g2264312	BLASTN	384	5e-12	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
13000	GM_186_B2_E10_T7	g3790154	BLASTN	441	7e-13	66	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
13001	GM_186_B2_E11_T7	g3695408	BLASTX	189	4e-14	51	(AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana]
13002	GM_186_B2_F01_MR	g3645899	BLASTX	281	1e-22	42	(U68408) 5' end not determined experimentally [Zea mays]
13003	GM_186_B2_F03_T7	g170029	BLASTN	419	6e-12	83	Glycine max cv. Dare nodulin 26 gene fragment.
13004	GM_186_B2_F04_MR	g2832608	BLASTX	183	3e-13	35	(AL021637) leucine rich repeat-like protein (fragment) [Arabidopsis thaliana]
13005	GM_186_B2_F10_MR	g629693	BLASTX	127	5e-16	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13006	GM_186_B2_G02_T7	g3650039	BLASTX	237	3e-18	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13007	GM_186_B2_G03_MR	g2792161	BLASTX	249	2e-20	55	(AJ223558) reverse transcriptase [Alstroemeria ligtu]
13008	GM_186_B2_G08_MR	g3650039	BLASTX	225	6e-17	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13009	GM_186_B2_G10_MR	g905361	BLASTX	214	9e-16	31	(U22103) gag-protease polyprotein [Glycine max]
13010	GM_186_B2_G11_MR	g4063760	BLASTX	290	2e-23	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13011	GM_186_B2_G12_MR	g3641845	BLASTX	247	1e-22	57	(AJ223358) stelar K+ outward rectifying channel [Arabidopsis thaliana]
13012	GM_186_B2_H02_T7	g507910	BLASTN	609	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13013	GM_186_B2_H03_MR	g2209031	BLASTX	134	1e-13	30	(AB001569) ORF of 1.56 kb [Daucus carota]
13014	GM_186_B2_H04_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13015	GM_186_B2_H09_T7	g2264312	BLASTN	373	8e-10	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
13016	GM_186_B2_H12_MR	g905361	BLASTX	186	9e-13	28	(U22103) gag-protease polyprotein [Glycine max]
13017	GM_187_A1_A10_MR	g2970556	BLASTX	142	2e-16	81	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]
13018	GM_187_A1_B02_MR	g507910	BLASTN	557	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13019	GM_187_A1_B03_MR	g1743410	BLASTX	150	7e-11	46	(Y09825) amino acid transporter [Solanum tuberosum]
13020	GM_187_A1_B05_MR	g1685003	BLASTX	310	9e-27	39	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13021	GM_187_A1_B10_MR	g3193221	BLASTN	465	5e-14	79	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
13022	GM_187_A1_C08_MR	g3777527	BLASTX	559	5e-52	92	(AF053008) gag-pol polyprotein [Glycine max]
13023	GM_187_A1_D03_MR	g905360	BLASTN	353	5e-09	77	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
13024	GM_187_A1_E03_MR	g3287696	BLASTX	258	2e-20	53	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
13025	GM_187_A1_F08_MR	g3337395	BLASTN	410	2e-11	68	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
13026	GM_187_A1_F10_MR	g2522228	BLASTX	226	6e-38	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
13027	GM_187_A1_F12_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13028	GM_187_A1_G06_MR	g3402755	BLASTX	298	3e-24	45	(AL031187) putative transposable element [Arabidopsis thaliana]
13029	GM_187_A1_G08_MR	g4063760	BLASTX	196	2e-13	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13030	GM_187_A1_G09_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13031	GM_187_A1_G10_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13032	GM_187_A2_A03_MR	g2522228	BLASTX	337	8e-30	47	(AB007466) reverse transcriptase-like protein [Vicia faba]
13033	GM_187_A2_A05_T7	g2827644	BLASTN	363	2e-09	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project).
13034	GM_187_A2_B03_MR	g507910	BLASTN	628	9e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
13035	GM_187_A2_B03_T7	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
13036	GM_187_A2_B04_T7	g4098966	BLASTN	1539	1e-63	83	Glycine max putative reistance gene analog genomic sequence
13037	GM_187_A2_B10_MR	g1666236	BLASTX	168	2e-11	32	(U76261) unknown [Hordeum vulgare]
13038	GM_187_A2_B11_MR	g122106	BLASTX	385	6e-35	100	HISTONE H4 gi 70771 pir HSZM4 histone H4 - maize gi 81642 pir S06904 histone H4 - Arabidopsis thaliana gi 2119028 pir S60475 histone H4 - garden pea gi 21795 (X00043) histone H4 [Triticum aestivum] gi 166740 (M17132) histone H4 [Arabidopsis thaliana] gi 166742 (M17133) histone H4 [Arabidopsis thaliana] gi 168499 (M36659) histone H4 (H4C13) [Zea mays] gi 168501 (M13370) histone H4 [Zea mays] gi 168503 (M13377) histone H4 [Zea mays] gi 498898 (U10042) histone H4 homolog [Pisum sativum] gi 1806285 gnl PID e263432 (Z79638) histone H4 homologue [Sesbania rostrata] gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13039	GM_187_A2_B11_T7	g421955	BLASTX	167	3e-18	42	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
13040	GM_187_A2_C01_T7	g170080	BLASTN	361	2e-09	68	Soybean seed lectin gene transposable element tgm1.
13041	GM_187_A2_C02_MR	g1633547	BLASTN	416	9e-12	63	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
13042	GM_187_A2_C05_T7	g3142328	BLASTN	1067	2e-41	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13043	GM_187_A2_C08_T7	g3337395	BLASTN	370	1e-09	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
13044	GM_187_A2_C10_MR	g18559	BLASTN	424	3e-12	69	G.max gene for catalase
13045	GM_187_A2_C12_T7	g2191126	BLASTN	238	9e-10	64	Arabidopsis thaliana BAC IG002N01
13046	GM_187_A2_D02_MR	g1666236	BLASTX	149	3e-09	28	(U76261) unknown [Hordeum vulgare]
13047	GM_187_A2_D07_MR	g505129	BLASTN	380	5e-13	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13048	GM_187_A2_D07_T7	g2462936	BLASTX	136	2e-20	40	(Y12321) open reading frame 2 [Brassica oleracea]
13049	GM_187_A2_D10_MR	g3907448	BLASTN	349	1e-08	62	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
13050	GM_187_A2_D11_MR	g3645899	BLASTX	213	2e-19	57	(U68408) 5' end not determined experimentally [Zea mays]
13051	GM_187_A2_D11_T7	g2586082	BLASTX	185	4e-12	32	(U72725) retrofit [Oryza longistaminata]
13052	GM_187_A2_D12_MR	g3777527	BLASTX	469	2e-42	94	(AF053008) gag-pol polyprotein [Glycine max]
13053	GM_187_A2_E03_MR	g2764526	BLASTN	544	1e-17	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13054	GM_187_A2_E08_MR	g4056486	BLASTX	182	2e-12	43	(AC005896) hypothetical protein [Arabidopsis thaliana]
13055	GM_187_A2_E10_T7	g4006831	BLASTX	216	1e-15	35	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13056	GM_187_A2_F01_T7	g2501460	BLASTX	168	4e-19	69	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
13057	GM_187_A2_F03_T7	g1769897	BLASTX	172	2e-11	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13058	GM_187_A2_F08_MR	g2764526	BLASTN	401	4e-11	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13059	GM_187_A2_F11_T7	g18559	BLASTN	963	1e-36	80	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13060	GM_187_A2_G01_MR	g170605	BLASTN	597	2e-20	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
13061	GM_187_A2_G03_T7	g3142328	BLASTN	1623	9e-67	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13062	GM_187_A2_G11_T7	g4038056	BLASTX	111	2e-09	41	(AC005897) putative transposon [Arabidopsis thaliana]
13063	GM_187_A2_H01_MR	g1666236	BLASTX	212	2e-16	32	(U76261) unknown [Hordeum vulgare]
13064	GM_187_A2_H01_T7	g3930515	BLASTX	164	1e-10	33	(AF059674) putative gag protein [Nicotiana tabacum]
13065	GM_187_A2_H02_T7	g840618	BLASTN	362	1e-09	61	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
13066	GM_187_A2_H04_T7	g4063760	BLASTX	340	8e-29	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13067	GM_187_A2_H05_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13068	GM_187_A2_H08_MR	g4063760	BLASTX	313	6e-26	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13069	GM_187_A2_H11_MR	g3810596	BLASTX	351	4e-30	51	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13070	GM_187_A2_H11_T7	g1769897	BLASTX	207	4e-15	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13071	GM_187_B2_A12_MR	g4063760	BLASTX	359	8e-31	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13072	GM_187_B2_B04_MR	g629693	BLASTX	250	2e-20	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13073	GM_187_B2_B07_MR	g1086249	BLASTX	206	8e-15	38	subtilisin-like protease - Alnus glutinosa gi 757522 (X85975) subtilisin-like protease [Alnus glutinosa]
13074	GM_187_B2_B12_MR	g2459406	BLASTN	446	4e-13	69	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]
13075	GM_187_B2_F08_MR	g100484	BLASTX	279	1e-22	50	hypothetical protein - garden snapdragon
13076	GM_187_B2_F10_MR	g4063760	BLASTX	155	4e-09	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13077	GM_187_B2_G02_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13078	GM_187_B2_G03_MR	g4115365	BLASTX	176	3e-11	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
13079	GM_187_B2_G12_MR	g3273127	BLASTN	370	1e-09	64	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-54, complete sequence [Plasmodium falciparum]
13080	GM_187_B2_H01_MR	g3142379	BLASTX	273	1e-22	64	(AF053008) envelope-like [Glycine max]
13081	GM_187_B2_H07_MR	g507910	BLASTN	615	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13082	GM_188_A2_A01_T7	g170606	BLASTN	649	1e-22	64	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
13083	GM_188_A2_A02_MR	g2522228	BLASTX	404	6e-37	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
13084	GM_188_A2_A07_MR	g3860321	BLASTX	178	1e-24	84	(AJ012687) beta-galactosidase [Cicer arietinum]
13085	GM_188_A2_A12_MR	g3687234	BLASTX	166	8e-22	55	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
13086	GM_188_A2_B01_T7	g3047060	BLASTN	378	5e-10	64	Arabidopsis thaliana BAC F7N22
13087	GM_188_A2_B04_T7	g2244916	BLASTX	153	3e-09	29	(Z97339) hypothetical protein [Arabidopsis thaliana]
13088	GM_188_A2_B08_T7	g3885341	BLASTX	369	3e-32	51	(AC005623) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13089	GM_188_A2_B10_MR	g2921211	BLASTX	176	1e-19	100	(AF026149) beta-ketoacyl-ACP synthase II [Perilla frutescens]
13090	GM_188_A2_C11_T7	g2121303	BLASTN	427	3e-12	65	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
13091	GM_188_A2_D01_T7	g4063760	BLASTX	294	3e-26	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13092	GM_188_A2_D04_T7	g4160362	BLASTN	378	5e-10	60	Saccharomyces cerevisiae complete mitochondrial genome
13093	GM_188_A2_D09_MR	g1736642	BLASTX	567	2e-52	86	(D90836) Invasin. [Escherichia coli]
13094	GM_188_A2_D10_T7	g1772985	BLASTX	160	3e-14	53	(Z83835) zeaxanthin epoxidase [Lycopersicon esculentum]
13095	GM_188_A2_D12_MR	g1518540	BLASTX	704	1e-68	95	(U53418) UDP-glucose dehydrogenase [Glycine max]
13096	GM_188_A2_D12_T7	g2642438	BLASTX	149	5e-09	36	(AC002391) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]
13097	GM_188_A2_E01_MR	g2618689	BLASTX	382	1e-34	85	(AC002510) unknown protein [Arabidopsis thaliana]
13098	GM_188_A2_E01_T7	g905361	BLASTX	119	2e-13	47	(U22103) gag-protease polyprotein [Glycine max]
13099	GM_188_A2_E02_T7	g507910	BLASTN	671	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
13100	GM_188_A2_E03_T7	g4038056	BLASTX	258	3e-20	44	(AC005897) putative transposon [Arabidopsis thaliana]
13101	GM_188_A2_E05_T7	g507910	BLASTN	585	8e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13102	GM_188_A2_E08_MR	g507910	BLASTN	662	3e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
13103	GM_188_A2_E08_T7	g507910	BLASTN	518	8e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13104	GM_188_A2_E12_MR	g2276452	BLASTN	362	3e-09	62	Homo sapiens shox gene, alternatively spliced products, complete cds
13105	GM_188_A2_F03_T7	g3377848	BLASTX	202	2e-21	53	(AF076274) contains similarity to reverse transcriptases (Pfam. rvt.hmm, score: 12.22) [Arabidopsis thaliana]
13106	GM_188_A2_F04_T7	g4140712	BLASTX	412	8e-45	53	(AF110183) putative integrase [Oryza sativa]
13107	GM_188_A2_F07_T7	g507910	BLASTN	472	1e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13108	GM_188_A2_F09_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13109	GM_188_A2_F10_T7	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13110	GM_188_A2_F12_MR	g3650035	BLASTX	154	4e-09	41	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
13111	GM_188_A2_G03_T7	g1531760	BLASTX	183	1e-12	62	(X97075) proline oxidase [Arabidopsis thaliana]
13112	GM_188_A2_G09_MR	g3097320	BLASTN	546	1e-17	66	Glycine max gene for Bd 30K, complete cds
13113	GM_188_A2_H01_MR	g3947433	BLASTN	412	1e-11	63	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
13114	GM_188_A2_H04_MR	g3746069	BLASTX	176	3e-11	31	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
13115	GM_188_A2_H06_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13116	GM_188_A2_H09_T7	g791097	BLASTN	348	8e-09	68	P.vulgaris plsB mRNA.
13117	GM_188_A2_H11_MR	g1165321	BLASTN	714	2e-25	81	Glycine max extensin (SbHRGP3) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13118	GM_188_A2_H11_T7	g113363	BLASTX	153	1e-12	59	ALCOHOL DEHYDROGENASE 1 gi 279445 pir DEPJA1 alcohol dehydrogenase (EC 1.1.1.1) 1 - garden petunia gi 20506 (X54106) alcohol dehydrogenase [Petunia hybrida]
13119	GM_188_B1_A01_T7	g507910	BLASTN	419	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13120	GM_188_B1_A05_T7	g3845184	BLASTN	247	8e-10	62	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence
13121	GM_188_B1_A06_T7	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence
13122	GM_188_B1_B04_T7	g3810596	BLASTX	255	2e-22	48	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13123	GM_188_B1_B06_T7	g3894156	BLASTN	364	2e-09	67	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]
13124	GM_188_B1_B09_T7	g2276452	BLASTN	361	3e-09	61	Homo sapiens shox gene, alternatively spliced products, complete cds
13125	GM_188_B1_C02_T7	g587603	BLASTN	383	2e-10	60	P.falciparum gene for beta subunit RNA polymerase
13126	GM_188_B1_C04_T7	g2665376	BLASTN	354	6e-09	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-15, complete sequence [Plasmodium falciparum]
13127	GM_188_B1_C09_T7	g3142328	BLASTN	1100	7e-43	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13128	GM_188_B1_E02_T7	g3142328	BLASTN	584	2e-19	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13129	GM_188_B1_E06_T7	g507910	BLASTN	340	9e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13130	GM_188_B1_E11_T7	g905361	BLASTX	437	3e-40	96	(U22103) gag-protease polyprotein [Glycine max]
13131	GM_188_B1_F05_T7	g2708743	BLASTX	188	2e-12	32	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
13132	GM_188_B1_F09_T7	g2194136	BLASTX	106	3e-09	31	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
13133	GM_188_B2_A11_MR	g100484	BLASTX	195	1e-13	48	hypothetical protein - garden snapdragon
13134	GM_188_B2_B06_MR	g3142328	BLASTN	894	2e-33	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13135	GM_188_B2_B06_T7	g13767	BLASTN	344	2e-09	65	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
13136	GM_188_B2_B07_T7	g2522228	BLASTX	177	3e-22	81	(AB007466) reverse transcriptase-like protein [Vicia faba]
13137	GM_188_B2_B09_MR	g2995405	BLASTX	186	1e-12	37	(Y12432) polyprotein [Ananas comosus]
13138	GM_188_B2_B12_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13139	GM_188_B2_D10_T7	g2970554	BLASTN	2009	7e-84	98	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
13140	GM_188_B2_E04_T7	g507910	BLASTN	463	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13141	GM_188_B2_E12_MR	g3142328	BLASTN	1166	7e-46	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13142	GM_188_B2_F05_MR	g2708743	BLASTX	217	1e-15	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
13143	GM_188_B2_F07_MR	g2522230	BLASTX	178	6e-13	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13144	GM_188_B2_F08_MR	g3097320	BLASTN	967	9e-37	78	Glycine max gene for Bd 30K, complete cds
13145	GM_188_B2_F10_T7	g1769897	BLASTX	270	2e-36	71	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13146	GM_188_B2_F12_T7	g3142328	BLASTN	1033	7e-40	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13147	GM_188_B2_G06_T7	g2225930	BLASTN	355	5e-09	66	Human DNA sequence from PAC 52202 on chromosome 6q21 contains ESTs, STSs and polymorphic CA repeat
13148	GM_188_B2_H03_T7	g905361	BLASTX	189	4e-13	32	(U22103) gag-protease polyprotein [Glycine max]
13149	GM_188_B2_H06_T7	g99755	BLASTX	165	1e-18	46	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
13150	GM_188_B2_H07_MR	g1769897	BLASTX	108	1e-08	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13151	GM_188_B2_H10_MR	g2129618	BLASTX	243	1e-18	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13152	GM_188_B2_H12_T7	g3142328	BLASTN	669	3e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13153	GM_189_A2_A02_MR	g507910	BLASTN	415	4e-12	79	Glycine max BSR-101 satellite SB92 genomic sequence.
13154	GM_189_A2_A02_T7	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13155	GM_189_A2_A03_T7	g18559	BLASTN	517	2e-16	66	G.max gene for catalase
13156	GM_189_A2_A07_T7	g2522228	BLASTX	329	6e-29	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
13157	GM_189_A2_A08_T7	g2982303	BLASTX	361	9e-55	87	(AF051236) hypothetical protein [Picea mariana]
13158	GM_189_A2_A09_MR	g507910	BLASTN	516	1e-16	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13159	GM_189_A2_A10_MR	g4038056	BLASTX	191	4e-13	48	(AC005897) putative transposon [Arabidopsis thaliana]
13160	GM_189_A2_A12_MR	g3450842	BLASTX	241	1e-18	71	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]
13161	GM_189_A2_A12_T7	g18559	BLASTN	886	4e-33	74	G.max gene for catalase
13162	GM_189_A2_B02_T7	g507910	BLASTN	413	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13163	GM_189_A2_B03_T7	g4063760	BLASTX	409	8e-51	76	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13164	GM_189_A2_B04_T7	g3283026	BLASTX	142	3e-14	59	putative transposase [Arabidopsis thaliana]
13165	GM_189_A2_C06_MR	g505129	BLASTN	367	1e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13166	GM_189_A2_C08_MR	g2443320	BLASTX	276	2e-27	44	(D85597) polyprotein [Oryza australiensis]
13167	GM_189_A2_C10_MR	g507910	BLASTN	412	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13168	GM_189_A2_C11_T7	g2443320	BLASTX	181	9e-16	47	(D85597) polyprotein [Oryza australiensis]
13169	GM_189_A2_D06_MR	g18559	BLASTN	383	3e-10	73	G.max gene for catalase
13170	GM_189_A2_D10_T7	g3142328	BLASTN	1654	4e-68	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13171	GM_189_A2_D11_MR	g3777527	BLASTX	589	2e-59	95	(AF053008) gag-pol polyprotein [Glycine max]
13172	GM_189_A2_D12_T7	g3426334	BLASTN	473	2e-14	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13173	GM_189_A2_E03_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13174	GM_189_A2_E08_MR	g2443320	BLASTX	297	1e-28	44	(D85597) polyprotein [Oryza australiensis]
13175	GM_189_A2_E08_T7	g507910	BLASTN	498	7e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13176	GM_189_A2_E09_T7	g2864621	BLASTX	153	2e-09	38	hypothetical protein [Arabidopsis thaliana]
13177	GM_189_A2_E11_MR	g4008006	BLASTX	182	2e-12	58	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]
13178	GM_189_A2_F01_MR	g2522227	BLASTX	184	2e-13	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
13179	GM_189_A2_F04_T7	g3142328	BLASTN	1422	1e-57	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13180	GM_189_A2_F09_MR	g1769898	BLASTX	188	2e-28	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13181	GM_189_A2_F10_MR	g2316016	BLASTX	157	1e-10	55	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
13182	GM_189_A2_F12_MR	g3395431	BLASTX	132	7e-11	86	(AC004683) unknown protein [Arabidopsis thaliana]
13183	GM_189_A2_G01_MR	g3777527	BLASTX	610	8e-64	92	(AF053008) gag-pol polyprotein [Glycine max]
13184	GM_189_A2_G06_MR	g3319362	BLASTX	183	7e-18	44	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13185	GM_189_A2_G07_T7	g2129618	BLASTX	154	4e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13186	GM_189_A2_G10_T7	g3695387	BLASTX	153	9e-11	46	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
13187	GM_189_A2_G11_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13188	GM_189_A2_H02_MR	g20613	BLASTN	576	4e-20	70	Phaseolus vulgaris tRNA-Pro(UGG2) gene
13189	GM_189_A2_H05_MR	g3183979	BLASTX	193	2e-13	46	(AJ005171) P69C protein [Lycopersicon esculentum]
13190	GM_189_A2_H06_T7	g1171499	BLASTX	308	9e-27	64	(Z68913) reverse transcriptase [Beta vulgaris]
13191	GM_189_A2_H11_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13192	GM_189_A2_H12_MR	g1840106	BLASTN	404	6e-12	67	Human fragile site locus (FRA16B) minisatellite repeat
13193	GM_189_B1_C12_T7	g2970554	BLASTN	892	3e-33	83	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
13194	GM_189_B1_D09_T7	g170605	BLASTN	369	7e-10	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
13195	GM_189_B2_A04_MR	g4063760	BLASTX	171	8e-11	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13196	GM_189_B2_B03_T7	g169940	BLASTN	388	1e-10	71	Glycine max chalcone synthase (chs6) gene, complete cds.
13197	GM_189_B2_B08_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence
13198	GM_189_B2_B10_T7	g4140691	BLASTX	567	3e-54	78	(AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
13199	GM_189_B2_B11_T7	g629693	BLASTX	145	9e-09	69	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13200	GM_189_B2_C04_MR	g4063756	BLASTN	660	9e-23	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13201	GM_189_B2_C04_T7	g1666236	BLASTX	229	2e-18	31	(U76261) unknown [Hordeum vulgare]
13202	GM_189_B2_C10_MR	g4063760	BLASTX	270	7e-42	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13203	GM_189_B2_C10_T7	g1769897	BLASTX	189	3e-13	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13204	GM_189_B2_C11_T7	g2129618	BLASTX	243	1e-18	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13205	GM_189_B2_D01_T7	g2764526	BLASTN	631	2e-21	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13206	GM_189_B2_D04_MR	g13767	BLASTN	453	3e-14	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
13207	GM_189_B2_D07_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13208	GM_189_B2_E02_T7	g3746069	BLASTX	129	3e-10	35	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
13209	GM_189_B2_E08_T7	g3142328	BLASTN	552	5e-18	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13210	GM_189_B2_E12_T7	g3142379	BLASTX	236	1e-18	57	(AF053008) envelope-like [Glycine max]
13211	GM_189_B2_G01_MR	g3599418	BLASTN	509	5e-16	90	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13212	GM_189_B2_G02_T7	g4063760	BLASTX	240	4e-18	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13213	GM_189_B2_G05_MR	g2826450	BLASTN	356	5e-09	61	Human Chromosome X, complete sequence [Homo sapiens]
13214	GM_189_B2_G05_T7	g2564750	BLASTN	617	8e-21	67	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13215	GM_189_B2_G07_T7	g3171154	BLASTN	354	6e-09	66	Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence [Homo sapiens]
13216	GM_189_B2_G10_MR	g4063760	BLASTX	512	4e-47	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13217	GM_189_B2_G11_MR	g1142703	BLASTN	292	4e-15	78	Glycine max satellite STR120-B.1.
13218	GM_189_B2_H02_T7	g1931647	BLASTX	199	3e-14	64	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]
13219	GM_189_B2_H05_MR	g2865437	BLASTX	131	3e-12	49	(AF039376) polyprotein [Arabidopsis arenosa]
13220	GM_189_B2_H08_MR	g507910	BLASTN	451	9e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13221	GM_189_B2_H08_T7	g4063760	BLASTX	185	3e-12	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13222	GM_190_A1_A01_T7	g2772557	BLASTN	374	7e-10	63	Homo sapiens BAC clone RG437L15 from 8q21, complete sequence [Homo sapiens]
13223	GM_190_A1_A08_MR	g3777527	BLASTX	584	7e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
13224	GM_190_A1_A09_T7	g3250687	BLASTX	275	3e-23	38	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
13225	GM_190_A1_B01_MR	g2443320	BLASTX	209	9e-15	46	(D85597) polyprotein [Oryza australiensis]
13226	GM_190_A1_B07_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13227	GM_190_A1_B07_T7	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13228	GM_190_A1_B08_MR	g4140712	BLASTX	305	1e-28	52	(AF110183) putative integrase [Oryza sativa]
13229	GM_190_A1_B12_MR	g3810596	BLASTX	163	5e-10	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13230	GM_190_A1_C01_T7	g130582	BLASTX	239	5e-18	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13231	GM_190_A1_C03_MR	g1617268	BLASTX	308	3e-33	67	(Z72153) acyl CoA synthetase [Brassica napus]
13232	GM_190_A1_C07_T7	g3097320	BLASTN	857	9e-32	69	Glycine max gene for Bd 30K, complete cds
13233	GM_190_A1_D04_MR	g3319351	BLASTX	208	1e-14	37	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
13234	GM_190_A1_D04_T7	g3935152	BLASTX	161	6e-10	75	(AC005106) T25N20.16 [Arabidopsis thaliana]
13235	GM_190_A1_D07_T7	g2654440	BLASTX	212	1e-16	52	(U70076) Lemir [Lycopersicon esculentum]
13236	GM_190_A1_D08_MR	g3142328	BLASTN	1169	5e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13237	GM_190_A1_E01_MR	g4063756	BLASTN	443	6e-13	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13238	GM_190_A1_E01_T7	g3810596	BLASTX	134	1e-11	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13239	GM_190_A1_E05_T7	g4102691	BLASTN	353	7e-10	81	Glycine max late-embryogenesis abundant protein mRNA, complete cds
13240	GM_190_A1_E06_MR	g507910	BLASTN	502	4e-16	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13241	GM_190_A1_E07_MR	g4006828	BLASTX	174	2e-14	48	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13242	GM_190_A1_F02_MR	g2462134	BLASTX	197	4e-14	35	(Y13368) reverse transcriptase [Beta vulgaris]
13243	GM_190_A1_G02_MR	g507910	BLASTN	388	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13244	GM_190_A1_G08_T7	g3046856	BLASTN	457	1e-13	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]
13245	GM_190_A1_G10_MR	g4063760	BLASTX	178	1e-11	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13246	GM_190_A1_H01_MR	g3777527	BLASTX	394	2e-34	78	(AF053008) gag-pol polyprotein [Glycine max]
13247	GM_190_A1_H01_T7	g2995405	BLASTX	478	6e-44	59	(Y12432) polyprotein [Ananas comosus]
13248	GM_190_A1_H08_T7	g1769898	BLASTX	399	5e-36	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13249	GM_190_A1_H11_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13250	GM_190_A2_A03_MR	g1184075	BLASTX	226	1e-16	43	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
13251	GM_190_A2_A10_MR	g4063756	BLASTN	534	4e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13252	GM_190_A2_B01_MR	g2764526	BLASTN	710	5e-25	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13253	GM_190_A2_B07_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13254	GM_190_A2_B07_T7	g507910	BLASTN	394	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13255	GM_190_A2_B08_T7	g1769899	BLASTX	140	6e-09	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13256	GM_190_A2_B11_T7	g2522227	BLASTX	228	3e-18	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
13257	GM_190_A2_C01_T7	g2462134	BLASTX	381	2e-34	53	(Y13368) reverse transcriptase [Beta vulgaris]
13258	GM_190_A2_C02_MR	g2245082	BLASTX	247	3e-20	45	(Z97343) SCARECROW homolog [Arabidopsis thaliana]
13259	GM_190_A2_C04_MR	g975703	BLASTN	876	1e-32	80	P.sativum GR gene
13260	GM_190_A2_C05_T7	g3142379	BLASTX	242	3e-19	66	(AF053008) envelope-like [Glycine max]
13261	GM_190_A2_C09_MR	g1769898	BLASTX	191	2e-13	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13262	GM_190_A2_C09_T7	g4063760	BLASTX	280	2e-22	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13263	GM_190_A2_D01_T7	g1666236	BLASTX	220	2e-17	31	(U76261) unknown [Hordeum vulgare]
13264	GM_190_A2_D04_T7	g1313926	BLASTX	152	3e-10	46	(X97677) non intermediate filament IFA binding protein [Brassica oleracea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13265	GM_190_A2_D08_MR	g3142328	BLASTN	724	7e-40	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13266	GM_190_A2_D10_MR	g3513747	BLASTX	175	5e-11	29	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
13267	GM_190_A2_E03_MR	g18559	BLASTN	934	3e-35	72	G.max gene for catalase
13268	GM_190_A2_E05_MR	g507910	BLASTN	413	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13269	GM_190_A2_E05_T7	g507910	BLASTN	348	4e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
13270	GM_190_A2_E10_T7	g905361	BLASTX	634	3e-61	94	(U22103) gag-protease polyprotein [Glycine max]
13271	GM_190_A2_F02_MR	g2462058	BLASTX	137	2e-17	46	(Y13389) reverse transcriptase [Antirrhinum majus]
13272	GM_190_A2_F05_MR	g99755	BLASTX	279	3e-25	44	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
13273	GM_190_A2_F07_T7	g2564046	BLASTN	352	7e-09	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]
13274	GM_190_A2_F12_MR	g629693	BLASTX	360	3e-32	49	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13275	GM_190_A2_G02_MR	g3142328	BLASTN	1402	1e-56	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13276	GM_190_A2_G04_MR	g3426334	BLASTN	429	2e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13277	GM_190_A2_G07_T7	g3860271	BLASTX	276	3e-22	45	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
13278	GM_190_A2_G09_T7	g170080	BLASTN	408	2e-11	81	Soybean seed lectin gene transposable element tgm1.
13279	GM_190_A2_G12_T7	g530207	BLASTX	227	6e-17	70	(L35272) heat shock protein [Glycine max]
13280	GM_190_A2_H01_MR	g2760171	BLASTN	351	8e-09	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]
13281	GM_190_A2_H10_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13282	GM_190_A2_H12_T7	g3810596	BLASTX	162	6e-10	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13283	GM_190_B1_A08_T7	g4063760	BLASTX	180	2e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13284	GM_190_B1_B01_T7	g507910	BLASTN	446	1e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13285	GM_190_B1_B03_T7	g4063760	BLASTX	337	1e-38	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13286	GM_190_B1_B04_T7	g3645899	BLASTX	236	1e-23	46	(U68408) 5' end not determined experimentally [Zea mays]
13287	GM_190_B1_B05_T7	g3056580	BLASTX	176	1e-11	51	(AC004255) T1F9.1 [Arabidopsis thaliana]
13288	GM_190_B1_C03_T7	g1806140	BLASTX	217	1e-26	97	(X97314) cdc2MsC [Medicago sativa]
13289	GM_190_B1_C11_T7	g3510347	BLASTN	583	3e-19	73	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13290	GM_190_B1_D02_T7	g3142328	BLASTN	452	2e-13	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13291	GM_190_B1_D11_T7	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13292	GM_190_B1_E09_T7	g3869065	BLASTN	365	2e-09	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
13293	GM_190_B1_E10_T7	g2129709	BLASTX	169	2e-10	38	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
13294	GM_190_B1_E11_T7	g3097320	BLASTN	871	2e-32	76	Glycine max gene for Bd 30K, complete cds
13295	GM_190_B1_E12_T7	g2462058	BLASTX	301	5e-26	56	(Y13389) reverse transcriptase [Antirrhinum majus]
13296	GM_190_B1_F11_T7	g4050011	BLASTN	352	7e-09	70	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
13297	GM_190_B1_G07_T7	g255572	BLASTN	471	2e-19	78	small auxin up RNA gene cluster orf 15A [Glycine max=soybeans, cv. Wayne, Genomic, 637 nt]
13298	GM_190_B1_G10_T7	g2997694	BLASTX	142	9e-16	48	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
13299	GM_190_B1_H01_T7	g3777527	BLASTX	286	7e-23	84	(AF053008) gag-pol polyprotein [Glycine max]
13300	GM_190_B1_H02_T7	g422418	BLASTX	154	4e-09	39	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
13301	GM_190_B1_H07_T7	g3142328	BLASTN	1249	1e-49	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13302	GM_190_B1_H10_T7	g3133272	BLASTN	429	2e-12	68	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence.
13303	GM_190_B2_A03_T7	g3859610	BLASTN	513	4e-16	66	Arabidopsis thaliana BAC T9E19
13304	GM_190_B2_A06_T7	g507910	BLASTN	482	4e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13305	GM_190_B2_B10_T7	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13306	GM_190_B2_D01_T7	g4156152	BLASTN	407	2e-11	62	Homo sapiens clone DJ56J10, complete sequence [Homo sapiens]
13307	GM_190_B2_D12_T7	g2315153	BLASTX	233	3e-22	74	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
13308	GM_190_B2_E04_T7	g3859610	BLASTN	478	1e-14	64	Arabidopsis thaliana BAC T9E19
13309	GM_190_B2_E05_T7	g507910	BLASTN	518	8e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13310	GM_190_B2_F01_T7	g995751	BLASTN	444	3e-13	63	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
13311	GM_190_B2_F04_T7	g2769655	BLASTN	353	7e-09	61	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13312	GM_190_B2_F08_T7	g3860247	BLASTX	131	6e-11	81	(AC005824) unknown protein [Arabidopsis thaliana]
13313	GM_190_B2_F11_T7	g3907448	BLASTN	394	9e-11	68	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
13314	GM_190_B2_G01_T7	g2129618	BLASTX	233	2e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13315	GM_190_B2_G02_T7	g3687234	BLASTX	299	2e-24	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
13316	GM_190_B2_H04_T7	g2443321	BLASTN	385	8e-11	61	Oryza australiensis retrotransposon RIRE1, LTR sequence.
13317	GM_190_B2_H06_T7	g507910	BLASTN	439	3e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13318	GM_191_A1_A01_MR	g507910	BLASTN	405	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13319	GM_191_A1_A01_T7	g3142328	BLASTN	728	5e-26	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13320	GM_191_A1_A05_MR	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13321	GM_191_A1_A05_T7	g4063760	BLASTX	433	1e-38	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13322	GM_191_A1_A10_MR	g3419855	BLASTN	441	7e-13	64	Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence [Homo sapiens]
13323	GM_191_A1_B09_T7	g4063756	BLASTN	420	6e-12	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13324	GM_191_A1_B12_T7	g342965	BLASTN	487	5e-16	66	paramecium species 7,227 mt dna dimer: replication init. region.
13325	GM_191_A1_C02_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13326	GM_191_A1_C02_T7	g1871190	BLASTX	310	6e-27	50	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
13327	GM_191_A1_C08_MR	g282965	BLASTX	251	6e-20	77	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia gi 20565 (Z13998) protein 3 [Petunia hybrida]
13328	GM_191_A1_C11_MR	g18559	BLASTN	771	6e-28	75	G.max gene for catalase
13329	GM_191_A1_D03_T7	g3142330	BLASTX	570	2e-54	94	(U96295) envelope-like [Glycine max]
13330	GM_191_A1_D04_T7	g3281847	BLASTN	311	1e-11	69	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)
13331	GM_191_A1_D08_T7	g2982459	BLASTX	225	6e-18	81	(AL022223) putative protein [Arabidopsis thaliana]
13332	GM_191_A1_D09_T7	g1778375	BLASTN	366	1e-09	88	Pisum sativum PsRT17-1 mRNA, complete cds
13333	GM_191_A1_E02_T7	g4063760	BLASTX	178	1e-11	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13334	GM_191_A1_E04_T7	g3687301	BLASTX	279	1e-22	50	(AJ006376) subtilisin-like protease [Lycopersicon esculentum] gi 3687309 gnl PID e1299614 (AJ006380) subtilisin-like protease [Lycopersicon esculentum]
13335	GM_191_A1_E08_MR	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13336	GM_191_A1_F02_MR	g2129965	BLASTX	206	6e-16	86	Sar1 homolog GTP-binding protein NTGB2 - common tobacco (fragment) gi 1184989 (U46928) NTGB2 [Nicotiana tabacum]
13337	GM_191_A1_F02_T7	g2950210	BLASTX	159	5e-10	84	(Y14615) Importin alpha-like protein [Arabidopsis thaliana]
13338	GM_191_A1_F03_T7	g4063760	BLASTX	448	3e-40	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13339	GM_191_A1_F08_T7	g2459412	BLASTX	273	4e-22	51	(AC002332) putative G9a protein [Arabidopsis thaliana]
13340	GM_191_A1_G06_MR	g507910	BLASTN	611	5e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
13341	GM_191_A1_G08_MR	g3142328	BLASTN	621	4e-21	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13342	GM_191_A1_G10_T7	g3176795	BLASTN	404	7e-12	67	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
13343	GM_191_A1_H06_T7	g3599418	BLASTN	969	6e-37	78	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13344	GM_191_A1_H09_T7	g1399164	BLASTN	377	7e-11	67	Oenothera elata subsp. hookeri chloroplast spacer between (trnG) and (trnH) genes
13345	GM_191_A1_H12_MR	g507910	BLASTN	594	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13346	GM_191_A1_H12_T7	g507910	BLASTN	621	2e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13347	GM_191_A2_A04_T7	g421954	BLASTX	306	2e-27	47	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
13348	GM_191_A2_A10_T7	g1167523	BLASTX	367	1e-31	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13349	GM_191_A2_B01_T7	g18559	BLASTN	1178	2e-46	88	G.max gene for catalase
13350	GM_191_A2_C01_T7	g3777527	BLASTX	764	7e-74	94	(AF053008) gag-pol polyprotein [Glycine max]
13351	GM_191_A2_C02_T7	g2642431	BLASTX	184	5e-12	43	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
13352	GM_191_A2_C08_T7	g3645899	BLASTX	166	9e-18	43	(U68408) 5' end not determined experimentally [Zea mays]
13353	GM_191_A2_C11_T7	g4050011	BLASTN	688	4e-24	68	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
13354	GM_191_A2_C12_T7	g4063760	BLASTX	369	6e-32	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13355	GM_191_A2_D02_T7	g170605	BLASTN	625	8e-22	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
13356	GM_191_A2_D06_T7	g100484	BLASTX	370	2e-32	55	hypothetical protein - garden snapdragon
13357	GM_191_A2_D10_T7	g4296	BLASTN	777	2e-28	98	S. carlsbergensis rDNA not transcribed spacer (NTS) sequence
13358	GM_191_A2_E11_T7	g3142328	BLASTN	803	2e-29	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13359	GM_191_A2_F09_T7	g3096935	BLASTX	121	6e-16	92	(AL023094) putative protein [Arabidopsis thaliana]
13360	GM_191_A2_F10_T7	g342967	BLASTN	258	3e-12	68	paramecium species 8,299 mt dna dimer: replication init. region.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13361	GM_191_A2_G01_T7	g3142328	BLASTN	894	2e-33	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13362	GM_191_A2_G02_T7	g3645899	BLASTX	197	1e-13	34	(U68408) 5' end not determined experimentally [Zea mays]
13363	GM_191_A2_G06_T7	g507910	BLASTN	396	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13364	GM_191_A2_H07_T7	g2244801	BLASTX	188	5e-14	66	(Z97336) hypothetical protein [Arabidopsis thaliana]
13365	GM_191_B1_A04_MR	g99922	BLASTX	299	2e-52	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13366	GM_191_B1_A04_T7	g3152618	BLASTX	235	3e-18	74	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]
13367	GM_191_B1_A05_MR	g169992	BLASTN	1860	2e-78	96	soybean leghemoglobin lba gene.
13368	GM_191_B1_A07_MR	g3645899	BLASTX	166	2e-20	42	(U68408) 5' end not determined experimentally [Zea mays]
13369	GM_191_B1_A07_T7	g1142701	BLASTN	861	1e-32	83	Glycine max satellite STR120-A.3.
13370	GM_191_B1_A08_MR	g2335061	BLASTN	386	2e-10	61	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
13371	GM_191_B1_A10_T7	g3046854	BLASTN	403	4e-11	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]
13372	GM_191_B1_B02_MR	g3128170	BLASTX	232	7e-18	55	(AC004521) hypothetical protein [Arabidopsis thaliana]
13373	GM_191_B1_B04_MR	g2586082	BLASTX	339	1e-28	50	(U72725) retrofit [Oryza longistaminata]
13374	GM_191_B1_B10_T7	g507910	BLASTN	355	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence
13375	GM_191_B1_B12_T7	g2244802	BLASTX	320	2e-26	51	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
13376	GM_191_B1_C09_T7	g4006828	BLASTX	152	7e-09	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13377	GM_191_B1_C10_MR	g2443320	BLASTX	158	5e-11	33	(D85597) polyprotein [Oryza australiensis]
13378	GM_191_B1_C10_T7	g3777527	BLASTX	258	6e-20	44	(AF053008) gag-pol polyprotein [Glycine max]
13379	GM_191_B1_D02_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13380	GM_191_B1_D05_MR	g2073400	BLASTN	384	3e-10	63	Caenorhabditis elegans cosmid Y6G8, complete sequence [Caenorhabditis elegans]
13381	GM_191_B1_E02_MR	g18559	BLASTN	350	8e-09	67	G.max gene for catalase
13382	GM_191_B1_E03_MR	g226407	BLASTX	240	5e-18	43	retrotransposon del1-46 [Lilium henryi]
13383	GM_191_B1_E05_MR	g3645899	BLASTX	468	1e-42	60	(U68408) 5' end not determined experimentally [Zea mays]
13384	GM_191_B1_F02_MR	g2244802	BLASTX	295	6e-24	37	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
13385	GM_191_B1_F02_T7	g3985957	BLASTN	358	4e-09	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
13386	GM_191_B1_F03_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13387	GM_191_B1_F07_T7	g130582	BLASTX	157	4e-16	65	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13388	GM_191_B1_F10_MR	g3941520	BLASTX	104	2e-10	57	(AF062914) putative transcription factor [Arabidopsis thaliana]
13389	GM_191_B1_G02_T7	g4063760	BLASTX	270	2e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13390	GM_191_B1_G04_MR	g507910	BLASTN	402	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13391	GM_191_B1_G04_T7	g3075397	BLASTX	374	2e-33	61	(AC004484) hypothetical protein [Arabidopsis thaliana]
13392	GM_191_B1_G05_MR	g2262105	BLASTX	332	2e-28	71	(AC002343) unknown protein [Arabidopsis thaliana]
13393	GM_191_B1_G08_T7	g421954	BLASTX	234	4e-20	47	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
13394	GM_191_B1_G12_T7	g2828280	BLASTX	172	9e-11	86	(AL021687) putative protein [Arabidopsis thaliana] gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]
13395	GM_191_B1_H05_T7	g2618701	BLASTX	189	4e-14	70	(AC002510) hypothetical protein [Arabidopsis thaliana]
13396	GM_191_B1_H07_MR	g3283026	BLASTX	176	7e-20	41	putative transposase [Arabidopsis thaliana]
13397	GM_191_B1_H07_T7	g531389	BLASTX	185	6e-15	47	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
13398	GM_191_B1_H10_T7	g531389	BLASTX	153	4e-10	41	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
13399	GM_191_B2_A04_MR	g100484	BLASTX	179	5e-12	39	hypothetical protein - garden snapdragon
13400	GM_191_B2_A05_MR	g1871192	BLASTX	179	6e-12	80	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
13401	GM_191_B2_B01_MR	g1087073	BLASTX	204	4e-15	56	(S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa] [Nicotiana tabacum]
13402	GM_191_B2_B02_MR	g4038056	BLASTX	340	5e-29	46	(AC005897) putative transposon [Arabidopsis thaliana]
13403	GM_191_B2_B10_MR	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13404	GM_191_B2_C01_MR	g976284	BLASTX	203	1e-15	39	reverse transcriptase [Arabidopsis thaliana]
13405	GM_191_B2_C02_MR	g18768	BLASTN	485	1e-15	72	Soybean Tgm6 transposable element 3' end
13406	GM_191_B2_C10_MR	g2245104	BLASTX	327	3e-29	73	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
13407	GM_191_B2_D01_MR	g3047066	BLASTX	163	3e-19	54	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
13408	GM_191_B2_E12_MR	g343819	BLASTN	378	6e-11	67	Saccharomyces exiguus mitochondrial Metf-tRNA, Pro-tRNA and putative ribonuclease P subunit.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13409	GM_191_B2_F02_MR	g2769655	BLASTN	430	2e-12	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
13410	GM_191_B2_G02_MR	g507910	BLASTN	513	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13411	GM_191_B2_G04_MR	g3873182	BLASTN	361	3e-09	61	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
13412	GM_191_B2_G06_MR	g18559	BLASTN	522	1e-16	75	G.max gene for catalase
13413	GM_191_B2_G10_MR	g3513745	BLASTX	205	3e-14	38	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
13414	GM_191_B2_H02_MR	g3599418	BLASTN	361	2e-09	87	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13415	GM_191_B2_H06_MR	g1769898	BLASTX	137	1e-14	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13416	GM_191_B2_H12_MR	g2997694	BLASTX	169	7e-17	48	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
13417	GM_192_A2_A01_MR	g3142328	BLASTN	729	5e-26	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13418	GM_192_A2_A02_T7	g13774	BLASTN	346	7e-09	64	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
13419	GM_192_A2_A03_MR	g4140712	BLASTX	238	5e-24	36	(AF110183) putative integrase [Oryza sativa]
13420	GM_192_A2_A05_MR	g18695	BLASTN	370	7e-10	68	Soybean nodulin 22 gene
13421	GM_192_A2_A07_T7	g505129	BLASTN	393	8e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13422	GM_192_A2_A09_MR	g4063760	BLASTX	561	2e-52	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13423	GM_192_A2_A12_MR	g3377834	BLASTX	207	6e-15	33	(AF075598) No definition line found [Arabidopsis thaliana]
13424	GM_192_A2_A12_T7	g4160362	BLASTN	413	1e-11	59	Saccharomyces cerevisiae complete mitochondrial genome
13425	GM_192_A2_B01_T7	g3097320	BLASTN	501	1e-15	69	Glycine max gene for Bd 30K, complete cds
13426	GM_192_A2_B02_MR	g905361	BLASTX	708	4e-69	95	(U22103) gag-protease polyprotein [Glycine max]
13427	GM_192_A2_B04_MR	g1142699	BLASTN	914	5e-35	83	Glycine max satellite STR120-A.1.
13428	GM_192_A2_B05_T7	g3097320	BLASTN	437	9e-13	73	Glycine max gene for Bd 30K, complete cds
13429	GM_192_A2_B09_T7	g3319362	BLASTX	96	7e-10	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13430	GM_192_A2_B12_MR	g18559	BLASTN	545	1e-17	83	G.max gene for catalase
13431	GM_192_A2_C02_MR	g507910	BLASTN	413	5e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13432	GM_192_A2_C04_T7	g4092470	BLASTN	680	1e-23	65	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
13433	GM_192_A2_C07_T7	g4063760	BLASTX	484	3e-44	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13434	GM_192_A2_C08_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13435	GM_192_A2_C08_T7	g507910	BLASTN	385	9e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence
13436	GM_192_A2_C10_MR	g2760170	BLASTN	457	1e-13	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]
13437	GM_192_A2_C12_MR	g4038056	BLASTX	353	2e-30	51	(AC005897) putative transposon [Arabidopsis thaliana]
13438	GM_192_A2_D04_T7	g2832623	BLASTX	255	5e-23	74	(AL021711) protein kinase - like protein [Arabidopsis thaliana]
13439	GM_192_A2_D07_T7	g507910	BLASTN	558	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13440	GM_192_A2_D08_T7	g3786000	BLASTX	151	4e-09	55	(AC005499) hypothetical protein [Arabidopsis thaliana]
13441	GM_192_A2_E02_MR	g505129	BLASTN	396	6e-11	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13442	GM_192_A2_E04_T7	g1370140	BLASTX	215	6e-17	67	(X98308) myb-related transcription factor [Lycopersicon esculentum]
13443	GM_192_A2_E05_MR	g2462134	BLASTX	373	1e-33	43	(Y13368) reverse transcriptase [Beta vulgaris]
13444	GM_192_A2_E05_T7	g3777527	BLASTX	386	2e-41	76	(AF053008) gag-pol polyprotein [Glycine max]
13445	GM_192_A2_E06_MR	g1773014	BLASTX	350	3e-30	55	(Y10338) chloride channel Stelc1 [Solanum tuberosum]
13446	GM_192_A2_E10_T7	g3193317	BLASTX	429	1e-39	62	(AF069299) similar to plant chalcone and stilbene synthases [Arabidopsis thaliana]
13447	GM_192_A2_F02_MR	g3777527	BLASTX	773	7e-75	98	(AF053008) gag-pol polyprotein [Glycine max]
13448	GM_192_A2_F02_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
13449	GM_192_A2_F03_MR	g4063760	BLASTX	365	2e-31	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13450	GM_192_A2_F03_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13451	GM_192_A2_F08_MR	g1666236	BLASTX	156	4e-10	29	(U76261) unknown [Hordeum vulgare]
13452	GM_192_A2_F12_MR	g3319351	BLASTX	220	6e-16	40	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
13453	GM_192_A2_G03_MR	g2462058	BLASTX	317	1e-27	53	(Y13389) reverse transcriptase [Antirrhinum majus]
13454	GM_192_A2_G04_T7	g18559	BLASTN	1086	3e-42	75	G.max gene for catalase
13455	GM_192_A2_G07_MR	g226407	BLASTX	393	2e-34	47	retrotransposon del1-46 [Lilium henryi]
13456	GM_192_A2_G07_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13457	GM_192_A2_G12_T7	g1710401	BLASTX	167	2e-11	75	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) gi 1044912 (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]
13458	GM_192_A2_H02_T7	g2811226	BLASTX	265	3e-21	91	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13459	GM_192_A2_H06_MR	g3097320	BLASTN	1177	3e-46	80	Glycine max gene for Bd 30K, complete cds
13460	GM_192_A2_H08_MR	g3097320	BLASTN	664	5e-23	79	Glycine max gene for Bd 30K, complete cds
13461	GM_192_A2_H10_T7	g703220	BLASTN	546	3e-18	74	Pisum sativum (clone HW16-26) gene fragment.
13462	GM_192_B2_A08_T7	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13463	GM_192_B2_B04_T7	g507910	BLASTN	363	8e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13464	GM_192_B2_B10_MR	g1658457	BLASTX	174	2e-12	75	(U75248) reverse transcriptase [Gossypium barbadense]
13465	GM_192_B2_C05_T7	g507910	BLASTN	352	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13466	GM_192_B2_C07_T7	g3650039	BLASTX	203	1e-14	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13467	GM_192_B2_C11_T7	g99922	BLASTX	278	2e-23	59	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13468	GM_192_B2_D10_T7	g1360633	BLASTN	386	2e-10	69	V.sativa mRNA for protein binding to ENOD12B promoter.
13469	GM_192_B2_E01_T7	g2085783	BLASTN	371	1e-09	64	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
13470	GM_192_B2_F06_MR	g3142328	BLASTN	355	5e-09	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13471	GM_192_B2_F12_T7	g507910	BLASTN	514	1e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13472	GM_192_B2_G08_T7	g1785739	BLASTX	161	3e-11	42	(Y08502) orf240b [Arabidopsis thaliana]
13473	GM_192_B2_G09_T7	g3377848	BLASTX	152	2e-09	46	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
13474	GM_192_B2_H03_T7	g3777527	BLASTX	375	2e-32	84	(AF053008) gag-pol polyprotein [Glycine max]
13475	GM_192_B2_H11_T7	g4063760	BLASTX	184	3e-12	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13476	GM_193_A1_A01_T7	g4063760	BLASTX	336	2e-28	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13477	GM_193_A1_A03_T7	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13478	GM_193_A1_A04_T7	g2995405	BLASTX	320	6e-27	52	(Y12432) polyprotein [Ananas comosus]
13479	GM_193_A1_A10_T7	g2196878	BLASTX	192	1e-17	87	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
13480	GM_193_A1_B04_T7	g2462749	BLASTX	221	1e-16	44	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
13481	GM_193_A1_B05_MR	g507910	BLASTN	534	2e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13482	GM_193_A1_B05_T7	g4063760	BLASTX	409	3e-36	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13483	GM_193_A1_B06_MR	g2129618	BLASTX	229	4e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13484	GM_193_A1_B12_MR	g2244915	BLASTX	185	2e-12	38	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13485	GM_193_A1_C02_T7	g1769899	BLASTX	217	4e-17	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13486	GM_193_A1_C03_T7	g99922	BLASTX	373	2e-48	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13487	GM_193_A1_C06_T7	g2129618	BLASTX	203	2e-14	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13488	GM_193_A1_C07_MR	g2462936	BLASTX	162	4e-15	40	(Y12321) open reading frame 2 [Brassica oleracea]
13489	GM_193_A1_D06_T7	g18767	BLASTN	374	2e-22	79	Soybean Tgm6 transposable element 5' end
13490	GM_193_A1_D07_MR	g417154	BLASTX	260	1e-20	61	HEAT SHOCK PROTEIN 82 gi 100685 pir S25541 heat shock protein 82 - rice (strain Taichung Native One) gi 20256 (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
13491	GM_193_A1_D08_MR	g507910	BLASTN	403	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13492	GM_193_A1_D08_T7	g507910	BLASTN	380	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13493	GM_193_A1_D12_MR	g2764526	BLASTN	455	1e-13	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13494	GM_193_A1_D12_T7	g4063756	BLASTN	492	3e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13495	GM_193_A1_E07_MR	g3513745	BLASTX	238	9e-18	42	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
13496	GM_193_A1_E10_T7	g3097320	BLASTN	1363	1e-54	82	Glycine max gene for Bd 30K, complete cds
13497	GM_193_A1_E12_MR	g4063760	BLASTX	209	7e-15	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13498	GM_193_A1_F08_MR	g3645899	BLASTX	231	2e-23	56	(U68408) 5' end not determined experimentally [Zea mays]
13499	GM_193_A1_F09_T7	g1345644	BLASTX	189	3e-13	50	CYTOCHROME P450 LXXXVI gi 940446 (X90458) cytochrome p450 [Arabidopsis thaliana]
13500	GM_193_A1_G02_T7	g1167523	BLASTX	206	2e-14	42	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13501	GM_193_A1_G06_T7	g549056	BLASTX	446	2e-41	71	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) gi 631651 pir S43059 CCT (chaperonin containing TCP-1) beta chain - mouse gi 468546 (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]
13502	GM_193_A1_G08_T7	g2245044	BLASTX	197	3e-13	49	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
13503	GM_193_A1_H06_T7	g1899158	BLASTN	526	4e-17	64	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13504	GM_193_A1_H07_T7	g13773	BLASTN	347	4e-09	62	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
13505	GM_193_A2_A03_T7	g1840106	BLASTN	429	3e-13	63	Human fragile site locus (FRA16B) minisatellite repeat
13506	GM_193_A2_A04_T7	g2842542	BLASTN	383	3e-10	61	Ipomoea purpurea DNA, LTR retrotransposon RTip1
13507	GM_193_A2_A05_T7	g3914402	BLASTX	226	3e-28	81	PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO I) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME I) (PPX I) >gi 2370333 gnl PID e337830 (Y13465) protoporphyrinogen oxidase [Nicotiana tabacum]
13508	GM_193_A2_A06_MR	g11748	BLASTN	1247	6e-60	91	Nicotiana debneyi chloroplast DNA for tRNA-Ile and ribosomal protein L2
13509	GM_193_A2_A06_T7	g133917	BLASTX	288	1e-24	92	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
13510	GM_193_A2_B02_MR	g2914758	BLASTN	428	3e-12	67	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
13511	GM_193_A2_B02_T7	g3075400	BLASTX	166	9e-11	47	(AC004484) putative thromboxane-A synthase [Arabidopsis thaliana] gi 3413720 (AC004747) putative thromboxin-A synthase [Arabidopsis thaliana]
13512	GM_193_A2_B03_MR	g1399302	BLASTN	783	7e-29	99	Glycine max phosphoinositide-specific phospholipase C P12 mRNA, complete cds.
13513	GM_193_A2_B06_MR	g3650039	BLASTX	235	5e-18	34	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13514	GM_193_A2_B06_T7	g1666236	BLASTX	213	1e-16	31	(U76261) unknown [Hordeum vulgare]
13515	GM_193_A2_B07_T7	g4092471	BLASTN	441	7e-13	67	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
13516	GM_193_A2_B08_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13517	GM_193_A2_B10_T7	g3695395	BLASTX	130	2e-12	63	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
13518	GM_193_A2_C02_MR	g3250687	BLASTX	246	3e-20	40	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
13519	GM_193_A2_C03_MR	g18559	BLASTN	418	7e-12	73	G.max gene for catalase
13520	GM_193_A2_C04_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13521	GM_193_A2_C05_T7	g3142328	BLASTN	990	7e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13522	GM_193_A2_C09_MR	g3645899	BLASTX	350	6e-31	59	(U68408) 5' end not determined experimentally [Zea mays]
13523	GM_193_A2_C09_T7	g4038062	BLASTX	194	2e-13	40	(AC005897) putative transposon MuDR [Arabidopsis thaliana]
13524	GM_193_A2_C10_MR	g3777527	BLASTX	148	2e-14	45	(AF053008) gag-pol polyprotein [Glycine max]
13525	GM_193_A2_D05_T7	g4160362	BLASTN	341	1e-10	62	Saccharomyces cerevisiae complete mitochondrial genome
13526	GM_193_A2_D07_MR	g3033389	BLASTX	168	1e-10	39	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
13527	GM_193_A2_D08_MR	g170029	BLASTN	362	2e-09	77	Glycine max cv. Dare nodulin 26 gene fragment.
13528	GM_193_A2_D12_T7	g2995405	BLASTX	315	1e-28	49	(Y12432) polyprotein [Ananas comosus]
13529	GM_193_A2_E01_T7	g4063756	BLASTN	546	1e-17	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13530	GM_193_A2_E06_MR	g3142328	BLASTN	1458	3e-59	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13531	GM_193_A2_E06_T7	g2462058	BLASTX	257	2e-21	42	(Y13389) reverse transcriptase [Antirrhinum majus]
13532	GM_193_A2_E07_MR	g3142328	BLASTN	773	5e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13533	GM_193_A2_E09_MR	g2462936	BLASTX	150	7e-13	41	(Y12321) open reading frame 2 [Brassica oleracea]
13534	GM_193_A2_F04_MR	g3777527	BLASTX	574	1e-53	83	(AF053008) gag-pol polyprotein [Glycine max]
13535	GM_193_A2_F04_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13536	GM_193_A2_F05_MR	g1236949	BLASTX	222	2e-16	93	(U50075) lipoxygenase L-5 [Glycine max]
13537	GM_193_A2_F07_MR	g4038056	BLASTX	352	3e-30	51	(AC005897) putative transposon [Arabidopsis thaliana]
13538	GM_193_A2_F08_MR	g2129618	BLASTX	264	7e-21	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13539	GM_193_A2_F12_T7	g21595	BLASTN	699	2e-25	70	S. tuberosum U2-22 gene for U2 snRNA
13540	GM_193_A2_G02_T7	g2792208	BLASTX	141	9e-09	35	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
13541	GM_193_A2_G04_MR	g3947735	BLASTX	323	3e-27	51	(AJ009720) NL27 [Solanum tuberosum]
13542	GM_193_A2_G04_T7	g2934885	BLASTX	187	1e-13	94	(L28004) TGACG-motif-binding factor [Glycine max]
13543	GM_193_A2_G07_MR	g3080426	BLASTX	194	2e-13	53	(AL022604) putative protein [Arabidopsis thaliana]
13544	GM_193_A2_H02_T7	g3337361	BLASTX	297	1e-37	65	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
13545	GM_193_A2_H04_T7	g3097320	BLASTN	438	9e-13	70	Glycine max gene for Bd 30K, complete cds
13546	GM_193_A2_H05_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13547	GM_193_A2_H05_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13548	GM_193_A2_H06_MR	g343938	BLASTN	292	2e-14	69	Yeast (S.cerevisiae) mitochondrial Ser-tRNA and ATPase proteolipid genes.
13549	GM_193_A2_H07_MR	g2864621	BLASTX	142	8e-21	38	hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13550	GM_193_A2_H08_MR	g2462134	BLASTX	379	3e-34	53	(Y13368) reverse transcriptase [Beta vulgaris]
13551	GM_193_B1_F03_MR	g559263	BLASTN	269	7e-09	58	Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.
13552	GM_193_B1_F08_MR	g226407	BLASTX	174	6e-19	47	retrotransposon del1-46 [Lilium henryi]
13553	GM_193_B1_G03_MR	g976178	BLASTX	167	8e-12	44	(L47183) reverse transcriptase [Arabidopsis thaliana]
13554	GM_193_B1_G09_MR	g507910	BLASTN	440	3e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13555	GM_193_B2_A01_MR	g2501353	BLASTX	337	1e-29	59	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
13556	GM_193_B2_A06_MR	g2501353	BLASTX	431	8e-40	66	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
13557	GM_193_B2_B04_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13558	GM_193_B2_B04_T7	g507910	BLASTN	378	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13559	GM_193_B2_B07_T7	g99922	BLASTX	486	3e-50	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13560	GM_193_B2_B10_MR	g3645899	BLASTX	415	6e-37	51	(U68408) 5' end not determined experimentally [Zea mays]
13561	GM_193_B2_C01_T7	g1769898	BLASTX	179	3e-14	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13562	GM_193_B2_C02_T7	g18559	BLASTN	362	2e-09	69	G max gene for catalase
13563	GM_193_B2_C03_T7	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13564	GM_193_B2_C08_T7	g3176811	BLASTN	374	8e-11	63	Homo sapiens allele 18 fragile site locus (FRA10B) minisatellite, 3' sequence
13565	GM_193_B2_D02_MR	g905361	BLASTX	195	9e-14	30	(U22103) gag-protease polyprotein [Glycine max]
13566	GM_193_B2_D04_T7	g2832629	BLASTX	172	2e-11	32	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]
13567	GM_193_B2_D05_T7	g3645899	BLASTX	203	1e-16	44	(U68408) 5' end not determined experimentally [Zea mays]
13568	GM_193_B2_D11_T7	g507910	BLASTN	573	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13569	GM_193_B2_D12_T7	g3319345	BLASTX	179	9e-12	35	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
13570	GM_193_B2_E04_T7	g130582	BLASTX	175	3e-11	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13571	GM_193_B2_E07_T7	g4063760	BLASTX	453	7e-41	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13572	GM_193_B2_E08_MR	g1431738	BLASTN	441	5e-13	87	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
13573	GM_193_B2_E08_T7	g2522230	BLASTX	151	4e-10	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13574	GM_193_B2_E09_T7	g2995405	BLASTX	244	8e-19	44	(Y12432) polyprotein [Ananas comosus]
13575	GM_193_B2_E12_T7	g3645899	BLASTX	397	5e-35	60	(U68408) 5' end not determined experimentally [Zea mays]
13576	GM_193_B2_F04_T7	g2244915	BLASTX	121	6e-11	31	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
13577	GM_193_B2_F05_T7	g3097320	BLASTN	1393	4e-56	79	Glycine max gene for Bd 30K, complete cds
13578	GM_193_B2_F08_T7	g3941729	BLASTN	506	8e-16	62	Homo sapiens chromosome 7 BAC clone F5, complete sequence [Homo sapiens]
13579	GM_193_B2_G02_MR	g130582	BLASTX	350	8e-30	46	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13580	GM_193_B2_G12_T7	g1769898	BLASTX	256	7e-24	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13581	GM_193_B2_H01_MR	g3777527	BLASTX	275	1e-21	51	(AF053008) gag-pol polyprotein [Glycine max]
13582	GM_193_B2_H01_T7	g100484	BLASTX	398	2e-35	53	hypothetical protein - garden snapdragon
13583	GM_193_B2_H02_MR	g18559	BLASTN	851	2e-38	73	G.max gene for catalase
13584	GM_193_B2_H07_MR	g3777527	BLASTX	456	5e-41	91	(AF053008) gag-pol polyprotein [Glycine max]
13585	GM_193_B2_H10_MR	g905361	BLASTX	247	2e-19	33	(U22103) gag-protease polyprotein [Glycine max]
13586	GM_194_A1_A01_MR	g4102181	BLASTN	367	1e-09	63	Mus musculus phosphoenolpyruvate carboxykinase (PEPCK) gene, complete cds
13587	GM_194_A1_A01_T7	g3645899	BLASTX	199	4e-23	48	(U68408) 5' end not determined experimentally [Zea mays]
13588	GM_194_A1_A11_MR	g130582	BLASTX	129	6e-09	63	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13589	GM_194_A1_B02_MR	g2995405	BLASTX	220	3e-33	53	(Y12432) polyprotein [Ananas comosus]
13590	GM_194_A1_B08_T7	g4063756	BLASTN	440	8e-13	61	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13591	GM_194_A1_B09_T7	g4063756	BLASTN	502	1e-15	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13592	GM_194_A1_B10_MR	g3377813	BLASTX	254	4e-21	56	(AF076275) No definition line found [Arabidopsis thaliana]
13593	GM_194_A1_C01_T7	g507910	BLASTN	704	3e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
13594	GM_194_A1_C02_T7	g3599418	BLASTN	659	7e-23	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13595	GM_194_A1_C03_MR	g1769897	BLASTX	159	3e-12	35	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13596	GM_194_A1_C04_T7	g1769897	BLASTX	173	6e-36	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13597	GM_194_A1_C10_T7	g4063760	BLASTX	203	3e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13598	GM_194_A1_C12_T7	g1172441	BLASTX	284	3e-24	52	POSSIBLE TRANSCRIPTION FACTOR POSF21 gi 99685 pir S21883 DNA-binding protein POSF21 - Arabidopsis thaliana gi 16429 (X61031) posF21 gene product [Arabidopsis thaliana]
13599	GM_194_A1_D01_MR	g1000971	BLASTN	234	4e-10	62	Hansenula wingei mitochondrial DNA, complete sequence
13600	GM_194_A1_D01_T7	g3845197	BLASTN	352	7e-09	60	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
13601	GM_194_A1_D04_MR	g3264544	BLASTN	351	8e-09	61	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
13602	GM_194_A1_D04_T7	g3810596	BLASTX	151	9e-09	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13603	GM_194_A1_D10_MR	g2443320	BLASTX	191	8e-21	40	(D85597) polyprotein [Oryza australiensis]
13604	GM_194_A1_E01_MR	g4038056	BLASTX	321	5e-27	52	(AC005897) putative transposon [Arabidopsis thaliana]
13605	GM_194_A1_E01_T7	g1906603	BLASTN	744	1e-26	66	Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence
13606	GM_194_A1_E02_T7	g3777527	BLASTX	773	7e-75	92	(AF053008) gag-pol polyprotein [Glycine max]
13607	GM_194_A1_E04_T7	g2443320	BLASTX	179	2e-16	36	(D85597) polyprotein [Oryza australiensis]
13608	GM_194_A1_E12_MR	g2522230	BLASTX	143	3e-09	29	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13609	GM_194_A1_F01_T7	g3097320	BLASTN	494	2e-15	70	Glycine max gene for Bd 30K, complete cds
13610	GM_194_A1_F07_MR	g507910	BLASTN	406	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13611	GM_194_A1_G02_MR	g1666236	BLASTX	146	6e-09	26	(U76261) unknown [Hordeum vulgare]
13612	GM_194_A1_H02_MR	g13373	BLASTN	472	4e-15	65	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
13613	GM_194_A1_H03_MR	g905361	BLASTX	404	2e-36	97	(U22103) gag-protease polyprotein [Glycine max]
13614	GM_194_A1_H04_MR	g3695395	BLASTX	163	2e-12	53	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
13615	GM_194_A1_H07_MR	g18559	BLASTN	625	3e-21	73	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13616	GM_194_A1_H08_MR	g2522227	BLASTX	200	2e-15	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
13617	GM_194_A2_A05_MR	g3097320	BLASTN	1001	3e-38	79	Glycine max gene for Bd 30K, complete cds
13618	GM_194_A2_A05_T7	g2808682	BLASTX	155	3e-09	39	(AJ002235) Hcr9-4C [Lycopersicon hirsutum]
13619	GM_194_A2_A06_MR	g4150930	BLASTN	441	7e-13	60	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
13620	GM_194_A2_A08_MR	g2522229	BLASTN	585	2e-19	64	Vicia faba mRNA expressed from retrotransposon-like gene
13621	GM_194_A2_A12_T7	g3319372	BLASTX	243	2e-18	37	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
13622	GM_194_A2_B01_MR	g336279	BLASTN	368	1e-09	61	Apis mellifera ligustica complete mitochondrial genome
13623	GM_194_A2_B01_T7	g3810596	BLASTX	275	5e-22	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13624	GM_194_A2_B02_T7	g3777527	BLASTX	167	3e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
13625	GM_194_A2_B04_MR	g3319362	BLASTX	306	3e-25	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13626	GM_194_A2_B06_T7	g1666236	BLASTX	228	3e-18	34	(U76261) unknown [Hordeum vulgare]
13627	GM_194_A2_B07_MR	g1644291	BLASTX	170	8e-18	69	(Z73295) receptor-like protein kinase [Catharanthus roseus]
13628	GM_194_A2_B11_T7	g3142328	BLASTN	2096	2e-88	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13629	GM_194_A2_C02_MR	g2264315	BLASTN	355	5e-09	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]
13630	GM_194_A2_C04_MR	g3777527	BLASTX	202	6e-29	50	(AF053008) gag-pol polyprotein [Glycine max]
13631	GM_194_A2_C05_MR	g3097320	BLASTN	387	2e-10	73	Glycine max gene for Bd 30K, complete cds
13632	GM_194_A2_C06_T7	g3097320	BLASTN	528	7e-17	69	Glycine max gene for Bd 30K, complete cds
13633	GM_194_A2_D02_MR	g170065	BLASTN	393	8e-11	75	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
13634	GM_194_A2_D04_MR	g507910	BLASTN	342	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13635	GM_194_A2_D04_T7	g507910	BLASTN	590	5e-20	86	Glycine max BSR-101 satellite SB92 genomic sequence.
13636	GM_194_A2_D05_MR	g3171875	BLASTN	372	9e-10	60	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1
13637	GM_194_A2_D07_MR	g2522228	BLASTX	632	4e-61	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
13638	GM_194_A2_D09_MR	g507910	BLASTN	580	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13639	GM_194_A2_E01_MR	g3777527	BLASTX	236	3e-21	41	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13640	GM_194_A2_E04_MR	g421955	BLASTX	223	1e-31	63	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
13641	GM_194_A2_E06_MR	g18695	BLASTN	354	4e-09	67	Soybean nodulin 22 gene
13642	GM_194_A2_E10_MR	g4063760	BLASTX	242	2e-18	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13643	GM_194_A2_F02_MR	g18559	BLASTN	740	2e-52	74	G.max gene for catalase
13644	GM_194_A2_F03_MR	g905361	BLASTX	437	3e-40	97	(U22103) gag-protease polyprotein [Glycine max]
13645	GM_194_A2_F03_T7	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence
13646	GM_194_A2_F08_T7	g4063760	BLASTX	448	2e-40	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13647	GM_194_A2_F09_MR	g1769898	BLASTX	348	7e-43	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13648	GM_194_A2_G02_MR	g1246823	BLASTX	162	4e-14	84	(X89865) unknown gene product [Phoenix dactylifera]
13649	GM_194_A2_G04_MR	g4140712	BLASTX	208	4e-16	62	(AF110183) putative integrase [Oryza sativa]
13650	GM_194_A2_G11_MR	g18559	BLASTN	1053	1e-40	74	G.max gene for catalase
13651	GM_194_A2_H12_MR	g507910	BLASTN	484	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13652	GM_194_B1_A01_MR	g3947719	BLASTX	237	3e-19	92	(AJ012653) ribosomal protein S28 [Prunus persica] >gi 3947721 gnl PID e1356377 (AJ012654) ribosomal protein S28 [Prunus persica] >gi 3947723 gnl PID e1356379 (AJ012655) ribosomal protein S28 [Prunus persica]
13653	GM_194_B1_A05_MR	g2522230	BLASTX	157	9e-11	34	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13654	GM_194_B1_A08_MR	g2462834	BLASTX	333	2e-29	47	(AF000657) hypothetical protein [Arabidopsis thaliana]
13655	GM_194_B1_B02_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13656	GM_194_B1_B02_T7	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13657	GM_194_B1_B04_T7	g1931642	BLASTX	316	8e-27	56	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
13658	GM_194_B1_B06_MR	g905361	BLASTX	276	2e-22	66	(U22103) gag-protease polyprotein [Glycine max]
13659	GM_194_B1_B08_T7	g3097320	BLASTN	940	2e-35	74	Glycine max gene for Bd 30K, complete cds
13660	GM_194_B1_B09_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13661	GM_194_B1_C01_MR	g3097320	BLASTN	1125	6e-44	79	Glycine max gene for Bd 30K, complete cds
13662	GM_194_B1_C02_T7	g3426334	BLASTN	548	8e-18	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13663	GM_194_B1_C06_T7	g2245073	BLASTN	353	2e-10	61	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
13664	GM_194_B1_C11_MR	g2462935	BLASTX	307	3e-25	45	(Y12321) open reading frame 1 [Brassica oleracea]
13665	GM_194_B1_C11_T7	g343840	BLASTN	427	1e-12	62	Yeast (S.cerevisiae) strain B mitochondrial petite mutant b-1 ori1 region.
13666	GM_194_B1_D01_MR	g2586082	BLASTX	305	6e-25	50	(U72725) retrofit [Oryza longistaminata]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13667	GM_194_B1_D09_T7	g99729	BLASTX	363	1e-32	46	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
13668	GM_194_B1_D12_MR	g4006828	BLASTX	219	4e-16	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13669	GM_194_B1_D12_T7	g629693	BLASTX	150	3e-09	26	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13670	GM_194_B1_E03_MR	g99922	BLASTX	392	1e-35	58	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13671	GM_194_B1_E04_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13672	GM_194_B1_E10_MR	g3033400	BLASTX	221	5e-16	79	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
13673	GM_194_B1_F02_MR	g322660	BLASTX	123	6e-19	48	S-receptor kinase-related protein - Chinese kale gi 17913 (Z18861) S-receptor kinase related protein [Brassica oleracea]
13674	GM_194_B1_F02_T7	g1666236	BLASTX	192	4e-14	32	(U76261) unknown [Hordeum vulgare]
13675	GM_194_B1_F03_MR	g3777527	BLASTX	228	9e-17	41	(AF053008) gag-pol polyprotein [Glycine max]
13676	GM_194_B1_F07_MR	g3282521	BLASTX	390	2e-39	53	tyrosine/dopa decarboxylase [Papaver somniferum]
13677	GM_194_B1_F10_T7	g905361	BLASTX	567	4e-57	90	(U22103) gag-protease polyprotein [Glycine max]
13678	GM_194_B1_F11_T7	g3142328	BLASTN	839	3e-36	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13679	GM_194_B1_G03_MR	g1769899	BLASTX	282	2e-34	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13680	GM_194_B1_G03_T7	g99922	BLASTX	466	2e-43	68	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13681	GM_194_B1_G05_T7	g2995405	BLASTX	223	1e-16	41	(Y12432) polyprotein [Ananas comosus]
13682	GM_194_B1_G09_MR	g2765093	BLASTX	159	5e-10	63	(Y10983) putative cytochrome P450 [Glycine max]
13683	GM_194_B1_G12_MR	g4063760	BLASTX	304	6e-25	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13684	GM_194_B1_H03_T7	g3142328	BLASTN	766	1e-27	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13685	GM_194_B1_H04_MR	g2911052	BLASTX	156	3e-21	56	(AL021961) putative protein [Arabidopsis thaliana]
13686	GM_194_B1_H12_T7	g3142328	BLASTN	633	1e-21	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13687	GM_195_A1_A03_MR	g2995405	BLASTX	226	8e-17	46	(Y12432) polyprotein [Ananas comosus]
13688	GM_195_A1_A04_MR	g1769897	BLASTX	126	2e-12	30	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13689	GM_195_A1_A05_MR	g507910	BLASTN	446	1e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13690	GM_195_A1_A09_MR	g2995405	BLASTX	223	1e-23	49	(Y12432) polyprotein [Ananas comosus]
13691	GM_195_A1_A10_MR	g2129618	BLASTX	193	3e-13	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13692	GM_195_A1_B01_MR	g507910	BLASTN	423	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13693	GM_195_A1_B08_MR	g99922	BLASTX	717	4e-70	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13694	GM_195_A1_B08_T7	g1167523	BLASTX	241	9e-22	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13695	GM_195_A1_B09_MR	g3142328	BLASTN	1715	6e-71	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13696	GM_195_A1_B10_MR	g531389	BLASTX	173	7e-11	41	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
13697	GM_195_A1_B11_MR	g3021268	BLASTX	384	2e-33	52	(AL022347) putative protein [Arabidopsis thaliana]
13698	GM_195_A1_B12_MR	g3264544	BLASTN	440	8e-13	64	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
13699	GM_195_A1_C01_T7	g1769898	BLASTX	274	3e-22	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13700	GM_195_A1_C08_MR	g99688	BLASTX	461	6e-43	93	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana gi 295789 (X16432) elongation factor 1-alpha [Arabidopsis thaliana]
13701	GM_195_A1_C09_MR	g905361	BLASTX	667	9e-65	97	(U22103) gag-protease polyprotein [Glycine max]
13702	GM_195_A1_D02_MR	g2822134	BLASTN	386	2e-10	61	Human Chromosome X, complete sequence [Homo sapiens]
13703	GM_195_A1_D04_T7	g507910	BLASTN	481	4e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13704	GM_195_A1_D06_MR	g3777527	BLASTX	559	1e-52	97	(AF053008) gag-pol polyprotein [Glycine max]
13705	GM_195_A1_D06_T7	g507910	BLASTN	659	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13706	GM_195_A1_D08_T7	g507910	BLASTN	522	6e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13707	GM_195_A1_D09_T7	g1061420	BLASTX	466	2e-43	87	(U38965) p-type H+-ATPase [Vicia faba]
13708	GM_195_A1_E02_MR	g100484	BLASTX	250	8e-22	44	hypothetical protein - garden snapdragon
13709	GM_195_A1_F02_T7	g1658455	BLASTX	129	2e-12	38	(U75247) reverse transcriptase [Gossypium barbadense]
13710	GM_195_A1_F05_T7	g99922	BLASTX	349	4e-31	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13711	GM_195_A1_G02_MR	g3080375	BLASTX	244	3e-19	42	(AL022580) putative protein [Arabidopsis thaliana]
13712	GM_195_A1_G04_MR	g4063760	BLASTX	292	1e-23	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13713	GM_195_A1_G04_T7	g3449326	BLASTN	616	9e-21	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]
13714	GM_195_A1_G08_MR	g1076758	BLASTX	176	1e-11	59	heat-shock protein precursor - rye gi 2130093 pir S65776 heat-shock protein, 82K, precursor - rye gi 556673 (Z30243) heat-shock protein [Secale cereale]
13715	GM_195_A1_G10_MR	g3273150	BLASTN	366	1e-09	64	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-81, complete sequence [Plasmodium falciparum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13716	GM_195_A1_G11_T7	g3142328	BLASTN	628	2e-21	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13717	GM_195_A1_H12_MR	g507910	BLASTN	697	7e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
13718	GM_195_A2_A04_MR	g4063760	BLASTX	472	7e-43	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13719	GM_195_A2_B04_MR	g905361	BLASTX	104	2e-10	28	(U22103) gag-protease polyprotein [Glycine max]
13720	GM_195_A2_C03_MR	g1167523	BLASTX	419	4e-37	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13721	GM_195_A2_C05_MR	g3319362	BLASTX	163	5e-10	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13722	GM_195_A2_D01_MR	g2288997	BLASTX	318	1e-26	63	(AC002335) hypothetical protein [Arabidopsis thaliana]
13723	GM_195_A2_D04_MR	g3377855	BLASTX	145	6e-09	38	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
13724	GM_195_A2_D05_MR	g507910	BLASTN	500	6e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13725	GM_195_A2_D11_MR	g2522228	BLASTX	451	7e-42	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
13726	GM_195_A2_E02_MR	g3820757	BLASTN	359	2e-09	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
13727	GM_195_A2_E11_MR	g3097320	BLASTN	450	2e-13	73	Glycine max gene for Bd 30K, complete cds
13728	GM_195_A2_F01_MR	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13729	GM_195_A2_G04_MR	g18559	BLASTN	547	9e-18	74	G.max gene for catalase
13730	GM_195_A2_H05_MR	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13731	GM_196_A1_A03_MR	g2828780	BLASTN	393	1e-10	62	Homo sapiens chromosome 17, clone 289A8, complete sequence [Homo sapiens]
13732	GM_196_A1_A04_MR	g3386534	BLASTX	263	1e-21	42	(AF078934) mariner transposase [Glycine max]
13733	GM_196_A1_A07_MR	g1666236	BLASTX	227	3e-18	34	(U76261) unknown [Hordeum vulgare]
13734	GM_196_A1_A10_MR	g3287269	BLASTN	509	5e-16	67	S.tuberosum mRNA for protein involved in starch metabolism
13735	GM_196_A1_B02_T7	g3171879	BLASTN	361	3e-09	65	Homo sapiens DNA sequence from PAC 357I16 on chromosome 1p36.13. Contains GSSs, genomic marker D1S449 and a CA repeat polymorphism, complete sequence [Homo sapiens]
13736	GM_196_A1_B03_MR	g3097320	BLASTN	481	1e-14	69	Glycine max gene for Bd 30K, complete cds
13737	GM_196_A1_B03_T7	g18559	BLASTN	1081	5e-42	74	G.max gene for catalase
13738	GM_196_A1_C04_T7	g3142328	BLASTN	864	4e-32	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13739	GM_196_A1_C06_MR	g3097320	BLASTN	866	3e-32	79	Glycine max gene for Bd 30K, complete cds
13740	GM_196_A1_C11_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13741	GM_196_A1_C12_MR	g507910	BLASTN	385	9e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13742	GM_196_A1_D06_T7	g2522228	BLASTX	83	6e-10	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
13743	GM_196_A1_D07_T7	g18700	BLASTN	1105	1e-43	80	Soybean nodulin-23 gene
13744	GM_196_A1_D12_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13745	GM_196_A1_D12_T7	g507910	BLASTN	373	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13746	GM_196_A1_E05_MR	g3097320	BLASTN	466	5e-14	73	Glycine max gene for Bd 30K, complete cds
13747	GM_196_A1_E07_T7	g3687234	BLASTX	229	5e-17	44	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
13748	GM_196_A1_F01_MR	g170606	BLASTN	417	5e-12	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
13749	GM_196_A1_F05_MR	g3776559	BLASTX	393	1e-35	75	(AC005388) Strong similarity to gene F14J9.26 gi 3482933 cdc2 protein kinase homolog from A. thaliana BAC gb AC003970. ESTs gb Z35332 and gb F19907 come from this gene. [Arabidopsis thaliana]
13750	GM_196_A1_F06_MR	g3599418	BLASTN	979	2e-37	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13751	GM_196_A1_F11_MR	g3395432	BLASTX	146	1e-21	80	(AC004683) unknown protein [Arabidopsis thaliana]
13752	GM_196_A1_G11_T7	g3142328	BLASTN	1112	2e-43	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13753	GM_196_A1_G12_MR	g4063756	BLASTN	707	7e-25	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13754	GM_196_A1_H01_MR	g507910	BLASTN	488	2e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13755	GM_196_A1_H07_T7	g2522230	BLASTX	209	3e-20	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13756	GM_196_A1_H08_MR	g1669680	BLASTN	391	1e-10	65	Human DNA sequence from PAC 293E14 contains ESTs, STS
13757	GM_196_A2_A04_MR	g3659406	BLASTN	375	7e-10	65	Homo sapiens Xp22 bins 29-30 BAC GSHB-227L7 (Genome Systems Human BAC Library) complete sequence [Homo sapiens]
13758	GM_196_A2_A05_MR	g3645899	BLASTX	402	1e-35	61	(U68408) 5' end not determined experimentally [Zea mays]
13759	GM_196_A2_A07_T7	g2827635	BLASTX	243	7e-19	52	(AL021636) predicted protein [Arabidopsis thaliana]
13760	GM_196_A2_A10_T7	g22491	BLASTX	128	2e-14	39	(X01380) ORF2 [Zea mays]
13761	GM_196_A2_B02_MR	g905361	BLASTX	206	6e-15	31	(U22103) gag-protease polyprotein [Glycine max]
13762	GM_196_A2_B02_T7	g169157	BLASTN	367	1e-09	64	Pisum sativum serine hydroxymethyltransferase mRNA, complete cds.
13763	GM_196_A2_B08_MR	g1705734	BLASTX	179	4e-16	81	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 2 (CDPK 2) gi 1362176 pir S56652 probable calcium-dependent protein kinase (clone OSCPK2) - rice gi 587498 (X81394) calcium-dependent protein kinase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13764	GM_196_A2_B11_MR	g99922	BLASTX	209	4e-16	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA), pid:e150225 [Glycine max]
13765	GM_196_A2_C01_MR	g3645899	BLASTX	191	6e-13	57	(U68408) 5' end not determined experimentally [Zea mays]
13766	GM_196_A2_C02_T7	g3540184	BLASTX	259	3e-20	55	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]
13767	GM_196_A2_D02_T7	g2522228	BLASTX	238	2e-26	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
13768	GM_196_A2_D06_MR	g4038056	BLASTX	285	4e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
13769	GM_196_A2_D07_MR	g507910	BLASTN	451	9e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13770	GM_196_A2_E12_MR	g4063760	BLASTX	209	3e-32	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13771	GM_196_A2_F02_MR	g18559	BLASTN	680	8e-24	76	G.max gene for catalase
13772	GM_196_A2_F07_MR	g3283026	BLASTX	241	1e-18	42	putative transposase [Arabidopsis thaliana]
13773	GM_196_A2_F07_T7	g1769897	BLASTX	136	2e-13	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13774	GM_196_A2_G02_MR	g507910	BLASTN	372	3e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13775	GM_196_A2_G02_T7	g507910	BLASTN	341	8e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13776	GM_196_A2_G04_T7	g3492889	BLASTN	460	1e-13	70	Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence [Homo sapiens]
13777	GM_196_A2_G07_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13778	GM_196_A2_G07_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13779	GM_196_A2_G10_T7	g4063760	BLASTX	493	4e-45	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13780	GM_196_A2_H10_MR	g4063760	BLASTX	199	9e-14	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13781	GM_196_B1_A02_MR	g3426334	BLASTN	437	9e-13	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13782	GM_196_B1_B10_MR	g4038056	BLASTX	229	4e-17	45	(AC005897) putative transposon [Arabidopsis thaliana]
13783	GM_196_B1_D08_MR	g2443320	BLASTX	196	2e-13	49	(D85597) polyprotein [Oryza australiensis]
13784	GM_196_B1_F06_MR	g1769898	BLASTX	172	7e-14	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13785	GM_196_B1_H01_MR	g3283026	BLASTX	144	5e-13	36	putative transposase [Arabidopsis thaliana]
13786	GM_196_B1_H06_MR	g2462134	BLASTX	304	7e-26	47	(Y13368) reverse transcriptase [Beta vulgaris]
13787	GM_196_B2_A02_MR	g3777527	BLASTX	516	2e-50	90	(AF053008) gag-pol polyprotein [Glycine max]
13788	GM_196_B2_A08_MR	g3377813	BLASTX	199	3e-15	50	(AF076275) No definition line found [Arabidopsis thaliana]
13789	GM_196_B2_A08_T7	g539602	BLASTX	216	3e-16	61	glycine hydroxymethyltransferase (EC 2.1.2.1) precursor, mitochondrial - human (fragment) gi 703093 (L11932) serine hydroxymethyltransferase [Homo sapiens]
13790	GM_196_B2_B05_T7	g507910	BLASTN	481	4e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13791	GM_196_B2_B07_MR	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13792	GM_196_B2_B10_MR	g2129709	BLASTX	253	2e-19	40	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
13793	GM_196_B2_B12_MR	g82309	BLASTX	187	6e-14	55	myb protein 315 - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13794	GM_196_B2_C12_MR	g4150930	BLASTN	428	3e-12	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
13795	GM_196_B2_D07_T7	g3097320	BLASTN	381	3e-10	68	Glycine max gene for Bd 30K, complete cds
13796	GM_196_B2_D10_MR	g507910	BLASTN	574	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13797	GM_196_B2_E01_MR	g4150930	BLASTN	479	1e-14	67	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
13798	GM_196_B2_F01_MR	g18737	BLASTN	349	8e-09	69	Glycine max RPRP3 gene for repetitive proline-rich protein 3
13799	GM_196_B2_F04_MR	g18559	BLASTN	363	2e-09	70	G.max gene for catalase
13800	GM_196_B2_F08_MR	g2190551	BLASTX	205	5e-15	60	(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb Z71181). ESTs gb H36844,gb AA394956 come from this gene. [Arabidopsis thaliana]
13801	GM_196_B2_F10_MR	g3142328	BLASTN	1083	4e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13802	GM_196_B2_G02_MR	g3097320	BLASTN	450	2e-13	69	Glycine max gene for Bd 30K, complete cds
13803	GM_196_B2_G08_MR	g3777527	BLASTX	621	1e-58	94	(AF053008) gag-pol polyprotein [Glycine max]
13804	GM_196_B2_H07_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13805	GM_196_B2_H12_T7	g507910	BLASTN	467	2e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13806	GM_197_A1_A02_MR	g3319362	BLASTX	163	4e-10	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13807	GM_197_A1_A08_T7	g3097320	BLASTN	553	5e-18	74	Glycine max gene for Bd 30K, complete cds
13808	GM_197_A1_A09_T7	g2586082	BLASTX	331	1e-27	49	(U72725) retrofit [Oryza longistaminata]
13809	GM_197_A1_A12_T7	g4063760	BLASTX	562	2e-52	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13810	GM_197_A1_B01_MR	g3859610	BLASTN	571	9e-19	64	Arabidopsis thaliana BAC T9E19
13811	GM_197_A1_B02_MR	g4006831	BLASTX	234	2e-17	39	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13812	GM_197_A1_B03_MR	g4063760	BLASTX	166	3e-10	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13813	GM_197_A1_B06_MR	g507910	BLASTN	423	2e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13814	GM_197_A1_B06_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13815	GM_197_A1_B12_MR	g2462134	BLASTX	242	5e-19	34	(Y13368) reverse transcriptase [Beta vulgaris]
13816	GM_197_A1_C01_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
13817	GM_197_A1_C02_T7	g4115365	BLASTX	175	4e-11	39	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
13818	GM_197_A1_C04_T7	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13819	GM_197_A1_C05_MR	g3777527	BLASTX	392	4e-34	47	(AF053008) gag-pol polyprotein [Glycine max]
13820	GM_197_A1_C05_T7	g3860247	BLASTX	150	2e-21	90	(AC005824) unknown protein [Arabidopsis thaliana]
13821	GM_197_A1_C06_MR	g1666236	BLASTX	162	9e-11	29	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13822	GM_197_A1_C07_T7	g1171978	BLASTX	503	2e-47	78	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) gi 304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] gi 2911051 gnl PID e1253339 (AL021961) poly(A)-binding protein [Arabidopsis thaliana]
13823	GM_197_A1_C09_T7	g2522230	BLASTX	223	1e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13824	GM_197_A1_C10_MR	g1769897	BLASTX	371	2e-33	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13825	GM_197_A1_C12_MR	g2522230	BLASTX	205	1e-24	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13826	GM_197_A1_D01_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13827	GM_197_A1_D01_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13828	GM_197_A1_D05_MR	g3377848	BLASTX	219	2e-22	56	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
13829	GM_197_A1_D07_MR	g3894211	BLASTN	438	9e-13	62	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
13830	GM_197_A1_D09_MR	g3142328	BLASTN	1789	2e-74	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13831	GM_197_A1_E02_MR	g507910	BLASTN	513	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13832	GM_197_A1_E03_MR	g2801423	BLASTN	670	3e-23	66	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
13833	GM_197_A1_E05_MR	g3510340	BLASTN	361	3e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]
13834	GM_197_A1_E11_T7	g3142328	BLASTN	1987	2e-83	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13835	GM_197_A1_F01_MR	g3947735	BLASTX	176	1e-11	37	(AJ009720) NL27 [Solanum tuberosum]
13836	GM_197_A1_F02_MR	g2522230	BLASTX	289	1e-24	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13837	GM_197_A1_F07_MR	g4115365	BLASTX	160	4e-13	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
13838	GM_197_A1_F12_T7	g18559	BLASTN	845	3e-31	77	G.max gene for catalase
13839	GM_197_A1_G01_T7	g3005576	BLASTX	210	1e-15	51	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]
13840	GM_197_A1_G05_T7	g4092470	BLASTN	409	2e-11	64	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
13841	GM_197_A1_G06_T7	g3142328	BLASTN	1834	2e-76	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13842	GM_197_A1_G08_T7	g3695395	BLASTX	267	2e-21	53	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
13843	GM_197_A1_H02_T7	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13844	GM_197_A1_H03_T7	g507910	BLASTN	366	6e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13845	GM_197_A1_H04_T7	g2764526	BLASTN	379	4e-10	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13846	GM_197_A2_A03_T7	g100484	BLASTX	289	9e-24	45	hypothetical protein - garden snapdragon
13847	GM_197_A2_A08_MR	g3845197	BLASTN	446	4e-13	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
13848	GM_197_A2_A10_T7	g13619	BLASTN	385	2e-11	60	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
13849	GM_197_A2_B01_T7	g2342684	BLASTX	392	1e-35	53	(AC000106) F7G19.14 [Arabidopsis thaliana]
13850	GM_197_A2_B02_MR	g1666236	BLASTX	193	3e-14	31	(U76261) unknown [Hordeum vulgare]
13851	GM_197_A2_B04_T7	g3461840	BLASTX	171	3e-14	27	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
13852	GM_197_A2_B05_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13853	GM_197_A2_B06_MR	g3046852	BLASTN	462	8e-14	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]
13854	GM_197_A2_B06_T7	g3777527	BLASTX	313	9e-26	42	(AF053008) gag-pol polyprotein [Glycine max]
13855	GM_197_A2_B07_MR	g3319362	BLASTX	368	6e-32	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13856	GM_197_A2_B08_MR	g3319345	BLASTX	172	5e-11	34	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
13857	GM_197_A2_B09_T7	g507910	BLASTN	374	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13858	GM_197_A2_C01_MR	g3777527	BLASTX	209	3e-25	34	(AF053008) gag-pol polyprotein [Glycine max]
13859	GM_197_A2_C03_T7	g170080	BLASTN	407	2e-11	69	Soybean seed lectin gene transposable element tgm1.
13860	GM_197_A2_C04_T7	g4160362	BLASTN	295	1e-12	67	Saccharomyces cerevisiae complete mitochondrial genome
13861	GM_197_A2_C05_T7	g2864621	BLASTX	133	4e-12	30	hypothetical protein [Arabidopsis thaliana]
13862	GM_197_A2_C08_MR	g1769903	BLASTX	150	4e-14	79	(X95738) proline transporter 2 [Arabidopsis thaliana]
13863	GM_197_A2_D01_MR	g3097320	BLASTN	461	8e-14	70	Glycine max gene for Bd 30K, complete cds
13864	GM_197_A2_D02_MR	g905361	BLASTX	883	1e-87	95	(U22103) gag-protease polyprotein [Glycine max]
13865	GM_197_A2_D03_T7	g3097320	BLASTN	772	6e-28	78	Glycine max gene for Bd 30K, complete cds
13866	GM_197_A2_D05_T7	g3845094	BLASTN	398	6e-11	60	Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence
13867	GM_197_A2_D09_T7	g4063760	BLASTX	231	4e-17	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13868	GM_197_A2_D11_MR	g1769897	BLASTX	534	1e-56	80	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13869	GM_197_A2_D11_T7	g905361	BLASTX	838	6e-83	98	(U22103) gag-protease polyprotein [Glycine max]
13870	GM_197_A2_E04_MR	g2462134	BLASTX	291	2e-24	43	(Y13368) reverse transcriptase [Beta vulgaris]
13871	GM_197_A2_E07_MR	g2275215	BLASTX	207	7e-16	64	(AC002337) hypothetical protein [Arabidopsis thaliana]
13872	GM_197_A2_E08_MR	g1769898	BLASTX	288	8e-24	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13873	GM_197_A2_E09_T7	g4063760	BLASTX	264	1e-20	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13874	GM_197_A2_E11_T7	g507910	BLASTN	341	8e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence
13875	GM_197_A2_G03_MR	g3947733	BLASTX	182	2e-12	36	(AJ009719) NL25 [Solanum tuberosum]
13876	GM_197_A2_H01_MR	g454847	BLASTN	439	7e-13	63	Glycine max ribosomal protein S11 gene, complete cds
13877	GM_197_A2_H04_MR	g2462058	BLASTX	262	7e-22	60	(Y13389) reverse transcriptase [Antirrhinum majus]
13878	GM_197_A2_H07_MR	g3548816	BLASTX	156	5e-09	42	(AC005313) LEA-like protein [Arabidopsis thaliana]
13879	GM_197_B1_B03_T7	g3645899	BLASTX	153	6e-09	53	(U68408) 5' end not determined experimentally [Zea mays]
13880	GM_197_B1_B06_T7	g4063760	BLASTX	251	3e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13881	GM_197_B1_C03_T7	g507910	BLASTN	351	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13882	GM_197_B1_C04_T7	g18559	BLASTN	731	4e-26	86	G.max gene for catalase
13883	GM_197_B1_E04_T7	g3777527	BLASTX	496	2e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
13884	GM_197_B1_G01_T7	g100484	BLASTX	276	2e-22	46	hypothetical protein - garden snapdragon
13885	GM_197_B1_G12_T7	g18559	BLASTN	382	3e-10	72	G.max gene for catalase
13886	GM_197_B1_H07_T7	g1666236	BLASTX	107	3e-10	26	(U76261) unknown [Hordeum vulgare]
13887	GM_198_A2_B04_T7	g3777527	BLASTX	209	1e-14	51	(AF053008) gag-pol polyprotein [Glycine max]
13888	GM_198_A2_B09_MR	g100484	BLASTX	224	9e-17	51	hypothetical protein - garden snapdragon
13889	GM_198_A2_B12_MR	g3250737	BLASTN	367	1e-09	64	Arabidopsis thaliana ASKbeta gene, complete CDS
13890	GM_198_A2_C01_T7	g3777527	BLASTX	181	1e-11	91	(AF053008) gag-pol polyprotein [Glycine max]
13891	GM_198_A2_C04_T7	g4063760	BLASTX	162	5e-24	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13892	GM_198_A2_D01_T7	g4038056	BLASTX	186	2e-12	46	(AC005897) putative transposon [Arabidopsis thaliana]
13893	GM_198_A2_D03_MR	g3250737	BLASTN	370	1e-09	65	Arabidopsis thaliana ASKbeta gene, complete CDS
13894	GM_198_A2_E04_T7	g3142328	BLASTN	668	3e-23	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13895	GM_198_A2_E05_MR	g18559	BLASTN	477	1e-14	71	G.max gene for catalase
13896	GM_198_A2_E11_T7	g2351061	BLASTN	411	2e-11	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19
13897	GM_198_A2_F07_T7	g3142328	BLASTN	688	4e-24	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13898	GM_198_A2_G11_T7	g3688600	BLASTX	278	2e-22	64	(AB009030) beta-Amyrin Synthase [Panax ginseng]
13899	GM_198_A2_G12_T7	g2264320	BLASTN	352	7e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
13900	GM_198_A2_H11_MR	g3142328	BLASTN	509	5e-16	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13901	GM_198_B1_A02_MR	g905361	BLASTX	122	2e-13	28	(U22103) gag-protease polyprotein [Glycine max]
13902	GM_198_B1_A08_MR	g905361	BLASTX	183	2e-12	31	(U22103) gag-protease polyprotein [Glycine max]
13903	GM_198_B1_A09_MR	g2065531	BLASTX	508	6e-48	70	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
13904	GM_198_B1_A10_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13905	GM_198_B1_B02_MR	g18559	BLASTN	739	2e-26	84	G.max gene for catalase
13906	GM_198_B1_B12_MR	g3645899	BLASTX	268	4e-21	60	(U68408) 5' end not determined experimentally [Zea mays]
13907	GM_198_B1_D03_MR	g2522228	BLASTX	193	8e-22	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
13908	GM_198_B1_D07_MR	g18559	BLASTN	906	5e-34	73	G.max gene for catalase
13909	GM_198_B1_E02_MR	g3777527	BLASTX	535	2e-49	94	(AF053008) gag-pol polyprotein [Glycine max]
13910	GM_198_B1_E11_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13911	GM_198_B1_F03_MR	g3097320	BLASTN	774	5e-28	81	Glycine max gene for Bd 30K, complete cds
13912	GM_198_B1_F06_MR	g18559	BLASTN	512	4e-16	70	G.max gene for catalase
13913	GM_198_B1_F08_MR	g1813978	BLASTN	342	2e-09	65	M.acuminata gene encoding putative partial protein homologous to pol gene
13914	GM_198_B1_G04_MR	g3281868	BLASTX	311	4e-26	54	(AL031004) putative protein [Arabidopsis thaliana]
13915	GM_198_B1_G07_MR	g2760316	BLASTN	507	7e-16	71	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
13916	GM_198_B1_G12_MR	g3337396	BLASTN	462	8e-14	67	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence [Homo sapiens]
13917	GM_198_B1_H11_MR	g342965	BLASTN	355	2e-09	61	paramecium species 7,227 mt dna dimer replication init. region.
13918	GM_199_A1_A03_T7	g2997694	BLASTX	183	1e-13	31	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
13919	GM_199_A1_B07_T7	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13920	GM_199_A1_C05_T7	g3282159	BLASTN	495	2e-15	65	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]
13921	GM_199_A1_C08_MR	g2769655	BLASTN	394	9e-11	62	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
13922	GM_199_A1_D03_T7	g507910	BLASTN	367	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13923	GM_199_A1_D08_MR	g18559	BLASTN	776	4e-28	71	G.max gene for catalase
13924	GM_199_A1_D09_T7	g507910	BLASTN	566	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13925	GM_199_A1_D12_T7	g507910	BLASTN	389	6e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13926	GM_199_A1_G02_T7	g2121303	BLASTN	380	4e-10	60	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
13927	GM_199_A1_G06_MR	g2995405	BLASTX	151	7e-09	55	(Y12432) polyprotein [Ananas comosus]
13928	GM_199_A1_G09_T7	g170606	BLASTN	500	8e-16	67	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
13929	GM_199_A1_H07_T7	g507910	BLASTN	492	1e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13930	GM_199_A1_H10_MR	g3142328	BLASTN	867	3e-32	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13931	GM_199_A2_A11_MR	g905361	BLASTX	307	8e-26	87	(U22103) gag-protease polyprotein [Glycine max]
13932	GM_199_A2_C01_MR	g3142328	BLASTN	561	2e-18	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13933	GM_199_A2_D02_MR	g507910	BLASTN	485	3e-15	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13934	GM_199_A2_F01_MR	g3786007	BLASTX	176	9e-12	63	(AC005499) hypothetical protein [Arabidopsis thaliana]
13935	GM_199_A2_G08_MR	g2995405	BLASTX	259	2e-20	60	(Y12432) polyprotein [Ananas comosus]
13936	GM_199_B1_A02_MR	g99922	BLASTX	707	5e-69	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13937	GM_199_B1_A09_MR	g3645899	BLASTX	103	1e-09	36	(U68408) 5' end not determined experimentally [Zea mays]
13938	GM_199_B1_A10_MR	g3097320	BLASTN	1175	3e-46	81	Glycine max gene for Bd 30K, complete cds
13939	GM_199_B1_A10_T7	g2129618	BLASTX	184	3e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13940	GM_199_B1_A11_MR	g1633547	BLASTN	356	5e-09	60	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
13941	GM_199_B1_A11_T7	g2979597	BLASTN	417	8e-12	65	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
13942	GM_199_B1_A12_MR	g4063756	BLASTN	444	5e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13943	GM_199_B1_A12_T7	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
13944	GM_199_B1_B02_MR	g498931	BLASTX	82	3e-11	36	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
13945	GM_199_B1_B05_T7	g2995405	BLASTX	286	3e-23	40	(Y12432) polyprotein [Ananas comosus]
13946	GM_199_B1_B06_T7	g85105	BLASTX	251	2e-19	41	pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 gi 8702 (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]
13947	GM_199_B1_B07_T7	g2462134	BLASTX	256	1e-20	38	(Y13368) reverse transcriptase [Beta vulgaris]
13948	GM_199_B1_B09_MR	g507910	BLASTN	622	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13949	GM_199_B1_B10_MR	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
13950	GM_199_B1_B10_T7	g2522230	BLASTX	150	4e-10	33	(AB007467) retrotransposon-like gene, the first amino acid was determined to be leucine [Vicia faba]
13951	GM_199_B1_B11_T7	g1480927	BLASTN	406	2e-11	86	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
13952	GM_199_B1_C08_MR	g3695019	BLASTX	137	4e-14	72	(AF055848) subtilisin-like protease [Arabidopsis thaliana]
13953	GM_199_B1_C08_T7	g2622367	BLASTX	286	2e-24	48	(AE000892) argininosuccinate synthase [Methanobacterium thermoautotrophicum]
13954	GM_199_B1_C09_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13955	GM_199_B1_D07_MR	g2133392	BLASTX	206	6e-16	37	cyst wall protein 1 - Giardia lamblia gi 606009 (U09330) cyst wall protein 1 [Giardia intestinalis] gi 1097262 prf 2113356A acidic Leu-rich protein [Giardia intestinalis]
13956	GM_199_B1_E02_T7	g4063760	BLASTX	206	2e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13957	GM_199_B1_E03_T7	g3645899	BLASTX	409	3e-36	60	(U68408) 5' end not determined experimentally [Zea mays]
13958	GM_199_B1_E05_T7	g1168518	BLASTX	158	7e-10	68	APURINIC ENDONUCLEASE-REDOX PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE) gi 472869 (X76912) ARP protein [Arabidopsis thaliana]
13959	GM_199_B1_E09_T7	g2443320	BLASTX	335	3e-28	44	(D85597) polyprotein [Oryza australiensis]
13960	GM_199_B1_E11_MR	g4063760	BLASTX	382	2e-33	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13961	GM_199_B1_F01_MR	g18559	BLASTN	1433	5e-58	91	G.max gene for catalase
13962	GM_199_B1_F02_T7	g3947733	BLASTX	150	5e-09	43	(AJ009719) NL25 [Solanum tuberosum]
13963	GM_199_B1_F06_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13964	GM_199_B1_F07_T7	g1142701	BLASTN	233	2e-18	75	Glycine max satellite STR120-A.3.
13965	GM_199_B1_F08_MR	g1066856	BLASTN	582	3e-19	74	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
13966	GM_199_B1_F11_T7	g2995405	BLASTX	336	1e-28	55	(Y12432) polyprotein [Ananas comosus]
13967	GM_199_B1_G05_MR	g100484	BLASTX	252	9e-20	57	hypothetical protein - garden snapdragon
13968	GM_199_B1_G07_MR	g1785739	BLASTX	159	3e-20	40	(Y08502) orf240b [Arabidopsis thaliana]
13969	GM_199_B1_G11_MR	g3097320	BLASTN	441	6e-13	65	Glycine max gene for Bd 30K, complete cds
13970	GM_199_B1_G11_T7	g3097320	BLASTN	427	3e-12	71	Glycine max gene for Bd 30K, complete cds
13971	GM_199_B1_G12_MR	g2522230	BLASTX	271	7e-23	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13972	GM_199_B1_H04_MR	g12137	BLASTN	457	1e-13	70	Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit gene
13973	GM_199_B1_H05_MR	g2829862	BLASTX	311	4e-27	49	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13974	GM_199_B2_A05_T7	g12144	BLASTN	635	5e-22	80	Pea chloroplast genes for F(O)-ATP synthase subunits a and c (partial)
13975	GM_199_B2_B01_T7	g2829109	BLASTN	409	2e-11	66	Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence [Homo sapiens]
13976	GM_199_B2_C03_MR	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence
13977	GM_199_B2_D04_T7	g421955	BLASTX	169	2e-11	49	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
13978	GM_199_B2_F10_T7	g3097320	BLASTN	858	8e-32	81	Glycine max gene for Bd 30K, complete cds
13979	GM_199_B2_H01_T7	g3645899	BLASTX	205	2e-14	54	(U68408) 5' end not determined experimentally [Zea mays]
13980	GM_200_A1_A04_T7	g4050011	BLASTN	558	3e-18	67	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
13981	GM_200_A1_A07_MR	g2443320	BLASTX	251	3e-19	43	(D85597) polyprotein [Oryza australiensis]
13982	GM_200_A1_A09_T7	g82695	BLASTX	168	8e-21	94	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 3 - maize (fragment) gi 293887 (L13431) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
13983	GM_200_A1_A10_MR	g4038056	BLASTX	301	7e-25	52	(AC005897) putative transposon [Arabidopsis thaliana]
13984	GM_200_A1_A11_MR	g22490	BLASTX	141	5e-09	45	(X01380) ORF1 [Zea mays]
13985	GM_200_A1_B12_T7	g4063760	BLASTX	209	8e-15	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13986	GM_200_A1_C08_MR	g3023281	BLASTX	178	1e-13	47	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
13987	GM_200_A1_D01_MR	g3644031	BLASTN	570	3e-19	80	Glycine max plasma membrane proton-ATPase mRNA, partial cds
13988	GM_200_A1_D02_MR	g4063760	BLASTX	380	4e-35	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13989	GM_200_A1_D03_T7	g905361	BLASTX	149	8e-09	83	(U22103) gag-protease polyprotein [Glycine max]
13990	GM_200_A1_D07_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13991	GM_200_A1_E03_MR	g3420054	BLASTX	162	6e-10	35	(AC004680) unknown protein [Arabidopsis thaliana]
13992	GM_200_A1_E08_MR	g3142328	BLASTN	1551	2e-63	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13993	GM_200_A1_E10_T7	g3688328	BLASTX	122	3e-09	54	(AJ228325) reverse transcriptase [Ginkgo biloba]
13994	GM_200_A1_F01_T7	g507910	BLASTN	382	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence
13995	GM_200_A1_F04_MR	g18559	BLASTN	349	9e-09	75	G.max gene for catalase
13996	GM_200_A1_F05_T7	g1769898	BLASTX	196	2e-16	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13997	GM_200_A1_F06_MR	g3777527	BLASTX	504	4e-46	91	(AF053008) gag-pol polyprotein [Glycine max]
13998	GM_200_A1_F06_T7	g3645899	BLASTX	242	3e-22	54	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13999	GM_200_A1_F07_MR	g3047066	BLASTX	178	5e-12	31	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
14000	GM_200_A1_F08_MR	g18559	BLASTN	742	1e-26	73	G.max gene for catalase
14001	GM_200_A1_G08_MR	g3142328	BLASTN	488	4e-15	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14002	GM_200_A1_H06_MR	g3142328	BLASTN	569	9e-19	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14003	GM_200_A1_H07_MR	g4056431	BLASTX	159	4e-10	86	(AC005990) Similar to gb AJ002532 endo-polygalacturonase from Arabidopsis thaliana and is a member of the polygalacturonase family PF 00295. [Arabidopsis thaliana]
14004	GM_200_A1_H08_MR	g3319362	BLASTX	256	5e-20	85	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14005	GM_200_A1_H11_MR	g3097320	BLASTN	656	1e-22	79	Glycine max gene for Bd 30K, complete cds
14006	GM_200_A2_A05_MR	g4063760	BLASTX	176	3e-11	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14007	GM_200_A2_A10_MR	g905361	BLASTX	295	1e-24	67	(U22103) gag-protease polyprotein [Glycine max]
14008	GM_200_A2_C03_T7	g99922	BLASTX	160	2e-19	84	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14009	GM_200_A2_C09_MR	g507910	BLASTN	341	8e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence
14010	GM_200_A2_C12_MR	g2443320	BLASTX	164	6e-10	53	(D85597) polyprotein [Oryza australiensis]
14011	GM_200_A2_D10_MR	g3645899	BLASTX	151	1e-08	41	(U68408) 5' end not determined experimentally [Zea mays]
14012	GM_200_A2_F10_MR	g3176806	BLASTN	365	2e-10	66	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
14013	GM_200_A2_G04_MR	g2462058	BLASTX	177	7e-13	46	(Y13389) reverse transcriptase [Antirrhinum majus]
14014	GM_200_A2_G09_T7	g2264320	BLASTN	467	5e-14	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
14015	GM_200_A2_H06_MR	g507910	BLASTN	500	6e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14016	GM_200_A2_H06_T7	g3142328	BLASTN	495	2e-15	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14017	GM_200_A2_H08_MR	g2565273	BLASTX	145	8e-09	43	(AF023481) o-methytransferase [Medicago sativa]
14018	GM_200_A2_H10_MR	g3510340	BLASTN	551	7e-18	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]
14019	GM_200_B1_A02_MR	g99922	BLASTX	428	1e-44	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14020	GM_200_B1_A04_T7	g629693	BLASTX	206	1e-31	62	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14021	GM_200_B1_A05_T7	g3319362	BLASTX	231	3e-17	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14022	GM_200_B1_A08_MR	g1040717	BLASTN	347	1e-09	60	D.polychroa microsatellite sequence (clone Dp ch1 F3)
14023	GM_200_B1_A10_MR	g3047068	BLASTX	166	4e-12	41	(AF058825) similar to maize transposon MuDR (GB.M76978) [Arabidopsis thaliana]
14024	GM_200_B1_A10_T7	g3142328	BLASTN	1164	8e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14025	GM_200_B1_A12_MR	g4063760	BLASTX	402	2e-35	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14026	GM_200_B1_B03_T7	g4092470	BLASTN	427	3e-12	64	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14027	GM_200_B1_B04_MR	g507910	BLASTN	618	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14028	GM_200_B1_B05_MR	g3142328	BLASTN	671	2e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14029	GM_200_B1_B07_MR	g4063760	BLASTX	285	2e-33	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14030	GM_200_B1_B07_T7	g2522228	BLASTX	158	4e-10	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
14031	GM_200_B1_B09_MR	g4063770	BLASTX	215	1e-15	40	(AB004906) transposase [Ipomoea purpurea]
14032	GM_200_B1_B11_MR	g1167523	BLASTX	350	8e-30	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14033	GM_200_B1_C05_MR	g1171583	BLASTN	357	4e-09	64	P.falciparum complete gene map of plastid-like DNA (IR-A)
14034	GM_200_B1_C05_T7	g2853071	BLASTN	350	9e-09	65	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSAII project)
14035	GM_200_B1_C08_T7	g507910	BLASTN	367	6e-10	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14036	GM_200_B1_C12_T7	g2218024	BLASTN	355	6e-10	64	Apis mellifera mitochondrial tRNA-Leu gene
14037	GM_200_B1_D01_T7	g1167523	BLASTX	136	2e-09	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14038	GM_200_B1_D03_T7	g170602	BLASTN	575	5e-20	64	Broad bean (V.faba) BamHI repetitive element, 900 bp family.
14039	GM_200_B1_D05_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14040	GM_200_B1_D08_T7	g4038056	BLASTX	170	8e-11	46	(AC005897) putative transposon [Arabidopsis thaliana]
14041	GM_200_B1_D09_MR	g2995405	BLASTX	123	4e-19	57	(Y12432) polyprotein [Ananas comosus]
14042	GM_200_B1_D09_T7	g2522228	BLASTX	505	1e-47	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
14043	GM_200_B1_E01_MR	g507910	BLASTN	527	3e-17	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14044	GM_200_B1_E10_T7	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14045	GM_200_B1_E12_MR	g531389	BLASTX	270	3e-33	63	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14046	GM_200_B1_F04_MR	g3142328	BLASTN	1178	2e-46	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14047	GM_200_B1_F06_MR	g4063760	BLASTX	239	4e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14048	GM_200_B1_F07_MR	g507910	BLASTN	499	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14049	GM_200_B1_F11_MR	g629693	BLASTX	363	1e-32	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14050	GM_200_B1_F12_MR	g18559	BLASTN	789	9e-29	74	G.max gene for catalase
14051	GM_200_B1_G02_T7	g3510344	BLASTN	455	2e-13	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
14052	GM_200_B1_G05_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14053	GM_200_B1_G08_MR	g3845197	BLASTN	407	2e-11	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14054	GM_200_B1_G10_MR	g2583123	BLASTX	180	2e-17	68	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]
14055	GM_200_B1_H01_T7	g3426334	BLASTN	484	7e-15	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
14056	GM_200_B1_H03_MR	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14057	GM_200_B1_H06_T7	g3930515	BLASTX	105	2e-10	45	(AF059674) putative gag protein [Nicotiana tabacum]
14058	GM_200_B1_H07_MR	g905361	BLASTX	179	5e-12	29	(U22103) gag-protease polyprotein [Glycine max]
14059	GM_200_B1_H09_T7	g1732513	BLASTX	191	2e-14	76	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
14060	GM_200_B1_H10_T7	g4092470	BLASTN	497	2e-15	68	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14061	GM_200_B2_C11_T7	g3142379	BLASTX	189	1e-17	86	(AF053008) envelope-like [Glycine max]
14062	GM_200_B2_E12_T7	g507910	BLASTN	460	4e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14063	GM_200_B2_G04_T7	g507910	BLASTN	683	3e-24	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14064	GM_201_A2_A02_MR	g18559	BLASTN	510	4e-16	66	G.max gene for catalase
14065	GM_201_A2_A06_MR	g3786021	BLASTX	239	9e-19	50	(AC005499) hypothetical protein [Arabidopsis thaliana]
14066	GM_201_A2_A12_MR	g2642333	BLASTN	845	3e-32	73	Sorghum bicolor tandemly repetitive Sau3A10 DNA element
14067	GM_201_A2_B03_MR	g4063760	BLASTX	182	6e-12	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14068	GM_201_A2_B04_MR	g2462134	BLASTX	224	4e-17	31	(Y13368) reverse transcriptase [Beta vulgaris]
14069	GM_201_A2_B07_MR	g3337395	BLASTN	482	1e-14	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
14070	GM_201_A2_B10_MR	g13988	BLASTN	388	2e-10	67	C. elegans complete mitochondrial genome
14071	GM_201_A2_B11_MR	g18559	BLASTN	822	3e-30	75	G.max gene for catalase
14072	GM_201_A2_C01_MR	g3777527	BLASTX	667	2e-63	90	(AF053008) gag-pol polyprotein [Glycine max]
14073	GM_201_A2_C03_MR	g507910	BLASTN	364	8e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14074	GM_201_A2_C06_MR	g3738325	BLASTX	212	5e-18	46	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]
14075	GM_201_A2_C10_MR	g3097320	BLASTN	1009	1e-38	79	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14076	GM_201_A2_D03_MR	g4063760	BLASTX	343	4e-34	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14077	GM_201_A2_D09_MR	g3142328	BLASTN	2035	1e-85	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14078	GM_201_A2_D11_MR	g3097320	BLASTN	380	4e-10	62	Glycine max gene for Bd 30K, complete cds
14079	GM_201_A2_E02_MR	g2129618	BLASTX	123	1e-12	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14080	GM_201_A2_E10_MR	g3319362	BLASTX	413	8e-37	77	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14081	GM_201_A2_F10_MR	g3777527	BLASTX	228	8e-17	42	(AF053008) gag-pol polyprotein [Glycine max]
14082	GM_201_A2_G02_MR	g507910	BLASTN	398	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14083	GM_201_A2_G04_MR	g3608480	BLASTN	401	4e-12	76	Petunia x hybrida ribosomal protein L27a mRNA, complete cds
14084	GM_201_A2_G06_MR	g905361	BLASTX	199	4e-14	33	(U22103) gag-protease polyprotein [Glycine max]
14085	GM_201_A2_H07_MR	g507910	BLASTN	396	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14086	GM_201_A2_H08_MR	g3777527	BLASTX	662	6e-63	93	(AF053008) gag-pol polyprotein [Glycine max]
14087	GM_201_A2_H09_MR	g507910	BLASTN	344	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14088	GM_201_B2_A05_MR	g507910	BLASTN	394	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14089	GM_201_B2_A11_MR	g3097320	BLASTN	534	4e-17	78	Glycine max gene for Bd 30K, complete cds
14090	GM_201_B2_D01_MR	g2522227	BLASTX	186	1e-13	48	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14091	GM_201_B2_D06_MR	g2352492	BLASTX	228	2e-17	64	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] gi 2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
14092	GM_201_B2_D09_MR	g1769899	BLASTX	122	8e-10	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14093	GM_201_B2_E11_MR	g2522228	BLASTX	238	6e-19	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
14094	GM_201_B2_F05_MR	g3176803	BLASTN	471	3e-15	67	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite sequence
14095	GM_201_B2_G09_MR	g226407	BLASTX	172	9e-11	52	retrotransposon del1-46 [Lilium henryi]
14096	GM_202_A1_A01_MR	g2995405	BLASTX	376	6e-33	58	(Y12432) polyprotein [Ananas comosus]
14097	GM_202_A1_A08_MR	g3176664	BLASTX	338	6e-30	76	(AC004393) Contains similarity to beta scruin gb Z47541 from Limulus polyphemus. ESTs gb T04493 and gb AA585955 come from this gene. [Arabidopsis thaliana]
14098	GM_202_A1_A08_T7	g3510346	BLASTN	449	3e-13	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]
14099	GM_202_A1_A11_MR	g3097320	BLASTN	352	7e-09	68	Glycine max gene for Bd 30K, complete cds
14100	GM_202_A1_B04_MR	g4107343	BLASTX	123	8e-09	47	(AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14101	GM_202_A1_B09_MR	g3395435	BLASTX	312	1e-26	47	(AC004683) myosin heavy chain-like protein [Arabidopsis thaliana]
14102	GM_202_A1_B10_MR	g3930515	BLASTX	125	2e-12	43	(AF059674) putative gag protein [Nicotiana tabacum]
14103	GM_202_A1_C07_MR	g2522227	BLASTX	158	2e-10	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14104	GM_202_A1_C11_MR	g1167523	BLASTX	234	2e-17	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14105	GM_202_A1_D01_MR	g905361	BLASTX	190	4e-13	29	(U22103) gag-protease polyprotein [Glycine max]
14106	GM_202_A1_D03_MR	g2224927	BLASTX	275	8e-24	55	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]
14107	GM_202_A1_D08_MR	g1769897	BLASTX	174	1e-11	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14108	GM_202_A1_D10_MR	g1769897	BLASTX	302	2e-25	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14109	GM_202_A1_F02_MR	g3858933	BLASTN	372	9e-10	75	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSAII project)
14110	GM_202_A1_F04_MR	g2454214	BLASTN	1906	2e-80	96	Glycine max nodule-specific phosphoribosylpyrophosphate amidotransferase (PRAT) gene, 5' upstream sequence and partial cds
14111	GM_202_A1_F05_MR	g507910	BLASTN	521	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14112	GM_202_A1_H10_MR	g4038056	BLASTX	169	1e-10	32	(AC005897) putative transposon [Arabidopsis thaliana]
14113	GM_202_A2_A03_T7	g507910	BLASTN	484	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14114	GM_202_A2_A04_T7	g18559	BLASTN	1080	6e-42	77	G.max gene for catalase
14115	GM_202_A2_B02_T7	g507910	BLASTN	587	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14116	GM_202_A2_C05_T7	g507910	BLASTN	341	8e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
14117	GM_202_A2_C10_T7	g4038056	BLASTX	341	4e-29	44	(AC005897) putative transposon [Arabidopsis thaliana]
14118	GM_202_A2_D07_T7	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14119	GM_202_A2_D12_T7	g3142330	BLASTX	182	2e-39	78	(U96295) envelope-like [Glycine max]
14120	GM_202_A2_E08_T7	g2264311	BLASTN	426	3e-12	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]
14121	GM_202_A2_E10_T7	g2462134	BLASTX	241	3e-25	49	(Y13368) reverse transcriptase [Beta vulgaris]
14122	GM_202_A2_F02_T7	g3402684	BLASTX	487	1e-45	67	(AC004697) hypothetical protein [Arabidopsis thaliana]
14123	GM_202_B1_A02_MR	g1840106	BLASTN	411	3e-12	65	Human fragile site locus (FRA16B) minisatellite repeat
14124	GM_202_B1_A07_MR	g3645899	BLASTX	213	6e-17	59	(U68408) 5' end not determined experimentally [Zea mays]
14125	GM_202_B1_A07_T7	g629693	BLASTX	205	4e-29	57	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14126	GM_202_B1_A12_MR	g20861	BLASTN	357	4e-09	71	P.sativum retrotransposon
14127	GM_202_B1_A12_T7	g387902	BLASTX	143	3e-09	30	(L23524) ORF [Hordeum vulgare]
14128	GM_202_B1_B03_MR	g467491	BLASTN	605	5e-21	73	Chlorella vulgaris genomic DNA, telomeric repeat
14129	GM_202_B1_B03_T7	g1167523	BLASTX	239	6e-18	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14130	GM_202_B1_B07_MR	g3142328	BLASTN	1103	5e-43	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14131	GM_202_B1_B10_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14132	GM_202_B1_C02_MR	g3513747	BLASTX	179	4e-17	46	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
14133	GM_202_B1_C06_MR	g4063760	BLASTX	326	3e-27	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14134	GM_202_B1_C10_T7	g905360	BLASTN	363	2e-09	79	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
14135	GM_202_B1_D02_T7	g3758836	BLASTN	333	6e-10	71	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
14136	GM_202_B1_D08_MR	g2264320	BLASTN	609	2e-20	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
14137	GM_202_B1_E01_T7	g1769898	BLASTX	150	4e-17	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14138	GM_202_B1_E09_MR	g3777527	BLASTX	526	2e-48	92	(AF053008) gag-pol polyprotein [Glycine max]
14139	GM_202_B1_F01_MR	g18559	BLASTN	669	3e-25	72	G.max gene for catalase
14140	GM_202_B1_F02_T7	g1906825	BLASTN	581	2e-19	76	A.thaliana hsp81.2 gene
14141	GM_202_B1_F05_MR	g2959734	BLASTX	170	3e-17	72	(Y13650) homologous to GATA-binding transcription factors [Arabidopsis thaliana]
14142	GM_202_B1_F05_T7	g2264318	BLASTN	472	3e-14	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
14143	GM_202_B1_F06_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14144	GM_202_B1_F09_MR	g218269	BLASTX	365	8e-33	86	(D12839) reverse transcriptase [Glycine max]
14145	GM_202_B1_F12_MR	g3283026	BLASTX	163	3e-10	30	putative transposase [Arabidopsis thaliana]
14146	GM_202_B1_G01_MR	g340796	BLASTN	411	2e-12	62	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
14147	GM_202_B1_G07_MR	g4063760	BLASTX	282	1e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14148	GM_202_B1_G09_MR	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
14149	GM_203_A1_A05_T7	g3777527	BLASTX	225	2e-16	81	(AF053008) gag-pol polyprotein [Glycine max]
14150	GM_203_A1_A06_MR	g840618	BLASTN	369	7e-10	59	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
14151	GM_203_A1_A07_MR	g4063756	BLASTN	597	6e-20	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14152	GM_203_A1_A08_MR	g4063760	BLASTX	336	2e-28	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14153	GM_203_A1_A10_MR	g2443329	BLASTX	156	2e-09	35	(D86122) Mei2-like protein [Arabidopsis thaliana]
14154	GM_203_A1_B02_MR	g4063760	BLASTX	175	3e-11	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14155	GM_203_A1_B06_MR	g3283026	BLASTX	284	3e-23	40	putative transposase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14156	GM_203_A1_B12_MR	g99729	BLASTX	238	2e-19	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
14157	GM_203_A1_C08_MR	g507910	BLASTN	582	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14158	GM_203_A1_C12_MR	g505129	BLASTN	385	2e-10	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
14159	GM_203_A1_D01_T7	g2842490	BLASTX	163	8e-11	40	(AL021749) heat-shock protein [Arabidopsis thaliana]
14160	GM_203_A1_D04_MR	g507910	BLASTN	634	5e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14161	GM_203_A1_D08_MR	g4006833	BLASTX	259	4e-20	39	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
14162	GM_203_A1_E03_MR	g2522230	BLASTX	170	4e-12	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14163	GM_203_A1_E06_MR	g4063756	BLASTN	506	8e-16	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14164	GM_203_A1_E07_MR	g4063760	BLASTX	454	5e-41	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14165	GM_203_A1_F03_MR	g3319372	BLASTX	239	5e-18	42	(AF077409) similar to reverse transcriptases (PFam: rvt hmm, score: 60.13) [Arabidopsis thaliana]
14166	GM_203_A1_F06_MR	g1418331	BLASTX	219	2e-16	32	(X95909) receptor like protein kinase [Arabidopsis thaliana]
14167	GM_203_A1_F11_T7	g2443320	BLASTX	180	1e-11	52	(D85597) polyprotein [Oryza australiensis]
14168	GM_203_A1_G09_MR	g1142703	BLASTN	273	8e-15	75	Glycine max satellite STR120-B.1.
14169	GM_203_A1_G10_MR	g3142328	BLASTN	1242	2e-49	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14170	GM_203_A1_G12_MR	g507910	BLASTN	414	4e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14171	GM_203_A1_H11_T7	g178823	BLASTN	336	5e-09	62	Human apolipoprotein B gene hypervariable region, 3' flank.
14172	GM_203_A2_A09_T7	g4038056	BLASTX	319	9e-27	50	(AC005897) putative transposon [Arabidopsis thaliana]
14173	GM_203_A2_B04_T7	g2244803	BLASTX	241	5e-24	44	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
14174	GM_203_A2_B07_T7	g3283026	BLASTX	197	7e-14	36	putative transposase [Arabidopsis thaliana]
14175	GM_203_A2_B09_T7	g1850550	BLASTX	103	5e-09	45	(U88030) reverse transcriptase [Secale cereale]
14176	GM_203_A2_C07_T7	g4063760	BLASTX	124	2e-12	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14177	GM_203_A2_C10_T7	g2522228	BLASTX	187	3e-13	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
14178	GM_203_A2_C12_T7	g3513747	BLASTX	175	5e-11	47	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
14179	GM_203_A2_D03_T7	g3668073	BLASTN	388	2e-10	65	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]
14180	GM_203_A2_D04_T7	g3097320	BLASTN	845	3e-31	82	Glycine max gene for Bd 30K, complete cds
14181	GM_203_A2_E02_T7	g4063760	BLASTX	296	4e-24	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14182	GM_203_A2_E03_T7	g905361	BLASTX	321	2e-47	82	(U22103) gag-protease polyprotein [Glycine max]
14183	GM_203_A2_E07_T7	g2764526	BLASTN	467	4e-14	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
14184	GM_203_A2_F03_T7	g2129618	BLASTX	152	7e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14185	GM_203_A2_F04_T7	g2586082	BLASTX	184	4e-16	48	(U72725) retrofit [Oryza longistaminata]
14186	GM_203_B1_A09_MR	g3142328	BLASTN	951	4e-36	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14187	GM_203_B1_B06_T7	g1167523	BLASTX	169	1e-10	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14188	GM_203_B1_B08_T7	g3645899	BLASTX	192	4e-13	50	(U68408) 5' end not determined experimentally [Zea mays]
14189	GM_203_B1_C03_T7	g416692	BLASTX	151	1e-12	70	AUXIN-INDUCED PROTEIN 6B gi 81764 pir JQ1098 auxin-induced protein 6B - soybean gi 255577 bbs 113700 (S44175) orf 6B [Glycine max=soybeans, cv. Wayne, Peptide, 90 aa] [Glycine max]
14190	GM_203_B1_D05_T7	g3599418	BLASTN	785	1e-28	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14191	GM_203_B1_D08_MR	g3142328	BLASTN	582	2e-19	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14192	GM_203_B1_F03_MR	g3142328	BLASTN	437	9e-13	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14193	GM_203_B1_G03_T7	g3928750	BLASTN	354	4e-09	75	Broad bean necrosis virus genes for triple-gene-block proteins and glycine-rich protein, partial and complete cds
14194	GM_203_B2_A01_MR	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14195	GM_203_B2_B04_MR	g507910	BLASTN	429	9e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14196	GM_203_B2_B05_MR	g2160694	BLASTX	534	1e-50	88	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
14197	GM_203_B2_B05_T7	g1002593	BLASTN	444	3e-13	69	Lycopersicon peruvianum self incompatibility (s11) gene, complete cds.
14198	GM_203_B2_B07_MR	g4156188	BLASTN	389	9e-13	68	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
14199	GM_203_B2_B08_MR	g13767	BLASTN	396	9e-12	61	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
14200	GM_203_B2_B09_MR	g4038056	BLASTX	330	6e-28	52	(AC005897) putative transposon [Arabidopsis thaliana]
14201	GM_203_B2_C01_MR	g3645899	BLASTX	232	5e-28	50	(U68408) 5' end not determined experimentally [Zea mays]
14202	GM_203_B2_C02_MR	g4038056	BLASTX	236	7e-18	49	(AC005897) putative transposon [Arabidopsis thaliana]
14203	GM_203_B2_D03_MR	g18559	BLASTN	916	2e-34	75	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14204	GM_203_B2_D08_MR	g3645899	BLASTX	175	3e-11	58	(U68408) 5' end not determined experimentally [Zea mays]
14205	GM_203_B2_F08_MR	g2098708	BLASTN	558	3e-18	69	Citrus sinensis pectinesterase (PECS-2.1) gene, complete cds.
14206	GM_203_B2_F10_MR	g1142702	BLASTN	342	6e-09	75	Glycine max satellite STR120-A.4.
14207	GM_203_B2_G04_MR	g2129618	BLASTX	268	3e-21	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14208	GM_203_B2_G06_MR	g3176768	BLASTN	396	7e-12	63	Homo sapiens allele 1 fragile site locus (FRA10B) minisatellite, 3' sequence
14209	GM_203_B2_G10_MR	g3810596	BLASTX	181	6e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14210	GM_203_B2_H07_MR	g1769898	BLASTX	439	1e-40	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14211	GM_204_A1_A01_T7	g3142328	BLASTN	855	9e-32	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14212	GM_204_A1_B02_T7	g3142328	BLASTN	469	3e-14	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14213	GM_204_A1_D03_T7	g100484	BLASTX	225	2e-19	63	hypothetical protein - garden snapdragon
14214	GM_204_A1_E04_T7	g3599418	BLASTN	1816	2e-75	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14215	GM_204_A1_F07_T7	g3176784	BLASTN	445	7e-14	64	Homo sapiens allele 7 fragile site locus (FRA10B) minisatellite sequence
14216	GM_204_A1_G09_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14217	GM_204_A1_G12_T7	g507910	BLASTN	346	5e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14218	GM_204_A1_H10_T7	g13581	BLASTN	351	1e-09	66	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
14219	GM_204_A2_A05_T7	g553114	BLASTX	101	3e-09	82	(M80491) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]
14220	GM_204_A2_B03_T7	g3645899	BLASTX	142	3e-16	36	(U68408) 5' end not determined experimentally [Zea mays]
14221	GM_204_A2_B06_T7	g3695395	BLASTX	163	3e-10	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14222	GM_204_A2_B11_T7	g507910	BLASTN	382	1e-10	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14223	GM_204_A2_D09_T7	g3264544	BLASTN	360	3e-09	65	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
14224	GM_204_A2_F01_T7	g99730	BLASTX	122	7e-16	51	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
14225	GM_204_A2_F12_T7	g905361	BLASTX	495	2e-46	93	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14226	GM_204_A2_G01_T7	g2225930	BLASTN	363	2e-09	64	Human DNA sequence from PAC 522O2 on chromosome 6q21 contains ESTs, STSs and polymorphic CA repeat
14227	GM_204_A2_G08_T7	g3687222	BLASTX	137	2e-16	36	(AC005169) hypothetical protein [Arabidopsis thaliana]
14228	GM_204_A2_H03_T7	g3142328	BLASTN	1347	4e-54	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14229	GM_204_A2_H04_T7	g3142328	BLASTN	1366	5e-55	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14230	GM_204_A2_H09_T7	g3845111	BLASTN	357	4e-09	61	Plasmodium falciparum chromosome 2, section 14 of 73 of the complete sequence
14231	GM_204_B1_A01_T7	g2894606	BLASTX	172	2e-11	67	(AL021889) putative protein [Arabidopsis thaliana]
14232	GM_204_B1_A03_MR	g4006838	BLASTN	477	2e-14	63	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
14233	GM_204_B1_A03_T7	g3142328	BLASTN	1745	3e-72	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14234	GM_204_B1_A09_MR	g18559	BLASTN	467	4e-14	78	G.max gene for catalase
14235	GM_204_B1_B09_T7	g4038056	BLASTX	242	1e-18	48	(AC005897) putative transposon [Arabidopsis thaliana]
14236	GM_204_B1_B11_MR	g1769898	BLASTX	454	3e-42	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14237	GM_204_B1_B12_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14238	GM_204_B1_B12_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14239	GM_204_B1_C02_T7	g3283026	BLASTX	194	1e-13	35	putative transposase [Arabidopsis thaliana]
14240	GM_204_B1_C12_MR	g100484	BLASTX	400	9e-36	50	hypothetical protein - garden snapdragon
14241	GM_204_B1_D03_MR	g2522228	BLASTX	470	6e-44	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
14242	GM_204_B1_D04_MR	g3777527	BLASTX	493	2e-59	90	(AF053008) gag-pol polyprotein [Glycine max]
14243	GM_204_B1_D10_MR	g2961349	BLASTX	350	6e-30	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
14244	GM_204_B1_D10_T7	g1881562	BLASTN	364	2e-09	62	Human cosmid g1346a045, complete sequence [Homo sapiens]
14245	GM_204_B1_D12_T7	g226407	BLASTX	188	2e-12	41	retrotransposon del1-46 [Lilium henryi]
14246	GM_204_B1_E06_MR	g3777527	BLASTX	175	5e-11	36	(AF053008) gag-pol polyprotein [Glycine max]
14247	GM_204_B1_E11_MR	g2865424	BLASTX	238	3e-23	48	(AF039371) polyprotein [Arabidopsis thaliana]
14248	GM_204_B1_F05_T7	g1769898	BLASTX	140	3e-15	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14249	GM_204_B1_F07_MR	g3930515	BLASTX	120	2e-12	35	(AF059674) putative gag protein [Nicotiana tabacum]
14250	GM_204_B1_F08_T7	g4038029	BLASTN	450	3e-13	62	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]
14251	GM_204_B1_F09_MR	g3688328	BLASTX	140	3e-18	65	(AJ228325) reverse transcriptase [Ginkgo biloba]
14252	GM_204_B1_F10_MR	g3142328	BLASTN	714	2e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14253	GM_204_B1_G08_MR	g1171583	BLASTN	353	6e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
14254	GM_204_B1_H03_MR	g4063760	BLASTX	316	3e-26	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14255	GM_204_B1_H08_T7	g2522227	BLASTX	147	3e-09	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14256	GM_204_B1_H11_MR	g3097320	BLASTN	894	2e-33	83	Glycine max gene for Bd 30K, complete cds
14257	GM_204_B2_A04_MR	g2995405	BLASTX	261	1e-20	58	(Y12432) polyprotein [Ananas comosus]
14258	GM_204_B2_A08_MR	g507910	BLASTN	382	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14259	GM_204_B2_C12_MR	g507910	BLASTN	374	3e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14260	GM_204_B2_D11_T7	g2586082	BLASTX	254	2e-19	53	(U72725) retrofit [Oryza longistaminata]
14261	GM_204_B2_E02_T7	g507910	BLASTN	368	5e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14262	GM_204_B2_E08_MR	g507910	BLASTN	354	2e-09	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14263	GM_204_B2_F01_MR	g3777527	BLASTX	253	2e-19	94	(AF053008) gag-pol polyprotein [Glycine max]
14264	GM_204_B2_F11_MR	g100484	BLASTX	159	9e-10	48	hypothetical protein - garden snapdragon
14265	GM_205_A1_A03_MR	g1769898	BLASTX	383	1e-37	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14266	GM_205_A1_A04_MR	g1167523	BLASTX	204	3e-14	38	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14267	GM_205_A1_A09_MR	g4140712	BLASTX	177	7e-13	40	(AF110183) putative integrase [Oryza sativa]
14268	GM_205_A1_B07_MR	g1066856	BLASTN	441	7e-13	68	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
14269	GM_205_A1_B08_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14270	GM_205_A1_B12_MR	g2522230	BLASTX	297	1e-25	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14271	GM_205_A1_C10_T7	g507910	BLASTN	506	3e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14272	GM_205_A1_C11_T7	g3548810	BLASTX	78	3e-11	77	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
14273	GM_205_A1_D01_MR	g1351780	BLASTX	228	2e-23	78	HYPOTHETICAL 23.2 KD PROTEIN (ORF 203) gi 984311 (U26948) unknown [Glycine max]
14274	GM_205_A1_D01_T7	g984307	BLASTN	1537	1e-62	96	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso...
14275	GM_205_A1_D04_T7	g3845197	BLASTN	436	1e-12	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14276	GM_205_A1_D05_MR	g3142328	BLASTN	1156	2e-45	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14277	GM_205_A1_D12_MR	g1167523	BLASTX	278	6e-25	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14278	GM_205_A1_E02_MR	g3142328	BLASTN	651	1e-38	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14279	GM_205_A1_E04_T7	g1621465	BLASTX	217	3e-29	82	(U73105) laccase [Liriodendron tulipifera]
14280	GM_205_A1_E05_MR	g3097320	BLASTN	978	3e-37	79	Glycine max gene for Bd 30K, complete cds
14281	GM_205_A1_E10_T7	g2854105	BLASTN	378	1e-10	67	Citrus limon copia-like retrotransposon Ccr15 reverse transcriptase pseudogene, partial sequence
14282	GM_205_A1_E11_MR	g4063760	BLASTX	232	3e-17	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14283	GM_205_A1_F02_T7	g2462134	BLASTX	196	5e-14	35	(Y13368) reverse transcriptase [Beta vulgaris]
14284	GM_205_A1_F03_MR	g130582	BLASTX	155	5e-09	30	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14285	GM_205_A1_F05_MR	g170029	BLASTN	396	7e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
14286	GM_205_A1_F11_MR	g4056489	BLASTX	266	3e-21	72	(AC005896) putative white protein [Arabidopsis thaliana]
14287	GM_205_A1_F12_MR	g18559	BLASTN	396	6e-11	72	G.max gene for catalase
14288	GM_205_A1_G03_MR	g3142328	BLASTN	645	3e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14289	GM_205_A1_G03_T7	g18559	BLASTN	382	3e-10	74	G.max gene for catalase
14290	GM_205_A1_G09_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14291	GM_205_A1_G10_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14292	GM_205_A1_G10_T7	g507910	BLASTN	388	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14293	GM_205_A1_G12_MR	g100484	BLASTX	354	9e-31	56	hypothetical protein - garden snapdragon
14294	GM_205_A1_H01_T7	g4050011	BLASTN	378	4e-10	61	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
14295	GM_205_A1_H06_T7	g3777527	BLASTX	200	2e-31	72	(AF053008) gag-pol polyprotein [Glycine max]
14296	GM_205_A1_H11_MR	g3777527	BLASTX	500	1e-45	84	(AF053008) gag-pol polyprotein [Glycine max]
14297	GM_205_A1_H12_T7	g3645899	BLASTX	169	1e-10	58	(U68408) 5' end not determined experimentally [Zea mays]
14298	GM_205_A2_A01_MR	g4038056	BLASTX	280	1e-22	50	(AC005897) putative transposon [Arabidopsis thaliana]
14299	GM_205_A2_A03_T7	g2443320	BLASTX	305	5e-25	45	(D85597) polyprotein [Oryza australiensis]
14300	GM_205_A2_A06_MR	g3142328	BLASTN	830	1e-30	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14301	GM_205_A2_A07_MR	g2995405	BLASTX	222	2e-16	37	(Y12432) polyprotein [Ananas comosus]
14302	GM_205_A2_A07_T7	g4063760	BLASTX	233	2e-28	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14303	GM_205_A2_A11_MR	g421953	BLASTX	163	7e-11	33	hypothetical protein 2 - potato transposon Tst1 gi 21432 (X52387) ORF2 [Solanum tuberosum]
14304	GM_205_A2_A12_T7	g2739003	BLASTN	575	3e-19	81	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
14305	GM_205_A2_B03_T7	g3337395	BLASTN	447	4e-13	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
14306	GM_205_A2_B05_MR	g3097320	BLASTN	480	1e-14	71	Glycine max gene for Bd 30K, complete cds
14307	GM_205_A2_C01_T7	g3142328	BLASTN	1880	2e-78	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14308	GM_205_A2_C05_MR	g342954	BLASTN	375	1e-10	63	paramecium species 4.51b mt dna dimer: replication init. region, clone-1.
14309	GM_205_A2_C08_MR	g2980793	BLASTX	341	3e-30	71	(AL022197) putative protein [Arabidopsis thaliana]
14310	GM_205_A2_C11_MR	g2995405	BLASTX	244	9e-19	40	(Y12432) polyprotein [Ananas comosus]
14311	GM_205_A2_D01_T7	g3645899	BLASTX	178	1e-11	33	(U68408) 5' end not determined experimentally [Zea mays]
14312	GM_205_A2_D07_MR	g2827662	BLASTX	368	3e-32	64	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14313	GM_205_A2_D08_MR	g507910	BLASTN	378	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14314	GM_205_A2_D12_MR	g99755	BLASTX	285	6e-32	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
14315	GM_205_A2_E04_MR	g731058	BLASTX	167	8e-12	62	URACIL-DNA GLYCOSYLASE (UDG) >gi 2118057 pir S39712 probable uracil-DNA glycosylase - Bacillus subtilis >gi 580875 (X73124) ipa-57d gene product [Bacillus subtilis] >gi 2636332 gnl PID e1186296 (Z99123) uracil-DNA glycosylase [Bacillus subtilis]
14316	GM_205_A2_E11_MR	g18559	BLASTN	1120	9e-44	75	G.max gene for catalase
14317	GM_205_A2_E11_T7	g3319363	BLASTX	307	2e-25	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
14318	GM_205_A2_F01_T7	g3549652	BLASTX	214	2e-15	49	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
14319	GM_205_B1_E09_T7	g507910	BLASTN	439	3e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14320	GM_205_B1_E11_T7	g3176694	BLASTN	366	8e-11	74	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]
14321	GM_205_B1_F10_T7	g2980777	BLASTX	173	1e-17	70	(AL022198) putative protein [Arabidopsis thaliana]
14322	GM_206_A1_A01_T7	g905360	BLASTN	949	3e-36	83	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
14323	GM_206_A1_C12_T7	g2262105	BLASTX	199	4e-14	80	(AC002343) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14324	GM_206_A1_D02_T7	g3142328	BLASTN	384	2e-10	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14325	GM_206_A1_D12_T7	g1666236	BLASTX	212	2e-16	30	(U76261) unknown [Hordeum vulgare]
14326	GM_206_A1_E08_T7	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14327	GM_206_A1_F02_T7	g507910	BLASTN	427	1e-12	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14328	GM_206_A1_F07_T7	g507910	BLASTN	560	1e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14329	GM_206_A1_G08_T7	g170080	BLASTN	469	3e-14	93	Soybean seed lectin gene transposable element tgm1.
14330	GM_206_A1_G10_T7	g1770127	BLASTN	345	2e-09	61	C.difficile pathogenicity locus, strain 2022 (566bp)
14331	GM_206_A1_H10_T7	g2921625	BLASTN	357	4e-09	62	Lupinus luteus leghemoglobin (Lbl) gene, complete cds
14332	GM_206_A1_H12_T7	g4103987	BLASTX	174	2e-16	89	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]
14333	GM_206_B1_A11_T7	g905361	BLASTX	580	1e-55	92	(U22103) gag-protease polyprotein [Glycine max]
14334	GM_206_B1_B07_T7	g3142328	BLASTN	650	2e-22	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14335	GM_206_B1_C04_T7	g2494415	BLASTX	380	2e-34	88	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) gi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine max]
14336	GM_206_B1_E07_T7	g13764	BLASTN	382	4e-11	65	Torulopsis glabrata mitochondrial DNA for ATPase 8 downstream of cytochrome oxidase 1 gene >gi 343953 gb M11874 YSLMTIG03 Yeast (T.glabrata) mitochondrial DNA between cytochrome oxidase subunit I and ATPase subunit 8 genes.
14337	GM_206_B1_F03_T7	g507910	BLASTN	519	8e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14338	GM_206_B1_H05_T7	g294042	BLASTN	300	7e-10	66	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
14339	GM_206_B1_H10_T7	g3097320	BLASTN	1120	1e-43	80	Glycine max gene for Bd 30K, complete cds
14340	GM_206_B1_H11_T7	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14341	GM_206_B1_H12_T7	g3097320	BLASTN	722	1e-25	73	Glycine max gene for Bd 30K, complete cds
14342	GM_208_A1_A01_T7	g2997694	BLASTX	187	6e-14	40	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
14343	GM_208_A1_A03_T7	g421955	BLASTX	143	3e-14	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
14344	GM_208_A1_A06_T7	g170067	BLASTN	372	7e-10	66	Soybean (G.max) proline-rich cell wall protein (SbPRP3) gene, complete cds.
14345	GM_208_A1_B09_T7	g4038056	BLASTX	169	2e-17	41	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14346	GM_208_A1_C03_T7	g2995405	BLASTX	146	9e-17	37	(Y12432) polyprotein [Ananas comosus]
14347	GM_208_A1_C09_T7	g4160362	BLASTN	318	9e-11	62	Saccharomyces cerevisiae complete mitochondrial genome
14348	GM_208_A1_C11_T7	g507910	BLASTN	523	5e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14349	GM_208_A1_D10_T7	g99729	BLASTX	141	6e-09	30	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
14350	GM_208_A1_D11_T7	g3777527	BLASTX	499	1e-45	88	(AF053008) gag-pol polyprotein [Glycine max]
14351	GM_208_A1_E02_T7	g3845316	BLASTN	379	4e-10	62	Plasmodium falciparum chromosome 2, section 65 of 73 of the complete sequence
14352	GM_208_A1_E04_T7	g130582	BLASTX	436	5e-39	66	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14353	GM_208_A1_E08_T7	g226407	BLASTX	261	3e-20	61	retrotransposon del1-46 [Lilium henryi]
14354	GM_208_A1_F11_T7	g1167523	BLASTX	201	6e-14	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14355	GM_208_A1_G06_T7	g2323254	BLASTN	354	6e-09	63	Human Chromosome X, complete sequence [Homo sapiens]
14356	GM_208_A1_G08_T7	g4063760	BLASTX	136	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14357	GM_208_A1_H08_T7	g3810596	BLASTX	289	2e-23	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14358	GM_208_B1_A10_MR	g3097320	BLASTN	661	7e-23	77	Glycine max gene for Bd 30K, complete cds
14359	GM_208_B1_A12_MR	g2522230	BLASTX	235	5e-19	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14360	GM_208_B1_B03_MR	g2522230	BLASTX	163	2e-11	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14361	GM_208_B1_B08_MR	g3142328	BLASTN	841	4e-31	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14362	GM_208_B1_B10_MR	g3176791	BLASTN	349	1e-09	62	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
14363	GM_208_B1_C01_MR	g4063760	BLASTX	189	2e-16	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14364	GM_208_B1_C02_MR	g3142328	BLASTN	717	2e-25	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14365	GM_208_B1_C03_T7	g1142702	BLASTN	419	2e-12	72	Glycine max satellite STR120-A.4.
14366	GM_208_B1_C05_MR	g2129618	BLASTX	225	1e-16	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14367	GM_208_B1_C05_T7	g3650039	BLASTX	176	1e-11	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
14368	GM_208_B1_D04_MR	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14369	GM_208_B1_D04_T7	g3377855	BLASTX	251	1e-20	81	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
14370	GM_208_B1_E06_T7	g3287696	BLASTX	453	2e-41	66	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
14371	GM_208_B1_E08_T7	g3650035	BLASTX	216	1e-15	39	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
14372	GM_208_B1_E10_T7	g294042	BLASTN	356	5e-09	64	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
14373	GM_208_B1_E11_T7	g3702735	BLASTN	349	1e-08	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]
14374	GM_208_B1_E12_T7	g294042	BLASTN	375	6e-10	65	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
14375	GM_208_B1_F03_T7	g2288979	BLASTN	402	4e-11	63	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]
14376	GM_208_B1_F09_T7	g13619	BLASTN	371	1e-10	61	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
14377	GM_208_B1_F12_T7	g3702323	BLASTX	569	2e-54	82	(AC005397) unknown protein [Arabidopsis thaliana]
14378	GM_208_B1_G03_T7	g507910	BLASTN	549	3e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14379	GM_208_B1_G04_T7	g905361	BLASTX	231	1e-17	41	(U22103) gag-protease polyprotein [Glycine max]
14380	GM_208_B1_G08_MR	g342964	BLASTN	354	7e-10	68	paramecium species 5.311 mt dna dimer: replication init. region.
14381	GM_208_B1_H10_MR	g1666236	BLASTX	164	6e-11	26	(U76261) unknown [Hordeum vulgare]
14382	GM_209_A1_A04_T7	g976178	BLASTX	278	1e-23	44	(L47183) reverse transcriptase [Arabidopsis thaliana]
14383	GM_209_A1_A05_T7	g3985931	BLASTN	351	1e-17	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]
14384	GM_209_A1_A07_MR	g507910	BLASTN	507	3e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14385	GM_209_A1_A08_T7	g18559	BLASTN	740	2e-26	77	G.max gene for catalase
14386	GM_209_A1_A10_MR	g3142328	BLASTN	1462	2e-59	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14387	GM_209_A1_B02_MR	g1666236	BLASTX	144	9e-09	32	(U76261) unknown [Hordeum vulgare]
14388	GM_209_A1_B02_T7	g3810596	BLASTX	243	3e-21	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14389	GM_209_A1_B05_MR	g3142328	BLASTN	808	1e-29	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14390	GM_209_A1_B06_MR	g905361	BLASTX	359	2e-31	92	(U22103) gag-protease polyprotein [Glycine max]
14391	GM_209_A1_B07_T7	g3810596	BLASTX	290	5e-30	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14392	GM_209_A1_B10_MR	g2522227	BLASTX	115	6e-10	57	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14393	GM_209_A1_B12_T7	g2160165	BLASTX	213	2e-15	39	(AC000132) F21M12.11 gene product [Arabidopsis thaliana]
14394	GM_209_A1_C02_T7	g18559	BLASTN	384	2e-10	69	G.max gene for catalase
14395	GM_209_A1_C05_MR	g905361	BLASTX	401	3e-36	94	(U22103) gag-protease polyprotein [Glycine max]
14396	GM_209_A1_C05_T7	g1666236	BLASTX	188	1e-13	30	(U76261) unknown [Hordeum vulgare]
14397	GM_209_A1_C06_T7	g18559	BLASTN	647	3e-22	73	G.max gene for catalase
14398	GM_209_A1_C08_T7	g3142328	BLASTN	686	4e-24	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14399	GM_209_A1_C10_T7	g976178	BLASTX	266	3e-22	46	(L47183) reverse transcriptase [Arabidopsis thaliana]
14400	GM_209_A1_D02_MR	g1840106	BLASTN	488	4e-16	65	Human fragile site locus (FRA16B) minisatellite repeat
14401	GM_209_A1_D02_T7	g2961349	BLASTX	287	3e-23	57	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
14402	GM_209_A1_D04_T7	g3810596	BLASTX	398	3e-35	48	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14403	GM_209_A1_D08_T7	g4063760	BLASTX	398	1e-45	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14404	GM_209_A1_E03_T7	g14222	BLASTN	403	3e-12	61	Saccharomyces cerevisiae mitochondrial gene aap1 for mitochondrial ATPase subunit 8
14405	GM_209_A1_E06_MR	g3785984	BLASTX	183	5e-12	37	(AC005560) putative reverse transcriptase [Arabidopsis thaliana]
14406	GM_209_A1_E07_MR	g2398523	BLASTX	151	1e-09	58	(Y13721) Transcription factor [Arabidopsis thaliana]
14407	GM_209_A1_E08_T7	g2335067	BLASTN	351	8e-09	60	Human BAC clone GS200K05 from 7q21-q22, complete sequence [Homo sapiens]
14408	GM_209_A1_E10_MR	g2995405	BLASTX	172	5e-11	38	(Y12432) polyprotein [Ananas comosus]
14409	GM_209_A1_E11_MR	g3461834	BLASTN	434	1e-12	64	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]
14410	GM_209_A1_F04_T7	g507910	BLASTN	402	1e-11	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14411	GM_209_A1_F08_T7	g2522228	BLASTX	258	3e-21	45	(AB007466) reverse transcriptase-like protein [Vicia faba]
14412	GM_209_A1_F10_T7	g99922	BLASTX	240	1e-19	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14413	GM_209_A1_G01_T7	g507910	BLASTN	597	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14414	GM_209_A1_G08_T7	g3097320	BLASTN	560	3e-18	80	Glycine max gene for Bd 30K, complete cds
14415	GM_209_A1_G09_MR	g531389	BLASTX	246	1e-18	48	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14416	GM_209_A1_G11_MR	g2245068	BLASTX	253	6e-21	76	(Z97342) serine protease homolog [Arabidopsis thaliana]
14417	GM_209_A1_H01_MR	g1658457	BLASTX	193	1e-23	75	(U75248) reverse transcriptase [Gossypium barbadense]
14418	GM_209_A1_H01_T7	g905361	BLASTX	743	7e-73	91	(U22103) gag-protease polyprotein [Glycine max]
14419	GM_209_A1_H08_T7	g3777527	BLASTX	113	9e-18	54	(AF053008) gag-pol polyprotein [Glycine max]
14420	GM_209_A1_H10_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14421	GM_209_A1_H11_T7	g4156185	BLASTN	418	8e-12	62	Homo sapiens PAC clone DJ0803F10 from 7q33-q36, complete sequence [Homo sapiens]
14422	GM_209_B1_A07_MR	g3695395	BLASTX	229	2e-17	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14423	GM_209_B1_A12_MR	g3777527	BLASTX	556	1e-51	86	(AF053008) gag-pol polyprotein [Glycine max]
14424	GM_209_B1_B08_MR	g507910	BLASTN	351	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14425	GM_209_B1_B12_MR	g4063770	BLASTX	156	2e-09	35	(AB004906) transposase [Ipomoea purpurea]
14426	GM_209_B1_C01_MR	g2501493	BLASTX	92	1e-10	54	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 4 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 4) gi 458547 (X77460) UTP-glucose glucosyltransferase [Manihot esculenta]
14427	GM_209_B1_C08_MR	g3142328	BLASTN	595	1e-41	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14428	GM_209_B1_D05_MR	g3600044	BLASTX	163	8e-10	50	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
14429	GM_209_B1_D09_MR	g507910	BLASTN	386	8e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14430	GM_209_B1_D10_MR	g2522228	BLASTX	203	5e-15	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
14431	GM_209_B1_D12_MR	g3941524	BLASTX	384	8e-35	75	(AF062916) putative transcription factor [Arabidopsis thaliana]
14432	GM_209_B1_E02_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14433	GM_209_B1_E04_MR	g976284	BLASTX	207	4e-16	37	reverse transcriptase [Arabidopsis thaliana]
14434	GM_209_B1_E05_MR	g3941524	BLASTX	341	3e-30	71	(AF062916) putative transcription factor [Arabidopsis thaliana]
14435	GM_209_B1_E06_MR	g2992164	BLASTX	210	2e-15	56	(AB012580) eIF3 p66 [Mus musculus]
14436	GM_209_B1_E11_MR	g100484	BLASTX	346	7e-30	62	hypothetical protein - garden snapdragon
14437	GM_209_B1_F06_MR	g507910	BLASTN	503	4e-16	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14438	GM_209_B1_F11_MR	g2522230	BLASTX	158	7e-11	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14439	GM_209_B1_G12_MR	g3319362	BLASTX	158	2e-09	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14440	GM_209_B1_H02_MR	g3777527	BLASTX	206	2e-14	40	(AF053008) gag-pol polyprotein [Glycine max]
14441	GM_209_B1_H09_MR	g507910	BLASTN	373	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14442	GM_209_B1_H11_MR	g3097320	BLASTN	646	3e-22	74	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14443	GM_210_A1_A03_MR	g170029	BLASTN	380	4e-10	79	Glycine max cv. Dare nodulin 26 gene fragment.
14444	GM_210_A1_B10_MR	g4063760	BLASTX	359	7e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14445	GM_210_A1_C08_MR	g3777527	BLASTX	158	3e-09	45	(AF053008) gag-pol polyprotein [Glycine max]
14446	GM_210_A1_E05_MR	g1666236	BLASTX	171	9e-12	37	(U76261) unknown [Hordeum vulgare]
14447	GM_210_A1_G04_MR	g507910	BLASTN	531	2e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14448	GM_210_A1_G07_MR	g3930515	BLASTX	100	5e-11	38	(AF059674) putative gag protein [Nicotiana tabacum]
14449	GM_210_A1_G08_MR	g1769898	BLASTX	353	1e-32	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14450	GM_210_A2_B01_MR	g3645899	BLASTX	227	9e-17	54	(U68408) 5' end not determined experimentally [Zea mays]
14451	GM_210_A2_C08_MR	g4115365	BLASTX	214	3e-15	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
14452	GM_210_A2_D05_MR	g3142379	BLASTX	216	2e-16	73	(AF053008) envelope-like [Glycine max]
14453	GM_210_A2_D11_MR	g3510336	BLASTN	494	3e-15	68	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
14454	GM_210_A2_E03_MR	g18575	BLASTN	511	3e-16	89	Soybean ENOD2A gene for Ngm-75
14455	GM_210_A2_F01_MR	g3645899	BLASTX	328	1e-27	56	(U68408) 5' end not determined experimentally [Zea mays]
14456	GM_210_A2_F03_MR	g4115365	BLASTX	228	9e-17	43	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
14457	GM_210_A2_F07_MR	g3142330	BLASTX	324	1e-27	86	(U96295) envelope-like [Glycine max]
14458	GM_210_A2_F10_MR	g3777527	BLASTX	642	8e-61	96	(AF053008) gag-pol polyprotein [Glycine max]
14459	GM_210_A2_F12_MR	g629693	BLASTX	219	7e-17	40	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14460	GM_210_A2_H02_MR	g1402883	BLASTX	176	6e-16	47	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
14461	GM_210_A2_H06_MR	g2995405	BLASTX	472	3e-43	62	(Y12432) polyprotein [Ananas comosus]
14462	GM_210_B1_A01_MR	g3063708	BLASTX	221	6e-16	42	(AL022537) putative protein [Arabidopsis thaliana]
14463	GM_210_B1_A03_T7	g2129618	BLASTX	192	4e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14464	GM_210_B1_A04_MR	g3097320	BLASTN	833	1e-30	82	Glycine max gene for Bd 30K, complete cds
14465	GM_210_B1_B01_MR	g4063760	BLASTX	202	4e-14	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14466	GM_210_B1_B04_T7	g3319362	BLASTX	179	2e-25	53	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19 29) [Arabidopsis thaliana]
14467	GM_210_B1_B06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14468	GM_210_B1_B06_T7	g507910	BLASTN	394	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14469	GM_210_B1_B10_T7	g4063756	BLASTN	458	1e-13	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14470	GM_210_B1_C09_T7	g4140712	BLASTX	307	1e-26	40	(AF110183) putative integrase [Oryza sativa]
14471	GM_210_B1_D03_T7	g226407	BLASTX	132	1e-11	54	retrotransposon del1-46 [Lilium henryi]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14472	GM_210_B1_D04_T7	g166884	BLASTN	1047	5e-41	78	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
14473	GM_210_B1_D08_T7	g2764525	BLASTN	946	4e-36	69	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
14474	GM_210_B1_D11_MR	g170080	BLASTN	460	7e-14	73	Soybean seed lectin gene transposable element tgm1.
14475	GM_210_B1_E02_T7	g18559	BLASTN	654	1e-22	75	G.max gene for catalase
14476	GM_210_B1_E04_MR	g1666236	BLASTX	166	3e-11	30	(U76261) unknown [Hordeum vulgare]
14477	GM_210_B1_E05_T7	g507910	BLASTN	873	8e-33	97	Glycine max BSR-101 satellite SB92 genomic sequence.
14478	GM_210_B1_E06_MR	g4063756	BLASTN	407	2e-11	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14479	GM_210_B1_F02_MR	g2129618	BLASTX	156	2e-09	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14480	GM_210_B1_F03_T7	g3142328	BLASTN	634	1e-21	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14481	GM_210_B1_F05_T7	g3097320	BLASTN	601	4e-20	79	Glycine max gene for Bd 30K, complete cds
14482	GM_210_B1_F11_MR	g416692	BLASTX	335	1e-29	74	AUXIN-INDUCED PROTEIN 6B gi 81764 pir JQ1098 auxin-induced protein 6B - soybean gi 255577 bbs 113700 (S44175) orf 6B [Glycine max=soybeans, cv. Wayne, Peptide, 90 aa] [Glycine max]
14483	GM_210_B1_F12_MR	g1769898	BLASTX	385	2e-34	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14484	GM_210_B2_A01_MR	g4038056	BLASTX	399	2e-35	52	(AC005897) putative transposon [Arabidopsis thaliana]
14485	GM_210_B2_A06_T7	g905361	BLASTX	171	4e-11	28	(U22103) gag-protease polyprotein [Glycine max]
14486	GM_210_B2_A10_MR	g2522227	BLASTX	217	4e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14487	GM_210_B2_B05_MR	g992916	BLASTN	473	2e-14	70	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
14488	GM_210_B2_B12_T7	g1769898	BLASTX	261	7e-21	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14489	GM_210_B2_C02_T7	g3913420	BLASTX	225	4e-30	77	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine decarboxylase [Pisum sativum]
14490	GM_210_B2_C05_MR	g2244950	BLASTN	350	9e-09	67	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5
14491	GM_210_B2_C07_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14492	GM_210_B2_D01_MR	g18559	BLASTN	752	5e-27	70	G.max gene for catalase
14493	GM_210_B2_D10_MR	g3645899	BLASTX	227	4e-29	45	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14494	GM_210_B2_D10_T7	g1402877	BLASTX	171	1e-11	73	(X98130) unknown [Arabidopsis thaliana] gi 1495257 gnl PID e242925 (X97485) orf03 [Arabidopsis thaliana]
14495	GM_210_B2_E06_T7	g3935157	BLASTX	182	4e-12	80	(AC005106) T25N20.21 [Arabidopsis thaliana]
14496	GM_210_B2_E08_T7	g3873182	BLASTN	444	5e-13	63	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
14497	GM_210_B2_E12_T7	g2351066	BLASTN	632	2e-21	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9
14498	GM_210_B2_F01_MR	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14499	GM_210_B2_F01_T7	g4092470	BLASTN	349	1e-08	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14500	GM_210_B2_F07_MR	g2464905	BLASTX	194	1e-14	67	(Z99708) minor allergen [Arabidopsis thaliana]
14501	GM_210_B2_F09_MR	g170080	BLASTN	430	2e-12	64	Soybean seed lectin gene transposable element tgm1.
14502	GM_210_B2_F10_MR	g507910	BLASTN	451	9e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14503	GM_210_B2_G02_MR	g3283026	BLASTX	318	7e-27	43	putative transposase [Arabidopsis thaliana]
14504	GM_210_B2_G04_MR	g2979567	BLASTN	350	9e-09	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence [Homo sapiens]
14505	GM_210_B2_G06_MR	g507910	BLASTN	413	5e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14506	GM_210_B2_G06_T7	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14507	GM_210_B2_G10_MR	g2462935	BLASTX	154	4e-13	40	(Y12321) open reading frame 1 [Brassica oleracea]
14508	GM_210_B2_H02_MR	g2522230	BLASTX	230	2e-18	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14509	GM_210_B2_H02_T7	g3142328	BLASTN	1084	4e-42	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14510	GM_210_B2_H04_MR	g3319372	BLASTX	217	1e-15	38	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
14511	GM_210_B2_H07_T7	g3930515	BLASTX	103	6e-10	45	(AF059674) putative gag protein [Nicotiana tabacum]
14512	GM_211_A1_A07_T7	g2323254	BLASTN	465	6e-14	62	Human Chromosome X, complete sequence [Homo sapiens]
14513	GM_211_A1_A09_MR	g4038056	BLASTX	311	6e-26	50	(AC005897) putative transposon [Arabidopsis thaliana]
14514	GM_211_A1_B12_T7	g3645899	BLASTX	192	2e-14	49	(U68408) 5' end not determined experimentally [Zea mays]
14515	GM_211_A1_C01_T7	g3142328	BLASTN	562	2e-18	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14516	GM_211_A1_C12_T7	g3142328	BLASTN	872	2e-32	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14517	GM_211_A1_D10_T7	g4063760	BLASTX	195	2e-13	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14518	GM_211_A1_E05_MR	g1142699	BLASTN	251	3e-12	69	Glycine max satellite STR120-A.1.
14519	GM_211_A1_E05_T7	g3550435	BLASTN	387	2e-10	62	Hordeum vulgare Hotr1 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14520	GM_211_A1_E06_T7	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14521	GM_211_A1_E10_MR	g2462134	BLASTX	337	1e-29	40	(Y13368) reverse transcriptase [Beta vulgaris]
14522	GM_211_A1_F02_T7	g4063760	BLASTX	293	8e-24	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14523	GM_211_A1_F05_T7	g1184075	BLASTX	162	7e-10	44	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
14524	GM_211_A1_F10_MR	g100484	BLASTX	353	1e-30	59	hypothetical protein - garden snapdragon
14525	GM_211_A1_F10_T7	g3426334	BLASTN	538	2e-17	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
14526	GM_211_A1_G10_T7	g507910	BLASTN	341	8e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
14527	GM_211_A2_A04_MR	g3097320	BLASTN	431	2e-12	67	Glycine max gene for Bd 30K, complete cds
14528	GM_211_A2_A04_T7	g4063760	BLASTX	613	5e-58	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14529	GM_211_A2_A07_MR	g4063760	BLASTX	352	5e-33	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14530	GM_211_A2_A10_T7	g2773249	BLASTX	112	9e-13	79	(AF039707) glutamate carboxypeptidase II [Rattus norvegicus]
14531	GM_211_A2_A11_MR	g507910	BLASTN	357	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14532	GM_211_A2_B02_MR	g3845197	BLASTN	378	5e-10	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14533	GM_211_A2_B03_MR	g3097320	BLASTN	370	1e-09	66	Glycine max gene for Bd 30K, complete cds
14534	GM_211_A2_B03_T7	g507910	BLASTN	479	5e-15	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14535	GM_211_A2_B04_MR	g4063760	BLASTX	472	7e-43	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14536	GM_211_A2_B05_MR	g3645899	BLASTX	392	2e-34	42	(U68408) 5' end not determined experimentally [Zea mays]
14537	GM_211_A2_B08_MR	g3645899	BLASTX	313	4e-30	54	(U68408) 5' end not determined experimentally [Zea mays]
14538	GM_211_A2_B10_MR	g3645899	BLASTX	291	1e-23	40	(U68408) 5' end not determined experimentally [Zea mays]
14539	GM_211_A2_B11_MR	g3319362	BLASTX	190	6e-13	32	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14540	GM_211_A2_B11_T7	g2522228	BLASTX	270	1e-22	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
14541	GM_211_A2_C01_T7	g2522227	BLASTX	156	3e-10	42	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14542	GM_211_A2_C02_T7	g1769898	BLASTX	437	2e-40	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14543	GM_211_A2_C03_MR	g1669680	BLASTN	370	1e-09	64	Human DNA sequence from PAC 293E14 contains ESTs, STS
14544	GM_211_A2_C05_MR	g2914758	BLASTN	496	2e-15	64	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
14545	GM_211_A2_C09_MR	g3142328	BLASTN	2339	4e-100	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14546	GM_211_A2_C09_T7	g170002	BLASTN	357	3e-09	67	soybean leghemoglobin pseudogene, segment 2.
14547	GM_211_A2_C11_MR	g2995405	BLASTX	359	1e-40	57	(Y12432) polyprotein [Ananas comosus]
14548	GM_211_A2_D03_MR	g1769897	BLASTX	203	1e-14	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14549	GM_211_A2_D05_T7	g4063760	BLASTX	545	1e-50	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14550	GM_211_A2_D06_T7	g2961349	BLASTX	287	4e-23	56	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
14551	GM_211_A2_D07_T7	g3779030	BLASTX	143	5e-09	29	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
14552	GM_211_A2_E03_T7	g18559	BLASTN	585	2e-19	81	G.max gene for catalase
14553	GM_211_A2_E07_T7	g3142328	BLASTN	1866	7e-78	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14554	GM_211_A2_E09_MR	g3097320	BLASTN	1504	4e-61	80	Glycine max gene for Bd 30K, complete cds
14555	GM_211_A2_E09_T7	g3142328	BLASTN	2020	6e-85	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14556	GM_211_A2_F04_MR	g836954	BLASTX	178	9e-12	41	(U20948) receptor protein kinase [Ipomoea trifida]
14557	GM_211_A2_F07_MR	g992916	BLASTN	947	9e-36	92	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
14558	GM_211_A2_F08_MR	g342964	BLASTN	386	2e-11	61	paramecium species 5,311 mt dna dimer: replication init. region.
14559	GM_211_A2_F09_MR	g905361	BLASTX	617	2e-59	90	(U22103) gag-protease polyprotein [Glycine max]
14560	GM_211_A2_G09_MR	g3777527	BLASTX	741	2e-71	93	(AF053008) gag-pol polyprotein [Glycine max]
14561	GM_211_A2_H01_MR	g1769897	BLASTX	195	2e-26	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14562	GM_211_B1_A04_MR	g1658457	BLASTX	297	1e-25	65	(U75248) reverse transcriptase [Gossypium barbadense]
14563	GM_211_B1_A08_MR	g2522227	BLASTX	236	4e-19	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14564	GM_211_B1_A10_T7	g1142701	BLASTN	1008	3e-39	82	Glycine max satellite STR120-A.3.
14565	GM_211_B1_A12_MR	g18559	BLASTN	832	1e-30	78	G.max gene for catalase
14566	GM_211_B1_B01_MR	g18559	BLASTN	519	2e-16	69	G.max gene for catalase
14567	GM_211_B1_B07_MR	g4063760	BLASTX	310	1e-25	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14568	GM_211_B1_B08_MR	g2995405	BLASTX	342	3e-41	58	(Y12432) polyprotein [Ananas comosus]
14569	GM_211_B1_C01_T7	g629693	BLASTX	162	1e-10	39	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14570	GM_211_B1_C05_MR	g507910	BLASTN	405	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14571	GM_211_B1_C05_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14572	GM_211_B1_D02_T7	g4063770	BLASTX	199	5e-14	41	(AB004906) transposase [Ipomoea purpurea]
14573	GM_211_B1_D07_MR	g2522230	BLASTX	170	4e-12	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14574	GM_211_B1_D08_T7	g2656030	BLASTN	720	2e-25	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
14575	GM_211_B1_D11_MR	g1707017	BLASTX	495	3e-46	76	(U78721) RNA helicase isolog [Arabidopsis thaliana]
14576	GM_211_B1_D12_MR	g2995405	BLASTX	257	4e-20	45	(Y12432) polyprotein [Ananas comosus]
14577	GM_211_B1_E01_T7	g3080426	BLASTX	151	8e-09	41	(AL022604) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14578	GM_211_B1_E02_T7	g3142328	BLASTN	1022	2e-39	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14579	GM_211_B1_E05_T7	g3426334	BLASTN	388	1e-10	61	Pisum sativum pectin methylesterase (repme1) gene, complete cds
14580	GM_211_B1_E12_MR	g4063760	BLASTX	429	3e-38	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14581	GM_211_B1_F01_MR	g2129618	BLASTX	154	4e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14582	GM_211_B1_F06_T7	g4038056	BLASTX	195	2e-13	39	(AC005897) putative transposon [Arabidopsis thaliana]
14583	GM_211_B1_G09_T7	g507910	BLASTN	372	3e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14584	GM_211_B1_H05_T7	g3777527	BLASTX	181	1e-11	89	(AF053008) gag-pol polyprotein [Glycine max]
14585	GM_211_B1_H10_T7	g507910	BLASTN	686	2e-24	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14586	GM_211_B1_H12_T7	g3746069	BLASTX	183	5e-12	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
14587	GM_211_B2_A01_MR	g4102692	BLASTX	345	9e-31	81	(AF004810) late-embryogenesis abundant protein [Glycine max]
14588	GM_211_B2_A06_MR	g1168972	BLASTX	242	1e-18	77	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA PRECURSOR gi 480969 pir S37557 clpA protein - rape (fragment) gi 406311 (X75328) clpA gene product [Brassica napus]
14589	GM_211_B2_A07_MR	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14590	GM_211_B2_A09_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14591	GM_211_B2_A10_MR	g1421730	BLASTX	178	5e-12	39	(U43082) RF2 [Zea mays]
14592	GM_211_B2_B01_MR	g3941725	BLASTN	486	6e-15	62	Homo sapiens clone BAC 72m22 chromosome 8 map 8p21, complete sequence [Homo sapiens]
14593	GM_211_B2_B04_T7	g3777527	BLASTX	241	3e-29	90	(AF053008) gag-pol polyprotein [Glycine max]
14594	GM_211_B2_B12_T7	g4063760	BLASTX	247	7e-19	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14595	GM_211_B2_C01_MR	g3319362	BLASTX	168	5e-21	56	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt hmm, score 19 29) [Arabidopsis thaliana]
14596	GM_211_B2_C04_MR	g18559	BLASTN	997	3e-38	77	G max gene for catalase
14597	GM_211_B2_D03_MR	g13619	BLASTN	405	3e-12	61	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
14598	GM_211_B2_D05_MR	g507910	BLASTN	610	6e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14599	GM_211_B2_D05_T7	g507910	BLASTN	362	9e-10	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14600	GM_211_B2_D12_MR	g3845197	BLASTN	466	5e-14	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14601	GM_211_B2_E04_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14602	GM_211_B2_F09_T7	g507910	BLASTN	481	4e-15	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14603	GM_211_B2_F04_T7	g2129618	BLASTX	171	6e-11	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14604	GM_211_B2_F05_MR	g226407	BLASTX	498	2e-45	62	retrotransposon del1-46 [Lilium henryi]
14605	GM_211_B2_F08_MR	g1840106	BLASTN	367	4e-10	62	Human fragile site locus (FRA16B) minisatellite repeat
14606	GM_211_B2_F10_MR	g4063756	BLASTN	402	4e-11	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14607	GM_211_B2_G01_MR	g3695395	BLASTX	166	1e-10	34	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14608	GM_211_B2_G04_T7	g3779021	BLASTX	142	3e-10	44	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
14609	GM_211_B2_G05_MR	g3645899	BLASTX	246	7e-19	44	(U68408) 5' end not determined experimentally [Zea mays]
14610	GM_211_B2_G07_T7	g3821288	BLASTN	389	5e-11	62	Pisum sativum repeated element highly similar to the BamHI repeated sequence families of Vicia faba
14611	GM_211_B2_G10_MR	g4063760	BLASTX	445	5e-40	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14612	GM_211_B2_G12_MR	g3128143	BLASTN	369	1e-09	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]
14613	GM_211_B2_H05_MR	g4038056	BLASTX	268	3e-21	43	(AC005897) putative transposon [Arabidopsis thaliana]
14614	GM_211_B2_H09_MR	g1142699	BLASTN	325	8e-19	71	Glycine max satellite STR120-A.1.
14615	GM_211_B2_H11_MR	g507910	BLASTN	404	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14616	GM_212_A1_A12_MR	g2865437	BLASTX	184	4e-12	41	(AF039376) polyprotein [Arabidopsis arenosa]
14617	GM_212_A1_B05_MR	g4063760	BLASTX	382	3e-33	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14618	GM_212_A1_C11_MR	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14619	GM_212_A1_D06_MR	g4063760	BLASTX	207	1e-14	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14620	GM_212_A1_D09_MR	g3142328	BLASTN	1142	8e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14621	GM_212_A1_D12_MR	g507910	BLASTN	646	1e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14622	GM_212_A1_E10_MR	g3097320	BLASTN	889	3e-33	80	Glycine max gene for Bd 30K, complete cds
14623	GM_212_A1_G01_MR	g2104945	BLASTN	293	2e-10	74	Glycine max copia-like retrotransposon Tgmr, complete sequence
14624	GM_212_A1_G04_MR	g2209031	BLASTX	167	7e-11	40	(AB001569) ORF of 1.56 kb [Daucus carota]
14625	GM_212_A1_G09_MR	g2522230	BLASTX	245	4e-20	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14626	GM_212_A1_G11_MR	g2522227	BLASTX	219	2e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14627	GM_212_A1_H09_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14628	GM_212_A1_H11_MR	g100484	BLASTX	409	9e-37	54	hypothetical protein - garden snapdragon
14629	GM_212_A2_A01_T7	g3176795	BLASTN	462	9e-15	68	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
14630	GM_212_A2_A02_T7	g2809251	BLASTX	315	2e-27	48	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14631	GM_212_A2_A03_T7	g4063756	BLASTN	421	6e-12	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14632	GM_212_A2_A12_MR	g1881585	BLASTX	155	1e-10	45	(U72489) remorin [Solanum tuberosum]
14633	GM_212_A2_B01_MR	g4063760	BLASTX	357	3e-32	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14634	GM_212_A2_B03_T7	g170029	BLASTN	460	8e-14	86	Glycine max cv. Dare nodulin 26 gene fragment.
14635	GM_212_A2_B06_MR	g3142328	BLASTN	909	3e-34	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14636	GM_212_A2_B11_MR	g905361	BLASTX	495	5e-50	96	(U22103) gag-protease polyprotein [Glycine max]
14637	GM_212_A2_C01_MR	g4115363	BLASTX	209	6e-15	46	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
14638	GM_212_A2_C03_T7	g1769898	BLASTX	385	2e-34	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14639	GM_212_A2_C04_MR	g3953470	BLASTX	150	6e-09	61	(AC002328) F20N2.15 [Arabidopsis thaliana]
14640	GM_212_A2_C05_MR	g1666236	BLASTX	209	4e-16	33	(U76261) unknown [Hordeum vulgare]
14641	GM_212_A2_C12_T7	g1928960	BLASTX	184	9e-16	63	(U92286) pyrroline-5-carboxylate synthetase [Actinidia deliciosa]
14642	GM_212_A2_D01_MR	g4063760	BLASTX	176	2e-11	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14643	GM_212_A2_D02_T7	g3142328	BLASTN	1573	2e-64	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14644	GM_212_A2_D06_MR	g4063756	BLASTN	421	6e-12	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14645	GM_212_A2_D08_T7	g4063760	BLASTX	203	3e-14	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14646	GM_212_A2_E02_T7	g2735745	BLASTN	361	1e-09	64	Oncorhynchus kisutch growth hormone 1 gene, intron C, complete sequence
14647	GM_212_A2_E04_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14648	GM_212_A2_E05_MR	g2656024	BLASTN	465	6e-14	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6
14649	GM_212_A2_E09_T7	g2129618	BLASTX	200	5e-14	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14650	GM_212_A2_E10_T7	g2618605	BLASTN	483	9e-15	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]
14651	GM_212_A2_F01_MR	g3513747	BLASTX	275	1e-21	50	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
14652	GM_212_A2_F05_T7	g3777527	BLASTX	637	3e-60	83	(AF053008) gag-pol polyprotein [Glycine max]
14653	GM_212_B1_A06_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14654	GM_212_B1_A08_MR	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14655	GM_212_B1_A11_MR	g18559	BLASTN	826	2e-30	75	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14656	GM_212_B1_C01_MR	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14657	GM_212_B1_C02_MR	g3273387	BLASTN	422	5e-12	66	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
14658	GM_212_B1_C04_MR	g1666236	BLASTX	179	3e-15	32	(U76261) unknown [Hordeum vulgare]
14659	GM_212_B1_C07_MR	g2351060	BLASTX	436	2e-40	82	(AB006660) sucrose-phosphate synthase [Citrus unshiu]
14660	GM_212_B1_D03_MR	g1480927	BLASTN	500	9e-16	91	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
14661	GM_212_B1_E12_MR	g3283026	BLASTX	139	2e-17	38	putative transposase [Arabidopsis thaliana]
14662	GM_212_B1_F01_MR	g703220	BLASTN	656	3e-23	76	Pisum sativum (clone HW16-26) gene fragment.
14663	GM_212_B1_F07_MR	g400636	BLASTX	166	6e-13	67	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST gi 320098 pir JQ1671 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - maize chloroplast gi 12420 (X62370) NADH Dehydrogenase subunit A [Zea mays] gi 902289 (X86563) NADH dehydrogenase ND1 [Zea mays]
14664	GM_212_B1_F09_MR	g2522230	BLASTX	257	2e-21	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14665	GM_212_B1_G12_MR	g1658455	BLASTX	342	2e-30	66	(U75247) reverse transcriptase [Gossypium barbadense]
14666	GM_213_A1_A01_T7	g3777527	BLASTX	142	2e-11	38	(AF053008) gag-pol polyprotein [Glycine max]
14667	GM_213_A1_A02_T7	g4063760	BLASTX	152	1e-08	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14668	GM_213_A1_A05_MR	g2443320	BLASTX	253	3e-20	46	(D85597) polyprotein [Oryza australiensis]
14669	GM_213_A1_A08_MR	g531389	BLASTX	274	1e-21	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14670	GM_213_A1_A09_T7	g507910	BLASTN	534	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14671	GM_213_A1_A10_T7	g2828293	BLASTX	244	1e-18	56	(AL021687) putative protein [Arabidopsis thaliana]
14672	GM_213_A1_A12_MR	g2462134	BLASTX	229	1e-17	51	(Y13368) reverse transcriptase [Beta vulgaris]
14673	GM_213_A1_B01_T7	g18559	BLASTN	355	5e-09	65	G.max gene for catalase
14674	GM_213_A1_B03_T7	g3097320	BLASTN	941	1e-35	73	Glycine max gene for Bd 30K, complete cds
14675	GM_213_A1_B08_MR	g18559	BLASTN	552	5e-18	74	G.max gene for catalase
14676	GM_213_A1_B08_T7	g100484	BLASTX	377	3e-33	52	hypothetical protein - garden snapdragon
14677	GM_213_A1_B11_T7	g1142699	BLASTN	1429	3e-58	88	Glycine max satellite STR120-A.1
14678	GM_213_A1_C05_T7	g1934969	BLASTN	262	1e-09	64	P.falciparum mRNA for AARP1 protein, partial
14679	GM_213_A1_C06_MR	g1167523	BLASTX	222	4e-16	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14680	GM_213_A1_D02_T7	g18559	BLASTN	1047	2e-40	76	G.max gene for catalase
14681	GM_213_A1_D03_MR	g3777527	BLASTX	310	2e-25	89	(AF053008) gag-pol polyprotein [Glycine max]
14682	GM_213_A1_E03_T7	g507910	BLASTN	353	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14683	GM_213_A1_E05_MR	g1769898	BLASTX	179	5e-12	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14684	GM_213_A1_E09_T7	g2120736	BLASTX	168	1e-10	32	X-Pro dipeptidyl-peptidase (EC 3.4.14.11) - Xanthomonas maltophilia gi 1753197 gnl PID d1012539 (D83263) dipeptidyl peptidase IV [Stenotrophomonas maltophilia]
14685	GM_213_A1_F03_T7	g169360	BLASTN	270	2e-14	92	P.vulgaris PVPK-1 protein, complete cds.
14686	GM_213_A1_F06_T7	g173088	BLASTX	182	6e-12	36	has homology to retroviral pol genes; ORF2 TYB3-2 (5' end of coding region not precisely determined)
14687	GM_213_A1_G01_T7	g507910	BLASTN	370	4e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14688	GM_213_A1_G05_T7	g2801423	BLASTN	416	9e-12	61	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
14689	GM_213_A1_G06_T7	g2315153	BLASTX	229	4e-18	76	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
14690	GM_213_A1_G07_T7	g4063760	BLASTX	405	7e-38	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14691	GM_213_A1_G08_T7	g2642431	BLASTX	433	1e-38	58	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
14692	GM_213_A1_G09_T7	g100484	BLASTX	438	6e-40	54	hypothetical protein - garden snapdragon
14693	GM_213_A1_H07_T7	g1633547	BLASTN	448	3e-13	63	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
14694	GM_213_A1_H12_T7	g4049647	BLASTN	405	3e-11	63	Melanoplus sanguinipes entomopoxvirus, complete genome
14695	GM_213_B1_A06_MR	g2160150	BLASTX	265	3e-22	69	(AC000375) EST gb T43829 comes from this gene. [Arabidopsis thaliana]
14696	GM_213_B1_A07_MR	g1589778	BLASTX	189	7e-13	77	(U62135) SPINDLY [Arabidopsis thaliana]
14697	GM_213_B1_A08_MR	g531389	BLASTX	223	3e-16	57	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14698	GM_213_B1_A09_MR	g170029	BLASTN	352	7e-09	81	Glycine max cv. Dare nodulin 26 gene fragment.
14699	GM_213_B1_A10_T7	g2522228	BLASTX	290	8e-25	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
14700	GM_213_B1_A12_MR	g3885339	BLASTX	222	2e-16	46	(AC005623) putative bzip protein [Arabidopsis thaliana]
14701	GM_213_B1_A12_T7	g3142328	BLASTN	1043	3e-40	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14702	GM_213_B1_B01_MR	g1041702	BLASTX	122	3e-11	64	(U30476) expansin At-EXP1 [Arabidopsis thaliana]
14703	GM_213_B1_B05_MR	g2244915	BLASTX	169	1e-10	41	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
14704	GM_213_B1_B09_T7	g421894	BLASTX	200	4e-29	78	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 5 - mung bean (fragment) gi 297850 (Z12134) ACC synthase [Vigna radiata] gi 553115 (M94863) 1-aminocyclopropane-1-carboxylate synthase [Vigna radiata]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14705	GM_213_B1_B12_MR	g2281100	BLASTX	204	1e-26	49	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]
14706	GM_213_B1_C03_MR	g507910	BLASTN	356	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
14707	GM_213_B1_C03_T7	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14708	GM_213_B1_C08_T7	g4150930	BLASTN	435	1e-12	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
14709	GM_213_B1_C10_MR	g3777527	BLASTX	258	2e-38	89	(AF053008) gag-pol polyprotein [Glycine max]
14710	GM_213_B1_C11_T7	g3024126	BLASTX	199	1e-14	94	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) gi 1655576 gnl PID e236742 (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]
14711	GM_213_B1_D04_MR	g3097320	BLASTN	813	9e-30	77	Glycine max gene for Bd 30K, complete cds
14712	GM_213_B1_D06_T7	g4063756	BLASTN	450	3e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14713	GM_213_B1_D12_T7	g170029	BLASTN	399	5e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
14714	GM_213_B1_E02_MR	g3097320	BLASTN	468	4e-14	71	Glycine max gene for Bd 30K, complete cds
14715	GM_213_B1_E04_MR	g2522228	BLASTX	195	4e-14	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
14716	GM_213_B1_E10_T7	g3142328	BLASTN	2032	2e-85	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14717	GM_213_B1_E11_T7	g4063760	BLASTX	189	9e-13	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14718	GM_213_B1_E12_T7	g2522230	BLASTX	313	3e-27	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14719	GM_213_B1_F02_T7	g3142328	BLASTN	1024	2e-39	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14720	GM_213_B1_G01_T7	g3097320	BLASTN	483	8e-15	74	Glycine max gene for Bd 30K, complete cds
14721	GM_214_A2_A02_MR	g2961384	BLASTX	147	1e-18	51	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]
14722	GM_214_A2_A03_T7	g3097320	BLASTN	586	2e-19	80	Glycine max gene for Bd 30K, complete cds
14723	GM_214_A2_A06_T7	g4063760	BLASTX	403	2e-35	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14724	GM_214_A2_A07_T7	g3142328	BLASTN	651	2e-22	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14725	GM_214_A2_A09_MR	g3551960	BLASTX	200	2e-23	49	(AF082033) senescence-associated protein 15 [Hemerocallis hybrid cultivar]
14726	GM_214_A2_A12_MR	g507910	BLASTN	413	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14727	GM_214_A2_B01_T7	g18559	BLASTN	723	9e-26	84	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14728	GM_214_A2_C01_MR	g2129709	BLASTX	248	6e-19	37	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
14729	GM_214_A2_C04_T7	g2842542	BLASTN	456	1e-13	60	Ipomoea purpurea DNA, LTR retrotransposon RTip1
14730	GM_214_A2_C07_T7	g3599418	BLASTN	509	5e-16	74	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14731	GM_214_A2_C08_MR	g4063760	BLASTX	165	4e-10	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14732	GM_214_A2_C11_MR	g3142328	BLASTN	660	7e-23	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14733	GM_214_A2_D10_MR	g507910	BLASTN	377	2e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14734	GM_214_A2_D11_MR	g1171591	BLASTN	313	2e-11	67	P.falciparum complete gene map of plastid-like DNA (IR-B)
14735	GM_214_A2_E03_MR	g3645899	BLASTX	449	1e-40	60	(U68408) 5' end not determined experimentally [Zea mays]
14736	GM_214_A2_E04_MR	g3367520	BLASTX	167	5e-11	48	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb D12522 from A. thaliana. [Arabidopsis thaliana]
14737	GM_214_A2_E10_MR	g2995405	BLASTX	182	2e-13	38	(Y12432) polyprotein [Ananas comosus]
14738	GM_214_A2_G10_T7	g3283026	BLASTX	238	3e-18	34	putative transposase [Arabidopsis thaliana]
14739	GM_214_A2_H09_T7	g4063760	BLASTX	156	3e-09	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14740	GM_214_B1_A10_MR	g3193306	BLASTX	101	5e-09	39	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]
14741	GM_214_B1_E03_MR	g3928116	BLASTN	364	2e-09	61	, complete sequence [Homo sapiens]
14742	GM_214_B1_E10_MR	g2522230	BLASTX	100	4e-10	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14743	GM_215_A1_A03_MR	g18559	BLASTN	1574	2e-64	89	G.max gene for catalase
14744	GM_215_A1_A07_MR	g3645899	BLASTX	442	8e-40	67	(U68408) 5' end not determined experimentally [Zea mays]
14745	GM_215_A1_B07_MR	g2623307	BLASTX	159	1e-09	69	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]
14746	GM_215_A1_C02_MR	g2341016	BLASTN	353	7e-09	66	Human PAC clone RG212D03, complete sequence [Homo sapiens]
14747	GM_215_A1_C04_MR	g4063760	BLASTX	436	5e-39	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14748	GM_215_A1_C05_MR	g507910	BLASTN	406	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14749	GM_215_A1_C06_MR	g1663537	BLASTX	321	4e-28	61	(U55803) disease resistance protein homolog [Glycine max]
14750	GM_215_A1_C10_MR	g3892061	BLASTX	209	2e-15	43	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
14751	GM_215_A1_D01_MR	g1769898	BLASTX	225	5e-17	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14752	GM_215_A1_D09_MR	g3096949	BLASTX	183	2e-12	35	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]
14753	GM_215_A1_D11_MR	g3695395	BLASTX	176	1e-11	34	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14754	GM_215_A1_F01_MR	g4063760	BLASTX	126	3e-16	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14755	GM_215_A1_F06_MR	g4038471	BLASTX	204	4e-19	90	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
14756	GM_215_A1_F12_MR	g2522230	BLASTX	180	3e-13	34	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14757	GM_215_A1_G03_MR	g1769898	BLASTX	321	2e-27	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14758	GM_215_A1_G04_MR	g1840106	BLASTN	385	5e-11	65	Human fragile site locus (FRA16B) minisatellite repeat
14759	GM_215_A1_H08_MR	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14760	GM_215_B1_A07_T7	g2245081	BLASTX	132	1e-09	82	(Z97343) myosin II heavy chain homolog [Arabidopsis thaliana]
14761	GM_215_B1_B08_T7	g4115363	BLASTX	160	1e-09	47	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
14762	GM_215_B1_C05_T7	g100484	BLASTX	261	1e-20	60	hypothetical protein - garden snapdragon
14763	GM_215_B1_E02_T7	g4063760	BLASTX	202	5e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14764	GM_215_B1_F12_T7	g166884	BLASTN	688	7e-25	76	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
14765	GM_215_B1_G06_T7	g3777527	BLASTX	180	3e-12	58	(AF053008) gag-pol polyprotein [Glycine max]
14766	GM_216_A1_A01_MR	g18559	BLASTN	703	8e-25	75	G.max gene for catalase
14767	GM_216_A1_A04_T7	g1091678	BLASTX	237	4e-18	39	activator-like transposable element [Pennisetum glaucum]
14768	GM_216_A1_B05_MR	g2769655	BLASTN	466	5e-14	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
14769	GM_216_A1_B07_MR	g4063756	BLASTN	387	2e-10	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14770	GM_216_A1_B07_T7	g3810596	BLASTX	117	2e-10	28	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14771	GM_216_A1_B08_MR	g18695	BLASTN	395	5e-11	69	Soybean nodulin 22 gene
14772	GM_216_A1_B09_MR	g1785729	BLASTN	513	4e-16	63	A.thaliana mitochondrial genome, part B
14773	GM_216_A1_B11_T7	g4092470	BLASTN	432	2e-12	66	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14774	GM_216_A1_C03_T7	g2258315	BLASTX	220	5e-16	48	(AF004878) resistance complex protein I2C-1 [Lycopersicon esculentum]
14775	GM_216_A1_D06_T7	g1173642	BLASTX	207	5e-17	93	(U36191) lipoxygenase [Glycine max] gi 1588566 prf 2208476A lipoxygenase [Glycine max]
14776	GM_216_A1_E01_MR	g3777527	BLASTX	804	3e-78	98	(AF053008) gag-pol polyprotein [Glycine max]
14777	GM_216_A1_E01_T7	g4063760	BLASTX	170	1e-10	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14778	GM_216_A1_E10_MR	g3319351	BLASTX	219	7e-16	55	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14779	GM_216_A2_B02_T7	g3097320	BLASTN	885	5e-33	85	Glycine max gene for Bd 30K, complete cds
14780	GM_216_A2_D05_T7	g4063760	BLASTX	159	4e-10	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14781	GM_216_A2_E06_T7	g3947735	BLASTX	124	4e-09	40	(AJ009720) NL27 [Solanum tuberosum]
14782	GM_216_A2_F06_T7	g4115341	BLASTX	189	1e-12	49	(U51100) chromaffin granule ATPase II [Bos taurus]
14783	GM_216_B2_A05_MR	g2655308	BLASTN	353	3e-09	60	Bactrocera xanthodes strain Samoa mitochondrial D-loop region, complete sequence
14784	GM_216_B2_B01_MR	g629693	BLASTX	257	2e-21	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14785	GM_216_B2_B05_MR	g507910	BLASTN	472	1e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14786	GM_216_B2_C04_MR	g3097320	BLASTN	488	5e-15	71	Glycine max gene for Bd 30K, complete cds
14787	GM_216_B2_C07_MR	g3142328	BLASTN	1118	1e-43	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14788	GM_216_B2_C08_MR	g18559	BLASTN	585	5e-28	74	G.max gene for catalase
14789	GM_216_B2_D02_MR	g3695395	BLASTX	127	1e-13	46	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14790	GM_216_B2_D03_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14791	GM_216_B2_D08_MR	g3777527	BLASTX	362	5e-31	85	(AF053008) gag-pol polyprotein [Glycine max]
14792	GM_216_B2_D12_MR	g3695387	BLASTX	249	4e-20	55	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
14793	GM_216_B2_E04_MR	g3777527	BLASTX	464	8e-42	83	(AF053008) gag-pol polyprotein [Glycine max]
14794	GM_216_B2_G04_MR	g3097320	BLASTN	457	1e-13	70	Glycine max gene for Bd 30K, complete cds
14795	GM_216_B2_G05_MR	g505129	BLASTN	349	8e-09	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
14796	GM_216_B2_G06_MR	g507910	BLASTN	657	4e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
14797	GM_216_B2_G07_MR	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14798	GM_216_B2_G09_MR	g505129	BLASTN	369	1e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
14799	GM_216_B2_H03_MR	g3928074	BLASTN	350	9e-09	68	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]
14800	GM_216_B2_H07_MR	g2462134	BLASTX	209	2e-15	33	(Y13368) reverse transcriptase [Beta vulgaris]
14801	GM_216_B2_H08_MR	g2564750	BLASTN	447	4e-13	62	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
14802	GM_217_A1_A03_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14803	GM_217_A1_A05_MR	g2997694	BLASTX	168	6e-12	47	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
14804	GM_217_A1_C02_MR	g99922	BLASTX	292	5e-43	64	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14805	GM_217_A1_C06_MR	g100484	BLASTX	183	4e-15	54	hypothetical protein - garden snapdragon
14806	GM_217_A1_C09_MR	g2522227	BLASTX	214	8e-17	57	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14807	GM_217_A1_D03_MR	g4038056	BLASTX	164	7e-17	48	(AC005897) putative transposon [Arabidopsis thaliana]
14808	GM_217_A1_D05_MR	g3776029	BLASTX	165	1e-11	64	(AJ010476) RNA helicase [Arabidopsis thaliana]
14809	GM_217_A1_E01_MR	g3645899	BLASTX	297	3e-24	51	(U68408) 5' end not determined experimentally [Zea mays]
14810	GM_217_A1_E02_MR	g4063760	BLASTX	101	4e-09	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14811	GM_217_A1_E07_MR	g905361	BLASTX	521	2e-57	92	(U22103) gag-protease polyprotein [Glycine max]
14812	GM_217_A1_E08_MR	g3142328	BLASTN	786	1e-28	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14813	GM_217_A2_B04_MR	g3687234	BLASTX	246	7e-23	55	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
14814	GM_217_A2_B06_MR	g3641865	BLASTX	150	7e-09	58	(AJ011010) beta-galactosidase [Cicer arietinum]
14815	GM_217_A2_B11_MR	g130582	BLASTX	159	2e-09	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14816	GM_217_A2_C01_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14817	GM_217_A2_D03_MR	g4063760	BLASTX	160	1e-09	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14818	GM_217_A2_E01_MR	g2995405	BLASTX	388	3e-34	57	(Y12432) polyprotein [Ananas comosus]
14819	GM_217_A2_F04_MR	g479178	BLASTX	201	7e-14	45	pol polyprotein - Volvox carteri f. nagariensis retrotransposon Osser gi 288597 (X69552) gag,protease,endonuclease, reverse transcriptase,RNaseH [Volvox carteri]
14820	GM_217_A2_F08_MR	g18559	BLASTN	1423	2e-57	88	G.max gene for catalase
14821	GM_217_A2_G01_MR	g3777527	BLASTX	171	1e-10	44	(AF053008) gag-pol polyprotein [Glycine max]
14822	GM_217_A2_G04_MR	g1666236	BLASTX	178	2e-12	31	(U76261) unknown [Hordeum vulgare]
14823	GM_217_A2_H01_MR	g3777527	BLASTX	171	1e-10	39	(AF053008) gag-pol polyprotein [Glycine max]
14824	GM_218_A1_A03_MR	g3777527	BLASTX	248	7e-19	40	(AF053008) gag-pol polyprotein [Glycine max]
14825	GM_218_A1_A05_T7	g3097320	BLASTN	423	4e-12	72	Glycine max gene for Bd 30K, complete cds
14826	GM_218_A1_B07_T7	g3201680	BLASTX	285	4e-23	47	(AF060941) extra-large G-protein [Arabidopsis thaliana]
14827	GM_218_A1_B09_T7	g3377834	BLASTX	154	3e-09	28	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14828	GM_218_A1_B11_T7	g114268	BLASTX	469	8e-44	62	L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE) gi 541907 pir S23763 gene Bp10 protein - rape gi 17789 (X64257) protein homologous to ascorbate oxidase [Brassica napus]
14829	GM_218_A1_C03_MR	g3142328	BLASTN	1349	3e-54	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14830	GM_218_A1_C03_T7	g2911075	BLASTX	182	3e-19	80	(AL021960) putative protein [Arabidopsis thaliana]
14831	GM_218_A1_C04_MR	g4063760	BLASTX	419	3e-37	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14832	GM_218_A1_C04_T7	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14833	GM_218_A1_C11_T7	g905361	BLASTX	153	3e-09	83	(U22103) gag-protease polyprotein [Glycine max]
14834	GM_218_A1_C12_T7	g100484	BLASTX	361	2e-31	54	hypothetical protein - garden snapdragon
14835	GM_218_A1_D04_MR	g2462936	BLASTX	107	4e-10	44	(Y12321) open reading frame 2 [Brassica oleracea]
14836	GM_218_A1_E03_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14837	GM_218_A1_E06_MR	g3930515	BLASTX	107	6e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
14838	GM_218_A1_E11_T7	g4115365	BLASTX	111	3e-11	48	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
14839	GM_218_A1_E12_T7	g3287696	BLASTX	196	3e-18	57	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
14840	GM_218_A1_F10_T7	g18695	BLASTN	395	5e-11	70	Soybean nodulin 22 gene
14841	GM_218_A1_G06_MR	g3097320	BLASTN	733	4e-26	74	Glycine max gene for Bd 30K, complete cds
14842	GM_218_A1_G06_T7	g3645899	BLASTX	358	8e-31	50	(U68408) 5' end not determined experimentally [Zea mays]
14843	GM_218_A1_G11_T7	g4063770	BLASTX	215	1e-15	35	(AB004906) transposase [Ipomoea purpurea]
14844	GM_218_A1_H04_MR	g3142328	BLASTN	1135	2e-44	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14845	GM_218_A2_A02_MR	g4038056	BLASTX	262	1e-20	50	(AC005897) putative transposon [Arabidopsis thaliana]
14846	GM_218_A2_A07_MR	g3097320	BLASTN	376	5e-10	62	Glycine max gene for Bd 30K, complete cds
14847	GM_218_A2_A08_MR	g3097320	BLASTN	541	2e-17	72	Glycine max gene for Bd 30K, complete cds
14848	GM_218_A2_A11_MR	g3142328	BLASTN	460	8e-14	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14849	GM_218_A2_B08_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14850	GM_218_A2_C01_MR	g1480927	BLASTN	1410	3e-58	91	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
14851	GM_218_A2_D07_MR	g3097320	BLASTN	406	2e-11	70	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14852	GM_218_A2_D09_MR	g3687234	BLASTX	164	4e-10	36	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
14853	GM_218_A2_F03_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
14854	GM_218_A2_F06_MR	g3097320	BLASTN	439	8e-13	68	Glycine max gene for Bd 30K, complete cds
14855	GM_218_A2_G03_MR	g3176795	BLASTN	344	6e-09	62	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
14856	GM_218_A2_G08_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14857	GM_218_B1_A04_MR	g2522230	BLASTX	250	1e-20	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14858	GM_218_B1_B01_MR	g18768	BLASTN	437	2e-13	71	Soybean Tgm6 transposable element 3' end
14859	GM_218_B1_B02_MR	g3645899	BLASTX	242	2e-18	43	(U68408) 5' end not determined experimentally [Zea mays]
14860	GM_218_B1_B05_MR	g1167523	BLASTX	435	7e-39	60	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14861	GM_218_B1_B07_MR	g507910	BLASTN	634	5e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14862	GM_218_B1_B11_MR	g18559	BLASTN	873	2e-32	72	G.max gene for catalase
14863	GM_218_B1_C01_MR	g3914535	BLASTX	208	3e-16	87	60S RIBOSOMAL PROTEIN L13A >gi 2791948 gnl PID e1237871 (AJ223363) ribosomal protein L13a [Lupinus luteus]
14864	GM_218_B1_C12_MR	g18559	BLASTN	843	3e-31	76	G.max gene for catalase
14865	GM_218_B1_D02_MR	g4160362	BLASTN	323	3e-09	62	Saccharomyces cerevisiae complete mitochondrial genome
14866	GM_218_B1_D09_MR	g2642443	BLASTX	341	5e-30	43	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]
14867	GM_218_B1_E01_MR	g4063760	BLASTX	377	1e-32	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14868	GM_218_B1_E11_MR	g4156185	BLASTN	586	2e-19	65	Homo sapiens PAC clone DJ0803F10 from 7q33-q36, complete sequence [Homo sapiens]
14869	GM_218_B1_F04_MR	g2995405	BLASTX	338	7e-29	67	(Y12432) polyprotein [Ananas comosus]
14870	GM_218_B1_G04_MR	g3097320	BLASTN	446	4e-13	69	Glycine max gene for Bd 30K, complete cds
14871	GM_218_B1_H04_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14872	GM_218_B2_A08_T7	g507910	BLASTN	580	1e-19	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14873	GM_218_B2_A11_T7	g2827715	BLASTX	224	1e-16	42	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
14874	GM_218_B2_B01_T7	g3687234	BLASTX	177	2e-24	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
14875	GM_218_B2_B05_MR	g3599418	BLASTN	359	3e-09	88	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14876	GM_218_B2_B07_MR	g3777527	BLASTX	307	4e-25	40	(AF053008) gag-pol polyprotein [Glycine max]
14877	GM_218_B2_B08_MR	g1732513	BLASTX	142	4e-09	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14878	GM_218_B2_B09_MR	g2995405	BLASTX	241	2e-34	65	(Y12432) polyprotein [Ananas comosus]
14879	GM_218_B2_C10_MR	g2315153	BLASTX	209	7e-16	74	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
14880	GM_218_B2_D04_MR	g3426334	BLASTN	417	7e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
14881	GM_218_B2_D05_T7	g3779030	BLASTX	154	2e-10	30	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
14882	GM_218_B2_D11_MR	g2121303	BLASTN	359	3e-09	60	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
14883	GM_218_B2_D11_T7	g2959767	BLASTX	312	1e-25	52	(AJ002584) AtMRP4 [Arabidopsis thaliana]
14884	GM_218_B2_E01_MR	g3097320	BLASTN	438	9e-13	71	Glycine max gene for Bd 30K, complete cds
14885	GM_218_B2_E02_MR	g3097320	BLASTN	472	2e-14	72	Glycine max gene for Bd 30K, complete cds
14886	GM_218_B2_E06_MR	g3097320	BLASTN	449	3e-13	70	Glycine max gene for Bd 30K, complete cds
14887	GM_218_B2_F05_MR	g3599418	BLASTN	895	1e-33	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14888	GM_218_B2_F07_MR	g3386611	BLASTX	279	5e-23	52	(AC004665) unknown protein [Arabidopsis thaliana]
14889	GM_219_B2_B01_T7	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14890	GM_219_B2_B03_T7	g133917	BLASTX	185	9e-14	79	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
14891	GM_219_B2_C10_T7	g950319	BLASTX	153	6e-09	50	(M11240) unknown protein [Drosophila melanogaster]
14892	GM_219_B2_D04_T7	g2160130	BLASTN	359	3e-09	62	Genomic sequence from Human 17, complete sequence [Homo sapiens]
14893	GM_219_B2_D06_T7	g905361	BLASTX	155	2e-09	32	(U22103) gag-protease polyprotein [Glycine max]
14894	GM_219_B2_D09_T7	g3142328	BLASTN	424	3e-12	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14895	GM_219_B2_D11_T7	g1666236	BLASTX	161	1e-10	28	(U76261) unknown [Hordeum vulgare]
14896	GM_219_B2_E09_T7	g18559	BLASTN	300	1e-10	74	G.max gene for catalase
14897	GM_219_B2_F01_T7	g1785729	BLASTN	364	2e-09	59	A.thaliana mitochondrial genome, part B
14898	GM_219_B2_F02_T7	g170065	BLASTN	361	2e-09	78	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
14899	GM_219_B2_G01_T7	g507910	BLASTN	455	6e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14900	GM_219_B2_H09_T7	g2995405	BLASTX	159	2e-11	60	(Y12432) polyprotein [Ananas comosus]
14901	GM_220_B1_A01_MR	g507910	BLASTN	361	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14902	GM_220_B1_B05_MR	g3193287	BLASTX	603	5e-58	80	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]
14903	GM_220_B1_E01_MR	g18559	BLASTN	782	2e-28	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14904	GM_220_B1_E04_MR	g2995405	BLASTX	341	3e-29	67	(Y12432) polyprotein [Ananas comosus]
14905	GM_220_B2_B06_T7	g4159704	BLASTN	596	7e-20	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence [Arabidopsis thaliana]
14906	GM_220_B2_B10_T7	g2129618	BLASTX	166	3e-16	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14907	GM_220_B2_B11_T7	g99922	BLASTX	206	1e-15	50	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14908	GM_220_B2_D08_T7	g22490	BLASTX	271	8e-23	36	(X01380) ORF1 [Zea mays]
14909	GM_220_B2_E01_T7	g13774	BLASTN	474	8e-15	66	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
14910	GM_220_B2_E12_T7	g3738114	BLASTN	560	3e-18	64	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
14911	GM_220_B2_H04_T7	g535454	BLASTX	162	2e-16	61	(U13940) cysteine proteinase [Alnus glutinosa]
14912	GM_220_B2_H10_T7	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
14913	GM_221_A1_A03_T7	g2801677	BLASTN	555	6e-19	67	Glycine max telomere-associated sequence STAS6
14914	GM_221_A1_B01_T7	g1743354	BLASTX	117	6e-12	67	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
14915	GM_221_A1_C03_T7	g2827662	BLASTX	283	4e-23	49	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14916	GM_221_A1_C05_T7	g3319366	BLASTX	192	2e-14	39	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
14917	GM_221_A1_C12_T7	g2687856	BLASTN	394	9e-11	63	Human genomic DNA sequence from cosmid B44H3 on chromosome 22, complete sequence [Homo sapiens]
14918	GM_221_A1_D05_T7	g507910	BLASTN	600	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14919	GM_221_A1_E04_T7	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14920	GM_221_A1_E11_T7	g507910	BLASTN	531	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14921	GM_221_A1_F10_T7	g1688049	BLASTX	254	5e-21	59	(D50034) 4-coumarate:CoA ligase [Nicotiana tabacum]
14922	GM_221_B1_B03_MR	g2443320	BLASTX	249	5e-19	63	(D85597) polyprotein [Oryza australiensis]
14923	GM_221_B1_C09_MR	g1769898	BLASTX	163	2e-10	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14924	GM_221_B1_E02_MR	g3777527	BLASTX	235	2e-17	44	(AF053008) gag-pol polyprotein [Glycine max]
14925	GM_221_B1_H12_T7	g18559	BLASTN	954	3e-36	84	G.max gene for catalase
14926	GM_222_B1_A02_MR	g1167523	BLASTX	177	2e-11	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14927	GM_222_B1_B02_MR	g3777527	BLASTX	173	7e-11	31	(AF053008) gag-pol polyprotein [Glycine max]
14928	GM_222_B1_D08_MR	g3319351	BLASTX	175	4e-11	62	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
14929	GM_222_B1_F11_MR	g2865437	BLASTX	153	9e-09	61	(AF039376) polyprotein [Arabidopsis arenosa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14930	GM_223_A1_A04_MR	g2351073	BLASTN	785	2e-28	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24
14931	GM_223_A1_A04_T7	g3810595	BLASTX	239	6e-18	42	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
14932	GM_223_A1_A05_MR	g1685114	BLASTN	369	1e-09	64	Dictyostelium discoideum putative transcription factor (stkA) mRNA, complete cds
14933	GM_223_A1_A09_MR	g1143381	BLASTX	164	5e-11	34	(Z49063) polygalacturonase inhibitor [Actinidia deliciosa]
14934	GM_223_A1_B02_T7	g3319366	BLASTX	191	2e-14	33	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
14935	GM_223_A1_B03_T7	g531389	BLASTX	90	3e-10	61	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14936	GM_223_A1_B07_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14937	GM_223_A1_B09_T7	g1480927	BLASTN	458	8e-14	81	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
14938	GM_223_A1_B12_MR	g2262107	BLASTX	152	3e-09	93	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
14939	GM_223_A1_B12_T7	g629693	BLASTX	138	1e-15	38	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14940	GM_223_A1_C07_MR	g507910	BLASTN	400	2e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14941	GM_223_A1_D01_MR	g3695387	BLASTX	256	6e-20	47	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
14942	GM_223_A1_D03_MR	g3599418	BLASTN	361	2e-09	82	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14943	GM_223_A1_D03_T7	g905361	BLASTX	474	4e-49	88	(U22103) gag-protease polyprotein [Glycine max]
14944	GM_223_A1_D06_T7	g1658062	BLASTX	496	1e-46	78	ACC synthase [Malus domestica]
14945	GM_223_A1_D07_T7	g2995405	BLASTX	388	3e-34	56	(Y12432) polyprotein [Ananas comosus]
14946	GM_223_A1_D11_MR	g3142328	BLASTN	1670	7e-69	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14947	GM_223_A1_D12_MR	g3599418	BLASTN	351	7e-09	80	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14948	GM_223_A1_D12_T7	g905361	BLASTX	625	2e-60	87	(U22103) gag-protease polyprotein [Glycine max]
14949	GM_223_A1_E01_T7	g3150396	BLASTN	415	1e-11	64	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence.
14950	GM_223_A1_E02_MR	g2316016	BLASTX	395	2e-34	60	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
14951	GM_223_A1_E03_T7	g507910	BLASTN	513	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14952	GM_223_A1_E04_MR	g3097320	BLASTN	421	5e-12	72	Glycine max gene for Bd 30K, complete cds
14953	GM_223_A1_E04_T7	g3779026	BLASTX	198	1e-13	39	(AC005171) putative retrotransposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14954	GM_223_A1_E05_MR	g1087068	BLASTN	365	5e-10	70	GH2/4=glutathione S-transferase {promoter} [Glycine max=soybeans, seedlings, Genomic, 858 nt]
14955	GM_223_A1_E10_MR	g2462936	BLASTX	110	1e-10	39	(Y12321) open reading frame 2 [Brassica oleracea]
14956	GM_223_A1_F03_MR	g4063760	BLASTX	242	4e-31	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14957	GM_223_A1_F04_T7	g3695395	BLASTX	218	3e-16	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14958	GM_223_A1_F07_MR	g3777527	BLASTX	574	1e-53	95	(AF053008) gag-pol polyprotein [Glycine max]
14959	GM_223_A1_F07_T7	g3142328	BLASTN	1611	3e-66	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14960	GM_223_A1_F09_T7	g3142328	BLASTN	1368	4e-55	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14961	GM_223_A1_F11_MR	g3930515	BLASTX	105	8e-10	35	(AF059674) putative gag protein [Nicotiana tabacum]
14962	GM_223_A1_G10_MR	g22491	BLASTX	102	2e-11	44	(X01380) ORF2 [Zea mays]
14963	GM_223_A1_G12_MR	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14964	GM_223_A1_H08_MR	g1771160	BLASTX	135	3e-15	48	(X98929) SBT1 [Lycopersicon esculentum] gi 3687305 gnl PID e1299610 (AJ006378) subtilisin-like protease [Lycopersicon esculentum]
14965	GM_223_A1_H10_MR	g4063760	BLASTX	323	6e-27	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14966	GM_223_B1_A03_T7	g507910	BLASTN	503	4e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14967	GM_223_B1_B07_T7	g3763850	BLASTN	745	1e-26	78	Glycine max GmENOD93 gene for early nodulin, complete cds
14968	GM_223_B1_C08_T7	g18559	BLASTN	455	1e-13	67	G.max gene for catalase
14969	GM_223_B1_D07_T7	g4050011	BLASTN	477	1e-14	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
14970	GM_223_B1_D08_T7	g2995405	BLASTX	265	5e-21	49	(Y12432) polyprotein [Ananas comosus]
14971	GM_223_B1_E02_T7	g1769899	BLASTX	169	4e-12	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14972	GM_224_A1_A03_T7	g130582	BLASTX	158	2e-09	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14973	GM_224_A1_A07_T7	g3645899	BLASTX	135	7e-16	43	(U68408) 5' end not determined experimentally [Zea mays]
14974	GM_224_A1_B03_T7	g3033375	BLASTX	406	4e-37	63	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
14975	GM_224_A1_B07_T7	g905361	BLASTX	308	6e-26	91	(U22103) gag-protease polyprotein [Glycine max]
14976	GM_224_A1_B11_T7	g3142328	BLASTN	1894	4e-79	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14977	GM_224_A1_B12_T7	g18768	BLASTN	400	1e-11	69	Soybean Tgm6 transposable element 3' end
14978	GM_224_A1_C02_T7	g1666236	BLASTX	188	1e-13	32	(U76261) unknown [Hordeum vulgare]
14979	GM_224_A1_C03_T7	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14980	GM_224_A1_D03_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14981	GM_224_A1_D11_T7	g507910	BLASTN	440	3e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14982	GM_224_A1_E05_T7	g2995405	BLASTX	468	7e-43	59	(Y12432) polyprotein [Ananas comosus]
14983	GM_224_A1_F11_T7	g3560029	BLASTN	462	5e-14	64	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
14984	GM_224_A1_G02_T7	g3142328	BLASTN	1418	2e-57	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14985	GM_224_A1_G03_T7	g3777527	BLASTX	752	1e-72	92	(AF053008) gag-pol polyprotein [Glycine max]
14986	GM_224_A1_H04_T7	g2801681	BLASTN	609	3e-21	69	Glycine max telomere-associated sequence STAS10
14987	GM_224_A1_H09_T7	g4063760	BLASTX	264	1e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14988	GM_225_B2_A01_T7	g3319351	BLASTX	380	5e-33	63	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
14989	GM_225_B2_A03_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14990	GM_225_B2_A03_T7	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14991	GM_225_B2_A04_T7	g3337395	BLASTN	367	1e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
14992	GM_225_B2_A08_T7	g905361	BLASTX	159	7e-10	100	(U22103) gag-protease polyprotein [Glycine max]
14993	GM_225_B2_A09_MR	g3777527	BLASTX	226	2e-16	35	(AF053008) gag-pol polyprotein [Glycine max]
14994	GM_225_B2_B01_T7	g1666236	BLASTX	111	4e-13	28	(U76261) unknown [Hordeum vulgare]
14995	GM_225_B2_B02_T7	g3319362	BLASTX	183	3e-12	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14996	GM_225_B2_B06_T7	g2864614	BLASTX	199	1e-14	40	(AL021811) putative protein [Arabidopsis thaliana]
14997	GM_225_B2_B07_MR	g4063760	BLASTX	419	3e-37	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14998	GM_225_B2_B08_T7	g100484	BLASTX	277	2e-22	53	hypothetical protein - garden snapdragon
14999	GM_225_B2_B11_MR	g1839022	BLASTX	142	1e-08	57	(Y11121) amino acid carrier [Ricinus communis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15000	GM_225_B2_C01_T7	g3142328	BLASTN	1520	5e-62	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15001	GM_225_B2_C05_MR	g3097320	BLASTN	904	7e-34	75	Glycine max gene for Bd 30K, complete cds
15002	GM_225_B2_C05_T7	g3777527	BLASTX	154	7e-10	36	(AF053008) gag-pol polyprotein [Glycine max]
15003	GM_225_B2_C12_MR	g505129	BLASTN	397	5e-11	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
15004	GM_225_B2_D01_T7	g22490	BLASTX	215	6e-17	46	(X01380) ORF1 [Zea mays]
15005	GM_225_B2_D04_MR	g507910	BLASTN	539	1e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15006	GM_225_B2_D07_MR	g2129618	BLASTX	249	3e-19	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15007	GM_225_B2_D09_T7	g3319362	BLASTX	157	2e-09	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15008	GM_225_B2_D10_MR	g421955	BLASTX	428	2e-39	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15009	GM_225_B2_E07_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15010	GM_225_B2_E07_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15011	GM_225_B2_E11_T7	g2828184	BLASTN	536	4e-17	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]
15012	GM_225_B2_F01_MR	g4063743	BLASTX	239	1e-23	63	(AC005851) hypothetical protein [Arabidopsis thaliana]
15013	GM_225_B2_F07_T7	g3600044	BLASTX	145	1e-09	39	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
15014	GM_226_A1_A12_MR	g3097320	BLASTN	407	2e-11	71	Glycine max gene for Bd 30K, complete cds
15015	GM_226_A1_B03_MR	g507910	BLASTN	491	1e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15016	GM_226_A1_B04_MR	g18559	BLASTN	449	2e-13	74	G.max gene for catalase
15017	GM_226_A1_B05_MR	g1142701	BLASTN	822	8e-31	86	Glycine max satellite STR120-A.3.
15018	GM_226_A1_C08_MR	g507910	BLASTN	351	3e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15019	GM_226_A1_C11_MR	g1172584	BLASTX	215	2e-18	42	POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE) gi 1076478 pir S52984 catechol oxidase (EC 1.10.3.1) precursor - apple tree gi 507280 (L29450) polyphenol oxidase [Malus domestica]
15020	GM_226_A1_D11_MR	g2052034	BLASTN	407	2e-11	68	Human DNA sequence from PAC 450C20 on chromosome X
15021	GM_226_B1_B03_MR	g2129618	BLASTX	235	9e-18	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15022	GM_226_B1_B09_MR	g4104931	BLASTX	160	7e-10	75	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
15023	GM_226_B1_F04_MR	g1707020	BLASTX	189	4e-13	30	(U78721) hypothetical protein [Arabidopsis thaliana]
15024	GM_226_B1_F06_MR	g2462058	BLASTX	252	8e-21	52	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15025	GM_227_B1_H12_MR	g3777527	BLASTX	175	3e-13	37	(AF053008) gag-pol polyprotein [Glycine max]
15026	GM_227_B2_A01_MR	g342953	BLASTN	494	3e-16	62	paramecium species 4.51a mt dna dimer: replication init. region.
15027	GM_227_B2_A03_MR	g3377855	BLASTX	373	2e-40	73	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96 80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
15028	GM_227_B2_A09_MR	g587603	BLASTN	347	1e-08	61	P.falciparum gene for beta subunit RNA polymerase
15029	GM_227_B2_B04_MR	g2462927	BLASTX	208	2e-15	65	(Y10342) putative amidase [Arabidopsis thaliana]
15030	GM_227_B2_B08_MR	g905361	BLASTX	428	3e-39	96	(U22103) gag-protease polyprotein [Glycine max]
15031	GM_227_B2_C04_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15032	GM_227_B2_D08_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15033	GM_227_B2_E02_MR	g905361	BLASTX	192	2e-13	29	(U22103) gag-protease polyprotein [Glycine max]
15034	GM_227_B2_E03_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15035	GM_227_B2_F03_MR	g4063760	BLASTX	295	5e-24	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15036	GM_228_A2_A05_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15037	GM_228_A2_B05_T7	g3097320	BLASTN	939	2e-35	81	Glycine max gene for Bd 30K, complete cds
15038	GM_228_A2_D03_T7	g3294511	BLASTN	357	4e-09	66	Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
15039	GM_228_A2_D05_T7	g255572	BLASTN	419	7e-13	75	small auxin up RNA gene cluster: orf 15A [Glycine max=soybeans, cv. Wayne, Genomic, 637 nt]
15040	GM_228_A2_G04_T7	g2706515	BLASTX	103	5e-13	56	(Y12689) isoflavone reductase-like protein [Citrus X paradisi]
15041	GM_229_A2_A11_T7	g507910	BLASTN	419	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15042	GM_229_A2_B04_T7	g118514	BLASTX	199	5e-17	93	TURGOR-RESPONSIVE PROTEIN 26G gi 100051 pir S11863 aldehyde dehydrogenase homolog - garden pea gi 20681 (X54359) 508 aa peptide [Pisum sativum]
15043	GM_229_A2_B06_MR	g4063760	BLASTX	173	9e-22	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15044	GM_229_A2_C07_MR	g3142328	BLASTN	480	1e-14	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15045	GM_229_A2_D01_T7	g2522228	BLASTX	270	1e-22	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
15046	GM_229_A2_D05_T7	g507910	BLASTN	354	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15047	GM_229_A2_D06_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15048	GM_229_A2_E08_MR	g3915082	BLASTX	149	1e-17	63	TUBULIN ALPHA CHAIN >gi 1220545 (M97956) alpha tubulin [Trypanosoma cruzi] >gi 1220548 (M96849) alpha tubulin [Trypanosoma cruzi]
15049	GM_229_A2_E11_T7	g2462936	BLASTX	369	3e-33	55	(Y12321) open reading frame 2 [Brassica oleracea]
15050	GM_229_A2_F01_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15051	GM_229_A2_F02_T7	g4092471	BLASTN	506	8e-16	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
15052	GM_229_A2_F09_T7	g99922	BLASTX	310	2e-47	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15053	GM_229_B2_A07_MR	g2642163	BLASTX	298	1e-24	55	(AC003000) hypothetical protein [Arabidopsis thaliana]
15054	GM_229_B2_B08_MR	g2760165	BLASTN	350	9e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
15055	GM_229_B2_C08_MR	g2244771	BLASTX	196	3e-13	80	(Z97335) kinesin homolog [Arabidopsis thaliana]
15056	GM_229_B2_C10_MR	g18559	BLASTN	1635	3e-67	85	G.max gene for catalase
15057	GM_229_B2_C12_MR	g3142328	BLASTN	723	9e-26	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15058	GM_229_B2_D08_MR	g1934969	BLASTN	359	3e-09	61	P.falciparum mRNA for AARP1 protein, partial
15059	GM_229_B2_E07_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15060	GM_229_B2_E08_MR	g4063756	BLASTN	365	2e-09	61	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15061	GM_240_B1_H12_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15062	GM_375_B2_B10_MR	g18559	BLASTN	777	3e-28	75	G.max gene for catalase
15063	GM_M01_A1_B09_MR	g1785739	BLASTX	163	1e-17	43	(Y08502) orf240b [Arabidopsis thaliana]
15064	GM_M01_A1_D05_MR	g3426334	BLASTN	354	5e-09	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15065	GM_M01_A1_G02_MR	g3645899	BLASTX	197	4e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
15066	GM_M01_A1_H11_MR	g1813979	BLASTX	135	2e-12	64	(Y10860) hypothetical protein [Musa acuminata]
15067	GM_M01_A2_A07_MR	g2292907	BLASTX	242	2e-18	44	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
15068	GM_M01_A2_A09_MF	g1531758	BLASTX	145	5e-11	90	(X98772) AUX1 [Arabidopsis thaliana] gi 3335360 (AC003028) unknown protein [Arabidopsis thaliana]
15069	GM_M01_A2_B01_MR	g2765244	BLASTX	220	2e-17	48	(Y12807) invertase inhibitor homolog [Arabidopsis thaliana]
15070	GM_M01_A2_B02_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15071	GM_M01_A2_B03_MF	g1850554	BLASTX	149	7e-10	57	(U88032) reverse transcriptase [Secale cereale]
15072	GM_M01_A2_B04_MR	g1814403	BLASTX	437	1e-39	80	(U84889) methionine synthase [Mesembryanthemum crystallinum]
15073	GM_M01_A2_B06_MF	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15074	GM_M01_A2_B09_MF	g4063760	BLASTX	279	3e-22	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15075	GM_M01_A2_B12_MF	g3777527	BLASTX	169	2e-10	33	(AF053008) gag-pol polyprotein [Glycine max]
15076	GM_M01_A2_C01_MF	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15077	GM_M01_A2_C01_MR	g507910	BLASTN	370	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15078	GM_M01_A2_C09_MF	g4063760	BLASTX	220	5e-16	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15079	GM_M01_A2_D01_MR	g3097320	BLASTN	457	1e-13	69	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15080	GM_M01_A2_D04_MF	g3176791	BLASTN	429	4e-13	61	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
15081	GM_M01_A2_D05_MR	g2465773	BLASTX	146	1e-09	37	(AF022186) homologous to orf238 in Porphyra purpurea [Cyanidium caldarium]
15082	GM_M01_A2_D07_MF	g4063760	BLASTX	195	2e-13	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15083	GM_M01_A2_D08_MF	g3283026	BLASTX	178	7e-12	36	putative transposase [Arabidopsis thaliana]
15084	GM_M01_A2_D11_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15085	GM_M01_A2_D11_MR	g402616	BLASTN	352	5e-09	86	G.max satellite DNA
15086	GM_M01_A2_E01_MF	g3097320	BLASTN	449	3e-13	70	Glycine max gene for Bd 30K, complete cds
15087	GM_M01_A2_E08_MR	g3777527	BLASTX	386	2e-33	51	(AF053008) gag-pol polyprotein [Glycine max]
15088	GM_M01_A2_E09_MR	g3097320	BLASTN	1082	6e-42	78	Glycine max gene for Bd 30K, complete cds
15089	GM_M01_A2_E11_MF	g3777527	BLASTX	384	2e-33	77	(AF053008) gag-pol polyprotein [Glycine max]
15090	GM_M01_A2_F01_MR	g4063756	BLASTN	699	1e-24	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15091	GM_M01_A2_F09_MF	g226407	BLASTX	302	1e-24	58	retrotransposon del1-46 [Lilium henryi]
15092	GM_M01_A2_G01_MR	g3097320	BLASTN	515	3e-16	70	Glycine max gene for Bd 30K, complete cds
15093	GM_M01_A2_G02_MR	g507910	BLASTN	345	6e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15094	GM_M01_A2_G03_MR	g18561	BLASTN	631	9e-22	85	G.max Gmachs1 gene for chalcone synthase
15095	GM_M01_A2_G11_MF	g4063760	BLASTX	253	1e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15096	GM_M01_A2_G12_MR	g1402883	BLASTX	171	2e-17	45	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
15097	GM_M01_A2_H03_MR	g507910	BLASTN	369	4e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15098	GM_M01_A2_H05_MF	g3142328	BLASTN	453	2e-13	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15099	GM_M01_A2_H11_MF	g3790154	BLASTN	358	4e-09	61	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
15100	GM_M01_A2_H12_MF	g3582000	BLASTX	157	9e-10	72	(AJ010942) hexose transporter protein [Lycopersicon esculentum]
15101	GM_M01_B1_A04_MF	g4050011	BLASTN	518	2e-16	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
15102	GM_M01_B1_A04_MR	g4063760	BLASTX	186	2e-12	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15103	GM_M01_B1_B06_MF	g2232254	BLASTX	195	6e-21	87	(AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
15104	GM_M01_B1_B07_MF	g2129618	BLASTX	209	6e-15	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
15105	GM_M01_B1_C06_MF	g3777527	BLASTX	600	2e-56	92	(AF053008) gag-pol polyprotein [Glycine max]
15106	GM_M01_B1_C07_MF	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
15107	GM_M01_B1_C08_MF	g3142328	BLASTN	1091	2e-42	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15108	GM_M01_B1_C08_MR	g507910	BLASTN	399	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15109	GM_M01_B1_D06_MR	g1142701	BLASTN	231	2e-17	72	Glycine max satellite STR120-A.3.
15110	GM_M01_B1_E02_MR	g4063760	BLASTX	210	5e-15	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15111	GM_M01_B1_E08_MR	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15112	GM_M01_B1_F04_MF	g2656031	BLASTN	591	1e-19	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
15113	GM_M01_B1_F05_MR	g1575536	BLASTX	156	3e-09	65	(U65533) regulator of nonsense transcript stability [Homo sapiens]
15114	GM_M01_B1_F06_MF	g507910	BLASTN	629	8e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15115	GM_M01_B1_F06_MR	g507910	BLASTN	368	5e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15116	GM_M01_B1_F09_MF	g2522226	BLASTN	564	1e-18	69	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
15117	GM_M01_B1_G02_MF	g729092	BLASTX	214	2e-19	88	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
15118	GM_M01_B1_H06_MF	g4063760	BLASTX	253	1e-19	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15119	GM_M01_B1_H06_MR	g3777527	BLASTX	431	2e-38	87	(AF053008) gag-pol polyprotein [Glycine max]
15120	GM_M01_B1_H10_MR	g2522228	BLASTX	202	6e-15	69	(AB007466) reverse transcriptase-like protein [Vicia faba]
15121	GM_M01_B1_H11_MF	g2852690	BLASTX	82	2e-09	48	(AF017754) resistance protein candidate [Lactuca sativa]
15122	GM_M01_B2_A02_MF	g3645899	BLASTX	287	3e-27	60	(U68408) 5' end not determined experimentally [Zea mays]
15123	GM_M01_B2_A04_MF	g2708743	BLASTX	233	2e-17	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
15124	GM_M01_B2_A05_MF	g3513745	BLASTX	228	1e-16	36	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
15125	GM_M01_B2_B01_MF	g2443320	BLASTX	241	3e-18	50	(D85597) polyprotein [Oryza australiensis]
15126	GM_M01_B2_B07_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15127	GM_M01_B2_B08_MF	g99922	BLASTX	548	3e-52	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15128	GM_M01_B2_C03_MF	g3452231	BLASTN	237	1e-08	63	Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15129	GM_M01_B2_C06_MF	g476213	BLASTN	663	2e-23	77	Glycine max Century 84 p24 oleosin isoform A gene, complete cds.
15130	GM_M01_B2_C11_MR	g3142328	BLASTN	892	2e-33	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15131	GM_M01_B2_D03_MF	g421955	BLASTX	306	2e-26	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15132	GM_M01_B2_D05_MF	g3608150	BLASTX	263	6e-22	52	(AC005314) putative peroxidase [Arabidopsis thaliana]
15133	GM_M01_B2_D11_MF	g4063760	BLASTX	312	8e-26	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15134	GM_M01_B2_E11_MF	g1071913	BLASTX	186	2e-13	72	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach gi 1066153 gnl PID d1007754 (D37963) cysteine synthase [Spinacia oleracea]
15135	GM_M01_B2_F01_MF	g905361	BLASTX	421	8e-54	86	(U22103) gag-protease polyprotein [Glycine max]
15136	GM_M01_B2_G03_MF	g3810596	BLASTX	176	9e-17	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
15137	GM_M01_B2_G06_MF	g4063760	BLASTX	192	5e-13	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15138	GM_M01_B2_G09_MR	g2522227	BLASTX	182	3e-13	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15139	GM_M01_B2_G11_MF	g3142328	BLASTN	1514	9e-62	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15140	GM_M01_B2_G12_MF	g3645899	BLASTX	147	5e-14	38	(U68408) 5' end not determined experimentally [Zea mays]
15141	GM_M01_B2_G12_MR	g3152618	BLASTX	200	2e-14	56	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]
15142	GM_M01_B2_H02_MF	g2462134	BLASTX	203	6e-19	40	(Y13368) reverse transcriptase [Beta vulgaris]
15143	GM_M01_B2_H05_MF	g4063760	BLASTX	484	4e-44	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15144	GM_M02_A1_A12_MR	g3599418	BLASTN	557	3e-18	71	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15145	GM_M02_A1_B07_MR	g992916	BLASTN	866	4e-32	84	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
15146	GM_M02_A1_B08_MR	g226407	BLASTX	254	1e-21	44	retrotransposon del1-46 [Lilium henryi]
15147	GM_M02_A1_B09_MR	g3142328	BLASTN	1050	1e-40	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15148	GM_M02_A1_B10_MF	g4063760	BLASTX	328	2e-27	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15149	GM_M02_A1_C10_MR	g2827663	BLASTX	412	3e-37	65	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
15150	GM_M02_A1_D03_MR	g2995405	BLASTX	462	3e-42	57	(Y12432) polyprotein [Ananas comosus]
15151	GM_M02_A1_D04_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15152	GM_M02_A1_D10_MR	g3449329	BLASTN	425	4e-12	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]
15153	GM_M02_A1_D11_MR	g3367567	BLASTN	395	8e-11	72	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)
15154	GM_M02_A1_E11_MF	g3777526	BLASTN	758	3e-27	97	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
15155	GM_M02_A1_F04_MR	g3702323	BLASTX	500	2e-49	77	(AC005397) unknown protein [Arabidopsis thaliana]
15156	GM_M02_A1_F08_MR	g3777527	BLASTX	535	3e-50	86	(AF053008) gag-pol polyprotein [Glycine max]
15157	GM_M02_A1_F09_MF	g1769899	BLASTX	91	3e-09	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15158	GM_M02_A1_F09_MR	g2443320	BLASTX	286	6e-23	49	(D85597) polyprotein [Oryza australiensis]
15159	GM_M02_A1_F10_MR	g1040717	BLASTN	364	2e-10	61	D.polychroa microsatellite sequence (clone Dp ch1 F3)
15160	GM_M02_A1_G08_MF	g2244994	BLASTX	261	9e-21	78	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]
15161	GM_M02_A1_H03_MR	g3097320	BLASTN	530	6e-17	72	Glycine max gene for Bd 30K, complete cds
15162	GM_M02_A1_H05_MR	g3661610	BLASTX	345	6e-29	81	(AF092565) splicing factor Prp8 [Homo sapiens]
15163	GM_M02_A1_H06_MR	g507910	BLASTN	420	2e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15164	GM_M02_A1_H07_MF	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15165	GM_M02_A1_H07_MR	g507910	BLASTN	403	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
15166	GM_M02_A2_A02_MF	g1854442	BLASTN	458	6e-14	75	Vigna unguiculata mRNA for CPRD8 protein, complete cds
15167	GM_M02_A2_B08_MF	g13767	BLASTN	423	6e-13	64	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
15168	GM_M02_A2_B10_MR	g3641780	BLASTN	360	3e-09	62	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
15169	GM_M02_A2_C04_MF	g3142328	BLASTN	1631	4e-67	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15170	GM_M02_A2_C05_MF	g507910	BLASTN	431	7e-13	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15171	GM_M02_A2_C12_MF	g3810595	BLASTX	160	1e-09	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
15172	GM_M02_A2_D08_MF	g3142328	BLASTN	735	3e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15173	GM_M02_A2_D11_MF	g2995405	BLASTX	237	5e-18	47	(Y12432) polyprotein [Ananas comosus]
15174	GM_M02_A2_E05_MF	g2522227	BLASTX	228	3e-18	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15175	GM_M02_A2_E07_MF	g2982431	BLASTX	262	2e-20	42	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
15176	GM_M02_A2_E08_MF	g1854442	BLASTN	497	1e-18	73	Vigna unguiculata mRNA for CPRD8 protein, complete cds
15177	GM_M02_A2_E12_MR	g4063760	BLASTX	219	7e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15178	GM_M02_A2_F02_MF	g3249094	BLASTN	391	1e-10	67	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]
15179	GM_M02_A2_F07_MF	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15180	GM_M02_A2_F11_MF	g507910	BLASTN	401	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15181	GM_M02_A2_G01_MF	g4063760	BLASTX	353	6e-31	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15182	GM_M02_A2_G09_MF	g1142701	BLASTN	1322	2e-53	84	Glycine max satellite STR120-A.3.
15183	GM_M02_A2_G12_MF	g2522228	BLASTX	199	1e-14	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
15184	GM_M02_A2_H05_MF	g3097320	BLASTN	465	5e-14	70	Glycine max gene for Bd 30K, complete cds
15185	GM_M02_A2_H05_MR	g118964	BLASTX	154	1e-09	31	DYNEIN HEAVY CHAIN (DYHC) gi 103902 pir S09598 dynein heavy chain - rainbow trout (fragment) gi 64319 (X15476) dynein (515 AA) [Oncorhynchus mykiss]
15186	GM_M02_B1_A04_MF	g2708743	BLASTX	182	2e-13	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
15187	GM_M02_B1_A07_MR	g2335065	BLASTN	365	2e-09	62	Human BAC clone RG180F08 from 7q31, complete sequence [Homo sapiens]
15188	GM_M02_B1_B03_MR	g3097320	BLASTN	901	9e-34	76	Glycine max gene for Bd 30K, complete cds
15189	GM_M02_B1_B12_MF	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15190	GM_M02_B1_B12_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15191	GM_M02_B1_C06_MF	g507910	BLASTN	546	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15192	GM_M02_B1_C08_MF	g2522230	BLASTX	159	6e-11	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15193	GM_M02_B1_C12_MR	g4063760	BLASTX	245	1e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15194	GM_M02_B1_D03_MR	g3142328	BLASTN	829	1e-30	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15195	GM_M02_B1_D05_MR	g3176077	BLASTN	500	7e-16	67	Medicago sativa mRNA for protein phosphatase 1, epsilon subunit
15196	GM_M02_B1_D10_MR	g3695388	BLASTX	187	6e-14	71	(AF096371) No definition line found [Arabidopsis thaliana]
15197	GM_M02_B1_D12_MF	g3097320	BLASTN	520	2e-16	69	Glycine max gene for Bd 30K, complete cds
15198	GM_M02_B1_E11_MR	g1769898	BLASTX	372	5e-33	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15199	GM_M02_B1_F02_MF	g100484	BLASTX	261	1e-20	68	hypothetical protein - garden snapdragon
15200	GM_M02_B1_F06_MF	g2924730	BLASTN	443	6e-13	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15201	GM_M02_B1_F06_MR	g2564046	BLASTN	372	9e-10	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]
15202	GM_M02_B1_F07_MF	g1514643	BLASTX	292	1e-23	61	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
15203	GM_M02_B1_F11_MF	g507910	BLASTN	695	8e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
15204	GM_M02_B1_F12_MF	g507910	BLASTN	344	6e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15205	GM_M02_B1_F12_MR	g3777527	BLASTX	477	3e-43	86	(AF053008) gag-pol polyprotein [Glycine max]
15206	GM_M02_B1_G03_MR	g3097320	BLASTN	364	2e-09	76	Glycine max gene for Bd 30K, complete cds
15207	GM_M02_B1_G06_MF	g3097320	BLASTN	483	8e-15	71	Glycine max gene for Bd 30K, complete cds
15208	GM_M02_B1_G10_MR	g3695388	BLASTX	145	2e-09	61	(AF096371) No definition line found [Arabidopsis thaliana]
15209	GM_M02_B2_A03_MF	g2245070	BLASTX	185	4e-12	55	(Z97342) hypothetical protein [Arabidopsis thaliana]
15210	GM_M02_B2_A07_MF	g3810596	BLASTX	152	6e-09	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
15211	GM_M02_B2_A12_MF	g99729	BLASTX	316	1e-27	46	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
15212	GM_M02_B2_B07_MF	g3645899	BLASTX	307	2e-25	53	(U68408) 5' end not determined experimentally [Zea mays]
15213	GM_M02_B2_B07_MR	g2443320	BLASTX	331	9e-28	53	(D85597) polyprotein [Oryza australiensis]
15214	GM_M02_B2_C07_MF	g4106979	BLASTN	366	2e-09	64	Homo sapiens chromosome 19, cosmid F15658, complete sequence [Homo sapiens]
15215	GM_M02_B2_C09_MF	g1769899	BLASTX	160	4e-11	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15216	GM_M02_B2_C11_MF	g507910	BLASTN	416	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
15217	GM_M02_B2_D02_MF	g3367528	BLASTX	185	5e-13	39	(AC004392) Strong similarity to gi 2160138 F19K23.6 gene product from A. thaliana BAC gb AC000375. [Arabidopsis thaliana]
15218	GM_M02_B2_D06_MR	g3150402	BLASTX	181	5e-17	79	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]
15219	GM_M02_B2_D09_MF	g2586081	BLASTX	188	5e-13	36	(U72725) receptor kinase-like protein [Oryza longistaminata]
15220	GM_M02_B2_D09_MR	g3033389	BLASTX	209	5e-15	39	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15221	GM_M02_B2_E01_MF	g2130082	BLASTX	199	7e-14	40	protein kinase Xa21 (EC 2.7.1.-) - rice gi 1122443 (U37133) receptor kinase-like protein [Oryza sativa] gi 2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] gi 1586408 prf 2203451A receptor kinase-like protein [Oryza sativa]
15222	GM_M02_B2_E03_MR	g3777526	BLASTN	465	5e-14	82	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
15223	GM_M02_B2_E12_MR	g1931640	BLASTX	156	9e-10	72	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]
15224	GM_M02_B2_F04_MF	g4063760	BLASTX	194	3e-13	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15225	GM_M02_B2_F05_MF	g4063756	BLASTN	433	2e-12	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15226	GM_M02_B2_F07_MR	g3142328	BLASTN	1458	3e-59	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15227	GM_M02_B2_F08_MR	g4115365	BLASTX	228	8e-17	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
15228	GM_M02_B2_G02_MF	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15229	GM_M02_B2_G11_MF	g3645899	BLASTX	153	1e-15	44	(U68408) 5' end not determined experimentally [Zea mays]
15230	GM_M02_B2_G12_MF	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15231	GM_M02_B2_G12_MR	g507910	BLASTN	406	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15232	GM_M02_B2_H01_MF	g3645899	BLASTX	314	4e-26	50	(U68408) 5' end not determined experimentally [Zea mays]
15233	GM_M02_B2_H03_MR	g3777527	BLASTX	246	1e-18	41	(AF053008) gag-pol polyprotein [Glycine max]
15234	GM_M02_B2_H05_MF	g2443320	BLASTX	287	4e-23	46	(D85597) polyprotein [Oryza australiensis]
15235	GM_M03_A1_A02_MR	g18559	BLASTN	672	2e-23	73	G.max gene for catalase
15236	GM_M03_A1_A05_MF	g4063760	BLASTX	477	2e-43	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15237	GM_M03_A1_B02_MF	g3046704	BLASTX	290	2e-23	43	(AL022223) putative protein [Arabidopsis thaliana]
15238	GM_M03_A1_B03_MF	g4006833	BLASTX	269	4e-21	42	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
15239	GM_M03_A1_B07_MF	g4063756	BLASTN	384	3e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15240	GM_M03_A1_B08_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15241	GM_M03_A1_B11_MF	g2245031	BLASTN	399	6e-11	66	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 7
15242	GM_M03_A1_C02_MR	g3777527	BLASTX	193	6e-13	45	(AF053008) gag-pol polyprotein [Glycine max]
15243	GM_M03_A1_C03_MF	g4063760	BLASTX	298	2e-43	77	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15244	GM_M03_A1_C05_MF	g3522932	BLASTN	371	1e-09	64	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
15245	GM_M03_A1_C06_MF	g3292817	BLASTX	99	7e-09	51	(AL031018) hypothetical protein [Arabidopsis thaliana]
15246	GM_M03_A1_C06_MR	g2493908	BLASTX	194	1e-20	52	CULLIN HOMOLOG 3 (CUL-3) gi 1381146 (U58089) Hs-CUL-3 [Homo sapiens]
15247	GM_M03_A1_C08_MR	g2443320	BLASTX	274	1e-21	48	(D85597) polyprotein [Oryza australiensis]
15248	GM_M03_A1_C09_MF	g3386534	BLASTX	360	3e-32	56	(AF078934) mariner transposase [Glycine max]
15249	GM_M03_A1_C11_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15250	GM_M03_A1_D01_MR	g4063760	BLASTX	511	4e-47	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15251	GM_M03_A1_D11_MR	g4063760	BLASTX	488	1e-44	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15252	GM_M03_A1_E01_MF	g3097320	BLASTN	842	4e-31	79	Glycine max gene for Bd 30K, complete cds
15253	GM_M03_A1_F03_MF	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15254	GM_M03_A1_F03_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15255	GM_M03_A1_F07_MF	g3097320	BLASTN	461	8e-14	70	Glycine max gene for Bd 30K, complete cds
15256	GM_M03_A1_F08_MF	g2769655	BLASTN	503	1e-15	65	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
15257	GM_M03_A1_F09_MF	g18559	BLASTN	882	6e-33	75	G.max gene for catalase
15258	GM_M03_A1_G02_MF	g4063760	BLASTX	492	5e-45	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15259	GM_M03_A1_G06_MF	g3777527	BLASTX	358	1e-30	97	(AF053008) gag-pol polyprotein [Glycine max]
15260	GM_M03_A1_G06_MR	g3983556	BLASTN	421	6e-12	62	Homo sapiens clone UWGC:r13c from 6p21, complete sequence [Homo sapiens]
15261	GM_M03_A1_G08_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15262	GM_M03_A1_G09_MR	g3402747	BLASTN	352	7e-09	60	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project)
15263	GM_M03_A1_G11_MF	g3645899	BLASTX	203	2e-28	51	(U68408) 5' end not determined experimentally [Zea mays]
15264	GM_M03_A1_H03_MR	g1666236	BLASTX	187	1e-13	36	(U76261) unknown [Hordeum vulgare]
15265	GM_M03_A1_H04_MF	g3746069	BLASTX	178	1e-13	34	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
15266	GM_M03_A1_H04_MR	g3142328	BLASTN	563	2e-18	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15267	GM_M03_A1_H06_MF	g2129618	BLASTX	153	8e-14	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15268	GM_M03_A1_H07_MF	g507910	BLASTN	552	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15269	GM_M03_A1_H07_MR	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15270	GM_M03_A1_H10_MF	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15271	GM_M03_A1_H11_MF	g4063760	BLASTX	522	3e-48	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15272	GM_M03_A1_H12_MF	g2160189	BLASTX	234	1e-17	57	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
15273	GM_M03_A2_A05_MR	g3142328	BLASTN	979	2e-37	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15274	GM_M03_A2_B05_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15275	GM_M03_A2_B06_MR	g1785744	BLASTX	147	1e-09	50	(Y08502) orf158 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15276	GM_M03_A2_B07_MF	g507910	BLASTN	609	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15277	GM_M03_A2_B07_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15278	GM_M03_A2_B10_MF	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15279	GM_M03_A2_B12_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15280	GM_M03_A2_C03_MF	g3777527	BLASTX	436	7e-39	55	(AF053008) gag-pol polyprotein [Glycine max]
15281	GM_M03_A2_C11_MF	g3650039	BLASTX	215	7e-16	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
15282	GM_M03_A2_D01_MR	g2384696	BLASTX	145	3e-15	62	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]
15283	GM_M03_A2_D02_MF	g3746069	BLASTX	188	1e-15	32	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
15284	GM_M03_A2_D02_MR	g3142328	BLASTN	650	2e-22	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15285	GM_M03_A2_D08_MR	g18559	BLASTN	445	4e-13	75	G.max gene for catalase
15286	GM_M03_A2_D12_MF	g3688173	BLASTX	159	2e-09	51	(AL031804) putative protein [Arabidopsis thaliana]
15287	GM_M03_A2_E01_MR	g2129618	BLASTX	146	2e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15288	GM_M03_A2_E02_MF	g3777527	BLASTX	154	7e-14	36	(AF053008) gag-pol polyprotein [Glycine max]
15289	GM_M03_A2_E04_MF	g3142328	BLASTN	482	8e-15	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15290	GM_M03_A2_E05_MF	g4063760	BLASTX	317	3e-26	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15291	GM_M03_A2_F01_MR	g2351071	BLASTN	358	4e-09	60	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3
15292	GM_M03_A2_F04_MF	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15293	GM_M03_A2_F04_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15294	GM_M03_A2_F05_MF	g2245104	BLASTX	401	3e-35	53	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
15295	GM_M03_A2_F07_MF	g479124	BLASTN	435	8e-13	65	C.parapsilosos mitochondrial DNA for right telomeric region and ATP6 gene
15296	GM_M03_A2_F08_MF	g1666236	BLASTX	145	7e-09	30	(U76261) unknown [Hordeum vulgare]
15297	GM_M03_A2_F11_MF	g3097320	BLASTN	386	2e-10	68	Glycine max gene for Bd 30K, complete cds
15298	GM_M03_A2_G03_MR	g1658457	BLASTX	363	1e-32	67	(U75248) reverse transcriptase [Gossypium barbadense]
15299	GM_M03_A2_G04_MR	g3292823	BLASTX	94	4e-10	30	(AL031018) putative protein [Arabidopsis thaliana]
15300	GM_M03_A2_G06_MF	g421954	BLASTX	289	3e-32	57	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
15301	GM_M03_A2_G12_MF	g3426334	BLASTN	382	3e-10	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15302	GM_M03_A2_H04_MF	g3097320	BLASTN	435	1e-12	68	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15303	GM_M03_A2_H06_MF	g3319362	BLASTX	262	1e-20	53	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15304	GM_M03_A2_H09_MR	g4063760	BLASTX	325	3e-27	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15305	GM_M03_A2_H10_MF	g3426334	BLASTN	373	7e-10	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15306	GM_M03_A2_H12_MF	g587603	BLASTN	353	5e-09	63	P.falciparum gene for beta subunit RNA polymerase
15307	GM_M03_B1_A01_MF	g629693	BLASTX	216	1e-16	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15308	GM_M03_B1_A04_MR	g3426334	BLASTN	569	9e-19	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15309	GM_M03_B1_A05_MF	g1769897	BLASTX	149	7e-09	27	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15310	GM_M03_B1_A08_MF	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15311	GM_M03_B1_A09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15312	GM_M03_B1_B03_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15313	GM_M03_B1_B07_MF	g3097320	BLASTN	557	3e-18	76	Glycine max gene for Bd 30K, complete cds
15314	GM_M03_B1_B08_MR	g507910	BLASTN	567	5e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15315	GM_M03_B1_B09_MF	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15316	GM_M03_B1_B12_MR	g507910	BLASTN	381	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15317	GM_M03_B1_C05_MF	g3845197	BLASTN	363	2e-09	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
15318	GM_M03_B1_C05_MR	g3687234	BLASTX	187	2e-12	42	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15319	GM_M03_B1_C08_MF	g2522230	BLASTX	190	3e-14	38	(AB007467) retrotransposon-like gene, the first amino acid was determined to be leucine [Vicia faba]
15320	GM_M03_B1_C08_MR	g629693	BLASTX	222	3e-17	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15321	GM_M03_B1_C09_MF	g100484	BLASTX	242	1e-18	41	hypothetical protein - garden snapdragon
15322	GM_M03_B1_C09_MR	g1142700	BLASTN	925	3e-35	88	Glycine max satellite STR120-A.2.
15323	GM_M03_B1_D01_MR	g3142328	BLASTN	901	7e-34	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15324	GM_M03_B1_D03_MR	g2970050	BLASTN	327	1e-15	77	Vigna radiata mRNA for ARG10, complete cds
15325	GM_M03_B1_D09_MR	g1809230	BLASTN	379	4e-10	66	Human BAC clone GS188P18, complete sequence [Homo sapiens]
15326	GM_M03_B1_E01_MF	g507910	BLASTN	402	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15327	GM_M03_B1_E02_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15328	GM_M03_B1_E08_MR	g18563	BLASTN	456	8e-14	63	G.max intergenic region DNA (between Gmachs1 and Gmachs3)
15329	GM_M03_B1_E09_MR	g2129503	BLASTX	186	1e-13	55	ACC oxidase (clone ACO2) oxidase - muskmelon gi 1183898 gnl PID e221405 (X95552) ACC oxidase [Cucumis melo]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15330	GM_M03_B1_E10_MR	g3645899	BLASTX	201	2e-23	37	(U68408) 5' end not determined experimentally [Zea mays]
15331	GM_M03_B1_F03_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15332	GM_M03_B1_F07_MF	g3820757	BLASTN	399	3e-11	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
15333	GM_M03_B1_F09_MF	g4115373	BLASTX	475	2e-43	72	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
15334	GM_M03_B1_F10_MF	g3953458	BLASTX	301	2e-25	80	(AC002328) F20N2.3 [Arabidopsis thaliana]
15335	GM_M03_B1_F12_MF	g18559	BLASTN	821	3e-30	75	G.max gene for catalase
15336	GM_M03_B1_G02_MR	g3645899	BLASTX	252	2e-19	42	(U68408) 5' end not determined experimentally [Zea mays]
15337	GM_M03_B1_G03_MR	g2462936	BLASTX	330	4e-29	46	(Y12321) open reading frame 2 [Brassica oleracea]
15338	GM_M03_B1_G07_MR	g2522228	BLASTX	335	1e-29	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
15339	GM_M03_B1_G09_MF	g1769898	BLASTX	152	4e-09	31	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15340	GM_M03_B1_H03_MR	g3599418	BLASTN	861	5e-32	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15341	GM_M03_B1_H06_MR	g2673917	BLASTX	445	1e-39	80	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
15342	GM_M03_B1_H08_MR	g1550659	BLASTX	116	8e-10	40	(Z80226) ptrBb [Mycobacterium tuberculosis]
15343	GM_M03_B2_A02_MR	g2522227	BLASTX	218	3e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15344	GM_M03_B2_A03_MF	g3645899	BLASTX	168	6e-12	43	(U68408) 5' end not determined experimentally [Zea mays]
15345	GM_M03_B2_A05_MF	g3930515	BLASTX	121	1e-10	47	(AF059674) putative gag protein [Nicotiana tabacum]
15346	GM_M03_B2_A05_MR	g2194136	BLASTX	163	7e-10	35	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
15347	GM_M03_B2_B01_MF	g507910	BLASTN	432	6e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
15348	GM_M03_B2_B01_MR	g3777527	BLASTX	536	2e-49	94	(AF053008) gag-pol polyprotein [Glycine max]
15349	GM_M03_B2_B02_MR	g130582	BLASTX	251	3e-19	51	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
15350	GM_M03_B2_B09_MR	g905361	BLASTX	517	7e-49	88	(U22103) gag-protease polyprotein [Glycine max]
15351	GM_M03_B2_C02_MF	g2244803	BLASTX	298	1e-25	41	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
15352	GM_M03_B2_C04_MF	g170029	BLASTN	423	4e-12	82	Glycine max cv. Dare nodulin 26 gene fragment.
15353	GM_M03_B2_C05_MF	g480618	BLASTX	172	2e-12	50	ATAF1 protein - Arabidopsis thaliana (fragment) gi 1345506 gnl PID e85756 (X74755) ATAF1 gene product [Arabidopsis thaliana]
15354	GM_M03_B2_C08_MF	g3108248	BLASTN	801	6e-30	71	Gossypium barbadense clone pXP027 repetitive DNA sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15355	GM_M03_B2_C08_MR	g12212	BLASTN	1138	8e-51	86	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
15356	GM_M03_B2_C11_MF	g178858	BLASTN	403	9e-12	64	Human restriction fragment length polymorphism 3' to the apolipoprotein B gene.
15357	GM_M03_B2_D04_MF	g2429543	BLASTX	204	3e-14	43	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
15358	GM_M03_B2_D04_MR	g294668	BLASTX	102	7e-09	48	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]
15359	GM_M03_B2_D09_MF	g100484	BLASTX	342	2e-29	58	hypothetical protein - garden snapdragon
15360	GM_M03_B2_E01_MF	g3097320	BLASTN	1036	7e-40	80	Glycine max gene for Bd 30K, complete cds
15361	GM_M03_B2_E12_MR	g2245116	BLASTX	204	9e-16	55	(Z97343) unnamed protein product [Arabidopsis thaliana]
15362	GM_M03_B2_F03_MF	g2493494	BLASTX	156	1e-17	46	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa]
15363	GM_M03_B2_F03_MR	g3513747	BLASTX	146	1e-13	37	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15364	GM_M03_B2_F06_MR	g3142328	BLASTN	624	3e-21	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15365	GM_M03_B2_F09_MR	g3777527	BLASTX	748	3e-72	94	(AF053008) gag-pol polyprotein [Glycine max]
15366	GM_M03_B2_F10_MR	g3097320	BLASTN	1271	2e-50	81	Glycine max gene for Bd 30K, complete cds
15367	GM_M03_B2_F12_MR	g3777527	BLASTX	726	8e-70	96	(AF053008) gag-pol polyprotein [Glycine max]
15368	GM_M03_B2_G01_MR	g3599418	BLASTN	354	5e-09	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15369	GM_M03_B2_G04_MF	g2827699	BLASTX	483	3e-44	69	(AL021684) predicted protein [Arabidopsis thaliana]
15370	GM_M03_B2_G04_MR	g1172555	BLASTX	254	5e-21	54	34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) gi 629720 pir S46936 34K porin - potato gi 1076682 pir A55364 porin (clone pPOM-34) - potato mitochondrion gi 516166 gnl PID e1188619 (X80386) 34 kDA porin [Solanum tuberosum]
15371	GM_M03_B2_G08_MR	g4063760	BLASTX	415	8e-37	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15372	GM_M03_B2_G09_MF	g3097320	BLASTN	475	2e-14	76	Glycine max gene for Bd 30K, complete cds
15373	GM_M03_B2_G10_MR	g3097320	BLASTN	567	1e-18	68	Glycine max gene for Bd 30K, complete cds
15374	GM_M03_B2_G11_MR	g507910	BLASTN	522	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15375	GM_M03_B2_G12_MR	g3319362	BLASTX	144	5e-10	45	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15376	GM_M03_B2_H01_MF	g1666236	BLASTX	177	2e-12	28	(U76261) unknown [Hordeum vulgare]
15377	GM_M03_B2_H01_MR	g3777527	BLASTX	231	2e-20	51	(AF053008) gag-pol polyprotein [Glycine max]
15378	GM_M03_B2_H02_MF	g3142328	BLASTN	907	4e-34	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15379	GM_M03_B2_H03_MR	g2230959	BLASTX	397	2e-35	52	(Y10149) subtilisin-like protease [Lycopersicon esculentum]
15380	GM_M03_B2_H04_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15381	GM_M03_B2_H04_MR	g3142379	BLASTX	157	7e-10	75	(AF053008) envelope-like [Glycine max]
15382	GM_M03_B2_H05_MF	g2708741	BLASTX	242	9e-18	86	(AC003952) hypothetical protein [Arabidopsis thaliana]
15383	GM_M03_B2_H05_MR	g2969943	BLASTN	365	2e-09	61	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
15384	GM_M03_B2_H06_MF	g18559	BLASTN	684	6e-24	73	G.max gene for catalase
15385	GM_M03_B2_H10_MF	g2288985	BLASTX	243	1e-18	56	(AC002335) hypothetical protein [Arabidopsis thaliana]
15386	GM_M04_A1_A02_MF	g4063760	BLASTX	426	5e-38	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15387	GM_M04_A1_B04_MF	g2924729	BLASTN	699	1e-24	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
15388	GM_M04_A1_C02_MF	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence
15389	GM_M04_A1_C09_MF	g3646936	BLASTN	364	2e-09	61	Caenorhabditis elegans cosmid Y47D3B, complete sequence [Caenorhabditis elegans]
15390	GM_M04_A1_D03_MF	g4063760	BLASTX	430	2e-46	76	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15391	GM_M04_A1_E07_MF	g3928116	BLASTN	407	2e-11	74	, complete sequence [Homo sapiens]
15392	GM_M04_A1_E11_MF	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15393	GM_M04_A1_F02_MF	g905361	BLASTX	149	3e-10	83	(U22103) gag-protease polyprotein [Glycine max]
15394	GM_M04_A1_F03_MF	g2522230	BLASTX	159	5e-11	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15395	GM_M04_A1_F04_MF	g2495209	BLASTX	191	2e-14	44	HYPOTHETICAL 12.9 KD PROTEIN SLR1417 gi 1651819 gnl PID d1017479 (D90900) hypothetical protein [Synechocystis sp.]
15396	GM_M04_A1_F08_MF	g4138583	BLASTX	233	8e-18	62	(Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
15397	GM_M04_A1_F09_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15398	GM_M04_A1_F11_MF	g2961370	BLASTN	383	3e-10	84	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)
15399	GM_M04_A1_G05_MF	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15400	GM_M04_A1_G06_MF	g2995405	BLASTX	196	6e-22	47	(Y12432) polyprotein [Ananas comosus]
15401	GM_M04_A1_G07_MF	g507910	BLASTN	675	7e-24	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
15402	GM_M04_A1_G12_MF	g4063770	BLASTX	193	2e-13	32	(AB004906) transposase [Ipomoea purpurea]
15403	GM_M04_A1_H03_MF	g18559	BLASTN	854	1e-31	78	G.max gene for catalase
15404	GM_M04_A1_H05_MF	g3142328	BLASTN	1237	4e-49	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15405	GM_M04_A1_H12_MF	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15406	GM_M04_A2_A04_MF	g507910	BLASTN	536	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15407	GM_M04_A2_A08_MR	g2443320	BLASTX	220	6e-16	32	(D85597) polyprotein [Oryza australiensis]
15408	GM_M04_A2_A10_MR	g3264565	BLASTN	378	5e-10	60	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
15409	GM_M04_A2_B02_MF	g507910	BLASTN	651	8e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15410	GM_M04_A2_B03_MF	g2407790	BLASTX	165	2e-10	44	(AF019910) grr1 [Glycine max]
15411	GM_M04_A2_B05_MF	g3777527	BLASTX	312	1e-25	50	(AF053008) gag-pol polyprotein [Glycine max]
15412	GM_M04_A2_B07_MF	g4140712	BLASTX	113	9e-11	31	(AF110183) putative integrase [Oryza sativa]
15413	GM_M04_A2_B07_MR	g1769897	BLASTX	304	8e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15414	GM_M04_A2_B09_MF	g507910	BLASTN	580	1e-19	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15415	GM_M04_A2_B10_MF	g3777527	BLASTX	686	2e-65	91	(AF053008) gag-pol polyprotein [Glycine max]
15416	GM_M04_A2_B11_MR	g3777527	BLASTX	312	1e-25	47	(AF053008) gag-pol polyprotein [Glycine max]
15417	GM_M04_A2_B12_MR	g3193306	BLASTX	205	2e-14	29	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB.AL021637) [Arabidopsis thaliana]
15418	GM_M04_A2_C02_MF	g905361	BLASTX	597	2e-57	87	(U22103) gag-protease polyprotein [Glycine max]
15419	GM_M04_A2_C06_MR	g2522228	BLASTX	367	4e-40	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
15420	GM_M04_A2_C07_MF	g18559	BLASTN	974	4e-37	74	G.max gene for catalase
15421	GM_M04_A2_C08_MR	g1669680	BLASTN	472	3e-14	63	Human DNA sequence from PAC 293E14 contains ESTs, STS
15422	GM_M04_A2_C12_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15423	GM_M04_A2_D04_MR	g905361	BLASTX	370	1e-32	89	(U22103) gag-protease polyprotein [Glycine max]
15424	GM_M04_A2_D05_MF	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15425	GM_M04_A2_D05_MR	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15426	GM_M04_A2_D06_MF	g2275186	BLASTN	403	4e-11	63	Human BAC clone RG020D02 from 7q22, complete sequence [Homo sapiens]
15427	GM_M04_A2_D07_MF	g3377848	BLASTX	107	1e-10	33	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
15428	GM_M04_A2_D07_MR	g4102839	BLASTX	180	3e-12	41	(AF016713) LeOPT1 [Lycopersicon esculentum]
15429	GM_M04_A2_E06_MR	g4063760	BLASTX	326	3e-27	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15430	GM_M04_A2_E08_MF	g905361	BLASTX	180	2e-14	36	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15431	GM_M04_A2_E11_MF	g2335100	BLASTX	432	4e-39	61	(AC002339) unknown protein [Arabidopsis thaliana]
15432	GM_M04_A2_F10_MR	g1840106	BLASTN	378	1e-10	64	Human fragile site locus (FRA16B) minisatellite repeat
15433	GM_M04_A2_G03_MR	g18559	BLASTN	433	1e-12	75	G.max gene for catalase
15434	GM_M04_A2_G06_MF	g1669374	BLASTN	362	3e-09	67	Human PAC clone 2G3A from 13q12-13q13, complete sequence [Homo sapiens]
15435	GM_M04_A2_G08_MF	g18559	BLASTN	368	1e-09	68	G.max gene for catalase
15436	GM_M04_A2_G10_MF	g3176795	BLASTN	421	1e-12	62	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
15437	GM_M04_A2_G11_MF	g2995405	BLASTX	338	8e-29	46	(Y12432) polyprotein [Ananas comosus]
15438	GM_M04_A2_G12_MR	g4063760	BLASTX	377	1e-32	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15439	GM_M04_A2_H02_MF	g629693	BLASTX	149	3e-09	30	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15440	GM_M04_A2_H03_MR	g3043726	BLASTX	193	3e-13	35	(AB011173) KIAA0601 protein [Homo sapiens]
15441	GM_M04_A2_H05_MF	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15442	GM_M04_A2_H05_MR	g507910	BLASTN	445	2e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15443	GM_M04_B1_A01_MR	g2522227	BLASTX	189	4e-14	49	(AB007466) retrotransposon-like gene, the first amino acid was determined to be glycine [Vicia faba]
15444	GM_M04_B1_A03_MR	g3273118	BLASTN	361	3e-09	59	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence [Plasmodium falciparum]
15445	GM_M04_B1_A04_MF	g4063760	BLASTX	211	5e-15	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15446	GM_M04_B1_A08_MR	g13536	BLASTN	347	7e-09	63	Yeast (S. cerevisiae) mitochondrial genes for several tRNAs (Thr(2), Cys(2) and His). >gi 343930 gb K00537 YSCMTTGO1 Yeast (S.cerevisiae) mitochondrial cap-oxi1 region: Thr-2, Cys-2 and His-tRNA genes.
15447	GM_M04_B1_B01_MR	g18559	BLASTN	916	2e-34	71	G.max gene for catalase
15448	GM_M04_B1_B04_MF	g629693	BLASTX	263	6e-22	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15449	GM_M04_B1_B05_MF	g730526	BLASTX	190	4e-31	80	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana gi 404166 (X75162) BBC1 protein [Arabidopsis thaliana]
15450	GM_M04_B1_B08_MR	g18559	BLASTN	1013	6e-39	76	G.max gene for catalase
15451	GM_M04_B1_B10_MR	g4159707	BLASTN	683	8e-24	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15452	GM_M04_B1_B12_MR	g1076387	BLASTX	332	3e-42	83	protein kinase homolog - Arabidopsis thaliana gi 717180 (X79279) protein kinase homologous to shaggy and glycogen synthase kinase-3 [Arabidopsis thaliana]
15453	GM_M04_B1_C01_MF	g99922	BLASTX	520	3e-49	67	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15454	GM_M04_B1_C01_MR	g99730	BLASTX	443	2e-43	57	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
15455	GM_M04_B1_C04_MF	g3777527	BLASTX	298	4e-24	48	(AF053008) gag-pol polyprotein [Glycine max]
15456	GM_M04_B1_C05_MR	g4063756	BLASTN	566	2e-18	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15457	GM_M04_B1_C08_MF	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15458	GM_M04_B1_C08_MR	g507910	BLASTN	522	6e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15459	GM_M04_B1_C11_MR	g3341679	BLASTX	298	7e-25	68	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]
15460	GM_M04_B1_C12_MR	g421954	BLASTX	220	2e-20	41	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
15461	GM_M04_B1_D07_MF	g507910	BLASTN	394	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15462	GM_M04_B1_D07_MR	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15463	GM_M04_B1_D10_MR	g4063756	BLASTN	515	3e-16	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15464	GM_M04_B1_E03_MF	g507910	BLASTN	532	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15465	GM_M04_B1_E03_MR	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15466	GM_M04_B1_E05_MF	g3142379	BLASTX	284	5e-24	83	(AF053008) envelope-like [Glycine max]
15467	GM_M04_B1_F05_MR	g3522932	BLASTN	655	1e-22	65	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
15468	GM_M04_B1_G02_MR	g507910	BLASTN	579	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15469	GM_M04_B1_G06_MF	g550452	BLASTX	177	1e-17	79	(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]
15470	GM_M04_B1_G07_MF	g4063760	BLASTX	207	1e-15	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15471	GM_M04_B1_G08_MF	g3810596	BLASTX	193	3e-13	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
15472	GM_M04_B1_G10_MR	g3097320	BLASTN	678	1e-23	70	Glycine max gene for Bd 30K, complete cds
15473	GM_M04_B1_H02_MF	g4063760	BLASTX	285	6e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15474	GM_M04_B1_H02_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15475	GM_M04_B1_H04_MR	g3142328	BLASTN	598	4e-20	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15476	GM_M04_B1_H05_MF	g1905780	BLASTN	373	6e-10	61	D.discoideum genes enocoding cytochrome C oxidase, subunits VIIe & VIIs
15477	GM_M04_B1_H08_MF	g3777527	BLASTX	246	1e-18	46	(AF053008) gag-pol polyprotein [Glycine max]
15478	GM_M04_B1_H09_MF	g550452	BLASTX	331	1e-51	98	(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]
15479	GM_M04_B1_H10_MF	g4063760	BLASTX	172	6e-12	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15480	GM_M04_B1_H12_MR	g3142328	BLASTN	722	5e-34	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15481	GM_M04_B2_A07_MF	g4063760	BLASTX	247	7e-19	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15482	GM_M04_B2_A07_MR	g507910	BLASTN	341	8e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15483	GM_M04_B2_B03_MF	g507910	BLASTN	670	1e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15484	GM_M04_B2_B03_MR	g507910	BLASTN	649	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15485	GM_M04_B2_B04_MF	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15486	GM_M04_B2_B05_MR	g4063760	BLASTX	372	3e-32	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15487	GM_M04_B2_B06_MF	g2462744	BLASTX	135	6e-09	32	(AC002292) Hypothetical protein [Arabidopsis thaliana]
15488	GM_M04_B2_B08_MF	g498931	BLASTX	103	1e-10	44	(Z12825) ORF167, homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
15489	GM_M04_B2_B09_MR	g4063760	BLASTX	358	1e-30	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15490	GM_M04_B2_B10_MR	g3142328	BLASTN	943	9e-36	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15491	GM_M04_B2_C03_MR	g3402749	BLASTX	252	3e-21	45	(AL031187) putative protein [Arabidopsis thaliana]
15492	GM_M04_B2_C04_MR	g1335862	BLASTX	313	1e-25	81	(U42608) clathrin heavy chain [Glycine max]
15493	GM_M04_B2_C05_MR	g3241921	BLASTN	457	1e-13	80	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCM23, complete sequence [Arabidopsis thaliana]
15494	GM_M04_B2_C10_MR	g507910	BLASTN	556	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15495	GM_M04_B2_C11_MF	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15496	GM_M04_B2_C11_MR	g4063760	BLASTX	225	2e-16	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15497	GM_M04_B2_D01_MF	g905361	BLASTX	644	2e-62	96	(U22103) gag-protease polyprotein [Glycine max]
15498	GM_M04_B2_D01_MR	g4063760	BLASTX	518	8e-48	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15499	GM_M04_B2_D07_MR	g905361	BLASTX	204	1e-14	35	(U22103) gag-protease polyprotein [Glycine max]
15500	GM_M04_B2_D12_MF	g2462134	BLASTX	147	9e-09	32	(Y13368) reverse transcriptase [Beta vulgaris]
15501	GM_M04_B2_D12_MR	g3522943	BLASTX	183	8e-13	57	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15502	GM_M04_B2_E03_MR	g2244747	BLASTN	372	9e-10	70	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 0
15503	GM_M04_B2_E04_MR	g4063760	BLASTX	424	9e-38	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15504	GM_M04_B2_E08_MF	g1769897	BLASTX	294	1e-28	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15505	GM_M04_B2_E08_MR	g4063760	BLASTX	214	2e-15	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15506	GM_M04_B2_E09_MF	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15507	GM_M04_B2_F12_MR	g3687234	BLASTX	165	3e-10	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15508	GM_M04_B2_G01_MF	g1755162	BLASTX	239	2e-19	72	(U75192) germin-like protein [Arabidopsis thaliana]
15509	GM_M04_B2_G03_MF	g507910	BLASTN	521	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15510	GM_M04_B2_G03_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15511	GM_M04_B2_G04_MF	g507910	BLASTN	352	3e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
15512	GM_M04_B2_G05_MR	g3928116	BLASTN	426	3e-12	65	, complete sequence [Homo sapiens]
15513	GM_M04_B2_G06_MR	g3337395	BLASTN	416	9e-12	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
15514	GM_M04_B2_G08_MF	g4092470	BLASTN	369	1e-09	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
15515	GM_M04_B2_G11_MF	g4056503	BLASTX	148	8e-10	77	(AC005896) unknown protein [Arabidopsis thaliana]
15516	GM_M04_B2_H03_MR	g170029	BLASTN	389	1e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
15517	GM_M04_B2_H04_MR	g1769898	BLASTX	158	8e-10	30	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15518	GM_M04_B2_H05_MF	g4063760	BLASTX	384	2e-33	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15519	GM_M04_B2_H05_MR	g507910	BLASTN	514	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15520	GM_M04_B2_H12_MR	g3510505	BLASTX	166	3e-10	45	(AF030881) pol polyprotein [Fugu rubripes]
15521	GM_M05_A1_A02_MR	g3142379	BLASTX	338	6e-30	68	(AF053008) envelope-like [Glycine max]
15522	GM_M05_A1_A05_MR	g3319366	BLASTX	160	6e-11	46	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
15523	GM_M05_A1_B05_MR	g9825	BLASTN	391	1e-10	68	Plasmodium falciparum 11-1 gene part 1
15524	GM_M05_A1_B08_MR	g507910	BLASTN	340	9e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15525	GM_M05_A1_B09_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15526	GM_M05_A1_D03_MR	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15527	GM_M05_A1_D06_MR	g3142379	BLASTX	217	2e-20	87	(AF053008) envelope-like [Glycine max]
15528	GM_M05_A1_D10_MR	g1272410	BLASTX	197	5e-15	97	(U52045) immunophilin precursor [Vicia faba]
15529	GM_M05_A1_G03_MR	g3152613	BLASTX	114	6e-13	36	(AC004482) hypothetical protein [Arabidopsis thaliana]
15530	GM_M05_A1_H03_MR	g3834390	BLASTX	117	9e-16	48	(AF039029) snurportin1 [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15531	GM_M05_A1_H04_MR	g462013	BLASTX	192	4e-25	88	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) gi 542022 pir S39558 HSP90 homolog - Madagascar periwinkle gi 348696 (L14594) heat shock protein 90 [Catharanthus roseus]
15532	GM_M05_B1_A07_MR	g4063760	BLASTX	172	7e-11	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15533	GM_M05_B1_A11_MR	g3641780	BLASTN	358	4e-09	61	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
15534	GM_M05_B1_A12_MR	g1142701	BLASTN	1388	2e-56	87	Glycine max satellite STR120-A.3.
15535	GM_M05_B1_D02_MR	g1589778	BLASTX	165	2e-15	76	(U62135) SPINDLY [Arabidopsis thaliana]
15536	GM_M05_B1_D04_MR	g4063760	BLASTX	145	3e-10	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15537	GM_M05_B1_D06_MR	g507910	BLASTN	419	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15538	GM_M05_B1_D11_MR	g99922	BLASTX	466	2e-43	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15539	GM_M05_B1_E08_MR	g18559	BLASTN	672	2e-23	74	G.max gene for catalase
15540	GM_M05_B1_G09_MR	g968986	BLASTN	439	6e-13	84	Glycine max ferritin gene, nuclear gene encoding chloroplast protein, complete cds
15541	GM_M05_B1_G10_MR	g4063760	BLASTX	246	8e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15542	GM_M05_B1_G12_MR	g1399304	BLASTN	394	6e-11	71	Glycine max phosphoinositide-specific phospholipase C P13 mRNA, complete cds.
15543	GM_M05_B1_H01_MR	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15544	GM_M05_B1_H03_MR	g3097320	BLASTN	369	1e-09	68	Glycine max gene for Bd 30K, complete cds
15545	GM_M05_B1_H06_MR	g178823	BLASTN	338	4e-09	62	Human apolipoprotein B gene hypervariable region, 3' flank.
15546	GM_M05_B2_A12_MF	g3805853	BLASTX	173	3e-11	60	(AL031986) putative protein [Arabidopsis thaliana]
15547	GM_M05_B2_B05_MF	g100484	BLASTX	374	6e-33	61	hypothetical protein - garden snapdragon
15548	GM_M05_B2_D02_MF	g2995405	BLASTX	408	2e-36	57	(Y12432) polyprotein [Ananas comosus]
15549	GM_M05_B2_D04_MF	g3142328	BLASTN	1530	2e-62	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15550	GM_M05_B2_D05_MF	g3777527	BLASTX	644	5e-61	92	(AF053008) gag-pol polyprotein [Glycine max]
15551	GM_M05_B2_E03_MF	g2541876	BLASTX	214	5e-16	36	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
15552	GM_M05_B2_E04_MF	g507910	BLASTN	388	6e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15553	GM_M05_B2_F05_MF	g2129618	BLASTX	233	1e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15554	GM_M05_B2_F10_MF	g3142379	BLASTX	140	2e-14	52	(AF053008) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15555	GM_M05_B2_F12_MF	g2497820	BLASTX	181	1e-24	81	DNA REPLICATION LICENSING FACTOR MCM3 HOMOLOG (REPLICATION ORIGIN ACTIVATOR) (ROA PROTEIN) gi 1076823 pir S52247 probable replication origin activator protein ROA - maize (fragment) gi 609290 (Z29368) ROA protein [Zea mays]
15556	GM_M05_B2_G07_MF	g1170507	BLASTX	109	4e-11	67	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) gi 100276 pir S22579 translation initiation factor eIF-4A - curled-leaved tobacco gi 19699 (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]
15557	GM_M05_B2_G09_MF	g14293	BLASTN	374	9e-11	69	Yeast R0 54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
15558	GM_M05_B2_G12_MF	g3777527	BLASTX	650	1e-61	94	(AF053008) gag-pol polyprotein [Glycine max]
15559	GM_M05_B2_H11_MF	g4063760	BLASTX	221	3e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15560	GM_M06_A1_A08_MR	g13597	BLASTN	293	1e-09	69	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile
15561	GM_M06_A1_A11_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15562	GM_M06_A1_A12_MR	g4160362	BLASTN	378	5e-10	61	Saccharomyces cerevisiae complete mitochondrial genome
15563	GM_M06_A1_B11_MR	g3643085	BLASTX	465	2e-43	66	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]
15564	GM_M06_A1_C08_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15565	GM_M06_A1_C10_MR	g3402755	BLASTX	307	2e-26	51	(AL031187) putative transposable element [Arabidopsis thaliana]
15566	GM_M06_A1_C11_MR	g3777527	BLASTX	659	2e-65	94	(AF053008) gag-pol polyprotein [Glycine max]
15567	GM_M06_A1_D06_MR	g226407	BLASTX	119	4e-11	38	retrotransposon del1-46 [Lilium henryi]
15568	GM_M06_A1_D07_MR	g1769898	BLASTX	303	2e-32	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15569	GM_M06_A1_E01_MR	g2132242	BLASTX	272	1e-22	49	hypothetical protein YPL235w - yeast (Saccharomyces cerevisiae) gi 1061254 (Z67751) putative protein [Saccharomyces cerevisiae] gi 1181253 (X94561) ATP/GTP binding site motif A (P-loop) [Saccharomyces cerevisiae] gi 1370486 gnl PID e246945 (Z73591) ORF YPL235w [Saccharomyces cerevisiae]
15570	GM_M06_A1_E04_MR	g2522228	BLASTX	339	2e-38	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
15571	GM_M06_A1_E12_MR	g3309583	BLASTX	164	4e-19	96	(AF073830) fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]
15572	GM_M06_A1_G07_MR	g2129618	BLASTX	160	1e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
15573	GM_M06_A1_H01_MR	g4102181	BLASTN	388	2e-10	63	Mus musculus phosphoenolpyruvate carboxykinase (PEPCK) gene, complete cds
15574	GM_M06_A1_H04_MR	g507910	BLASTN	464	2e-14	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15575	GM_M06_A1_H06_MR	g507910	BLASTN	415	4e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15576	GM_M06_A1_H10_MR	g2129618	BLASTX	157	2e-09	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15577	GM_M06_A2_A05_MR	g629693	BLASTX	152	2e-09	31	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15578	GM_M06_A2_A07_MR	g507910	BLASTN	543	6e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15579	GM_M06_A2_A09_MF	g2764526	BLASTN	443	5e-13	67	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
15580	GM_M06_A2_B11_MF	g18768	BLASTN	351	2e-09	70	Soybean Tgm6 transposable element 3' end
15581	GM_M06_A2_C02_MR	g3452140	BLASTX	357	6e-32	82	(AJ004901) resistance protein [Glycine max]
15582	GM_M06_A2_C04_MF	g2979597	BLASTN	453	2e-13	67	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
15583	GM_M06_A2_C09_MR	g4063760	BLASTX	116	2e-13	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15584	GM_M06_A2_D09_MR	g507910	BLASTN	380	1e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
15585	GM_M06_A2_D10_MR	g905361	BLASTX	174	2e-11	28	(U22103) gag-protease polyprotein [Glycine max]
15586	GM_M06_A2_E01_MF	g2245021	BLASTX	144	7e-11	74	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]
15587	GM_M06_A2_E04_MF	g3142328	BLASTN	685	3e-29	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15588	GM_M06_A2_E04_MR	g3492803	BLASTX	164	4e-11	48	(AJ002479) ENBP1 [Medicago truncatula]
15589	GM_M06_A2_F04_MR	g4063760	BLASTX	427	4e-38	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15590	GM_M06_A2_F06_MR	g3142328	BLASTN	944	8e-36	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15591	GM_M06_A2_F08_MF	g18559	BLASTN	552	5e-18	72	G.max gene for catalase
15592	GM_M06_A2_H01_MR	g1480927	BLASTN	461	6e-14	78	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
15593	GM_M06_A2_H11_MR	g2129618	BLASTX	151	1e-14	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15594	GM_M06_B1_A02_MF	g3033389	BLASTX	177	1e-11	38	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15595	GM_M06_B1_A05_MF	g166884	BLASTN	609	3e-21	77	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
15596	GM_M06_B1_A08_MF	g3142328	BLASTN	1101	6e-43	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15597	GM_M06_B1_A11_MR	g1167523	BLASTX	300	2e-24	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
15598	GM_M06_B1_A12_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15599	GM_M06_B1_A12_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15600	GM_M06_B1_B10_MF	g507910	BLASTN	391	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15601	GM_M06_B1_B10_MR	g507910	BLASTN	350	3e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15602	GM_M06_B1_B11_MF	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15603	GM_M06_B1_B11_MR	g507910	BLASTN	394	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15604	GM_M06_B1_B12_MR	g1666236	BLASTX	169	1e-11	35	(U76261) unknown [Hordeum vulgare]
15605	GM_M06_B1_C06_MF	g1167523	BLASTX	172	8e-11	41	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
15606	GM_M06_B1_C09_MF	g3377856	BLASTX	283	9e-23	50	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
15607	GM_M06_B1_D04_MF	g1769898	BLASTX	130	4e-15	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15608	GM_M06_B1_D09_MF	g99922	BLASTX	285	2e-24	92	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15609	GM_M06_B1_D10_MR	g3869075	BLASTN	400	5e-11	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
15610	GM_M06_B1_E02_MF	g2764526	BLASTN	393	1e-10	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
15611	GM_M06_B1_E07_MF	g2351060	BLASTX	488	7e-46	70	(AB006660) sucrose-phosphate synthase [Citrus unshiu]
15612	GM_M06_B1_E09_MF	g2979562	BLASTX	351	6e-31	54	(AC003680) unknown protein [Arabidopsis thaliana] gi 3386623 (AC004665) unknown protein [Arabidopsis thaliana]
15613	GM_M06_B1_E10_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15614	GM_M06_B1_E11_MR	g4063760	BLASTX	205	2e-14	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15615	GM_M06_B1_F01_MF	g2995179	BLASTN	362	3e-09	63	Homo sapiens DNA sequence from PAC 262D12 on chromosome q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIK...
15616	GM_M06_B1_F06_MR	g3645899	BLASTX	245	1e-23	50	(U68408) 5' end not determined experimentally [Zea mays]
15617	GM_M06_B1_F12_MR	g4160362	BLASTN	443	6e-13	63	Saccharomyces cerevisiae complete mitochondrial genome
15618	GM_M06_B1_G12_MR	g4063760	BLASTX	497	1e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15619	GM_M06_B1_H02_MF	g1769897	BLASTX	295	9e-25	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15620	GM_M06_B1_H06_MF	g3650026	BLASTN	425	4e-12	63	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15621	GM_M06_B1_H07_MF	g3176803	BLASTN	333	6e-09	59	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite sequence
15622	GM_M06_B1_H08_MF	g905361	BLASTX	698	4e-68	93	(U22103) gag-protease polyprotein [Glycine max]
15623	GM_M06_B1_H08_MR	g3142328	BLASTN	619	5e-21	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15624	GM_M06_B1_H11_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15625	GM_M06_B1_H11_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15626	GM_M06_B2_A10_MR	g18559	BLASTN	548	8e-18	74	G.max gene for catalase
15627	GM_M06_B2_A12_MR	g3687234	BLASTX	153	3e-14	60	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15628	GM_M06_B2_B08_MR	g4063760	BLASTX	230	4e-17	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15629	GM_M06_B2_B12_MR	g728905	BLASTX	199	1e-13	42	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
15630	GM_M06_B2_C04_MF	g3142328	BLASTN	655	1e-22	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15631	GM_M06_B2_C10_MF	g3142328	BLASTN	748	7e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15632	GM_M06_B2_D09_MR	g507910	BLASTN	372	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15633	GM_M06_B2_D12_MF	g3777527	BLASTX	528	1e-48	93	(AF053008) gag-pol polyprotein [Glycine max]
15634	GM_M06_B2_E10_MR	g3097320	BLASTN	683	7e-24	75	Glycine max gene for Bd 30K, complete cds
15635	GM_M06_B2_F08_MR	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15636	GM_M06_B2_F09_MF	g2342690	BLASTX	127	2e-16	58	(AC000106) Similar to Homo copine I (gb U83246). [Arabidopsis thaliana]
15637	GM_M06_B2_G01_MF	g3608154	BLASTX	167	4e-12	47	(AC005314) unknown protein [Arabidopsis thaliana]
15638	GM_M06_B2_G07_MF	g2995405	BLASTX	215	2e-26	49	(Y12432) polyprotein [Ananas comosus]
15639	GM_M06_B2_G12_MR	g507910	BLASTN	686	2e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15640	GM_M06_B2_H05_MF	g3097320	BLASTN	836	8e-31	74	Glycine max gene for Bd 30K, complete cds
15641	GM_M06_B2_H08_MF	g3097320	BLASTN	372	8e-10	71	Glycine max gene for Bd 30K, complete cds
15642	GM_M07_A1_A03_MR	g4063760	BLASTX	419	3e-37	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15643	GM_M07_A1_A04_MF	g3142328	BLASTN	554	4e-18	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15644	GM_M07_A1_A05_MR	g2501565	BLASTX	104	3e-09	43	HYPOTHETICAL 40.2 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION gi 1078518 pir S55087 hypothetical protein YMR101c - yeast (Saccharomyces cerevisiae) gi 854438 (Z49807) unknown [Saccharomyces cerevisiae]
15645	GM_M07_A1_A07_MF	g169934	BLASTN	665	8e-24	80	G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds.
15646	GM_M07_A1_A07_MR	g2887437	BLASTX	128	2e-13	88	(AB007893) KIAA0433 [Homo sapiens]
15647	GM_M07_A1_A08_MR	g3513747	BLASTX	265	1e-20	47	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15648	GM_M07_A1_A12_MR	g3097320	BLASTN	402	4e-11	68	Glycine max gene for Bd 30K, complete cds
15649	GM_M07_A1_B08_MR	g3928097	BLASTX	243	7e-20	73	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]
15650	GM_M07_A1_C02_MF	g4063760	BLASTX	225	1e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15651	GM_M07_A1_C02_MR	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15652	GM_M07_A1_C07_MF	g2462753	BLASTX	137	2e-09	67	(AC002292) putative polygalacturonase [Arabidopsis thaliana]
15653	GM_M07_A1_C09_MR	g728905	BLASTX	181	8e-12	44	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
15654	GM_M07_A1_C10_MF	g507910	BLASTN	461	3e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15655	GM_M07_A1_D02_MR	g3645899	BLASTX	222	6e-22	52	(U68408) 5' end not determined experimentally [Zea mays]
15656	GM_M07_A1_D03_MR	g3097320	BLASTN	785	2e-28	78	Glycine max gene for Bd 30K, complete cds
15657	GM_M07_A1_D10_MR	g2129618	BLASTX	170	8e-11	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15658	GM_M07_A1_E01_MF	g20854	BLASTN	400	3e-11	68	Pea rbcS-3A gene for ribulose 1.5-bisphosphate carboxylase (RBC) small subunit
15659	GM_M07_A1_F08_MR	g18559	BLASTN	365	2e-09	75	G.max gene for catalase
15660	GM_M07_A1_F12_MF	g2104945	BLASTN	651	2e-22	69	Glycine max copia-like retrotransposon Tgmr, complete sequence
15661	GM_M07_A1_G05_MF	g3193221	BLASTN	358	3e-09	77	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
15662	GM_M07_A1_G08_MR	g3426334	BLASTN	491	3e-15	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
15663	GM_M07_A1_G09_MF	g2522228	BLASTX	187	5e-16	44	(AB007466) reverse transcriptase-like protein [Vicia faba]
15664	GM_M07_A1_G12_MF	g4063760	BLASTX	195	3e-13	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15665	GM_M07_A1_H01_MR	g4006828	BLASTX	182	4e-12	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
15666	GM_M07_A1_H02_MF	g2583128	BLASTX	367	5e-33	74	(AC002387) hypothetical protein [Arabidopsis thaliana]
15667	GM_M07_A1_H03_MF	g3930515	BLASTX	121	1e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
15668	GM_M07_A1_H09_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15669	GM_M07_A2_A07_MF	g729092	BLASTX	349	2e-30	64	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
15670	GM_M07_A2_A09_MF	g100484	BLASTX	335	1e-28	58	hypothetical protein - garden snapdragon
15671	GM_M07_A2_B05_MR	g2129618	BLASTX	204	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15672	GM_M07_A2_B10_MF	g422028	BLASTX	268	2e-22	73	transcription factor OBF3.1, ocs element-binding - maize gi 297020 (X69153) ocs-element binding factor 3.1 [Zea mays]
15673	GM_M07_A2_B12_MR	g1769899	BLASTX	261	8e-22	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15674	GM_M07_A2_C03_MR	g3142330	BLASTX	311	3e-32	89	(U96295) envelope-like [Glycine max]
15675	GM_M07_A2_C04_MR	g3738114	BLASTN	377	5e-10	62	Homo sapiens chromosome Y, clone 264,M.20, complete sequence [Homo sapiens]
15676	GM_M07_A2_C11_MR	g2462749	BLASTX	184	1e-12	66	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
15677	GM_M07_A2_D02_MR	g421955	BLASTX	148	2e-26	60	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15678	GM_M07_A2_D08_MF	g18559	BLASTN	477	1e-14	69	G.max gene for catalase
15679	GM_M07_A2_D10_MF	g2462834	BLASTX	178	5e-13	44	(AF000657) hypothetical protein [Arabidopsis thaliana]
15680	GM_M07_A2_D12_MF	g2924781	BLASTX	144	3e-19	47	(AC002334) putative cellulose synthase [Arabidopsis thaliana]
15681	GM_M07_A2_E02_MR	g4038056	BLASTX	194	2e-13	38	(AC005897) putative transposon [Arabidopsis thaliana]
15682	GM_M07_A2_F04_MR	g2326372	BLASTX	167	2e-21	82	(Y14404) putative arabinose kinase [Arabidopsis thaliana]
15683	GM_M07_A2_F06_MR	g4063760	BLASTX	309	2e-25	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15684	GM_M07_A2_H03_MR	g18559	BLASTN	323	4e-11	70	G.max gene for catalase
15685	GM_M07_A2_H04_MR	g3033389	BLASTX	123	1e-10	43	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15686	GM_M07_A2_H08_MR	g2522230	BLASTX	257	2e-21	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15687	GM_M07_B1_A01_MF	g340797	BLASTN	339	4e-09	70	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
15688	GM_M07_B1_B10_MF	g1769898	BLASTX	159	7e-10	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15689	GM_M07_B1_C06_MR	g4063760	BLASTX	405	1e-35	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15690	GM_M07_B1_C07_MR	g3845197	BLASTN	408	2e-11	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
15691	GM_M07_B1_C08_MF	g1165321	BLASTN	672	2e-23	80	Glycine max extensin (SbHRGP3) gene, complete cds
15692	GM_M07_B1_C08_MR	g3142328	BLASTN	1068	2e-41	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15693	GM_M07_B1_C09_MR	g4140712	BLASTX	118	9e-09	34	(AF110183) putative integrase [Oryza sativa]
15694	GM_M07_B1_D06_MR	g507910	BLASTN	627	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
15695	GM_M07_B1_D07_MR	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15696	GM_M07_B1_E02_MF	g3928086	BLASTX	204	1e-15	54	(AC005770) unknown protein [Arabidopsis thaliana]
15697	GM_M07_B1_E06_MR	g3142328	BLASTN	433	1e-12	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15698	GM_M07_B1_F08_MF	g1040717	BLASTN	336	4e-09	65	D.polychroa microsatellite sequence (clone Dp ch1 F3)
15699	GM_M07_B1_G07_MF	g3091216	BLASTX	103	3e-18	58	(AF060192) putative resistance protein [Glycine max]
15700	GM_M07_B1_G09_MF	g100484	BLASTX	339	4e-29	57	hypothetical protein - garden snapdragon
15701	GM_M07_B1_G10_MR	g2921317	BLASTX	246	8e-37	83	(AF034108) beta-1,3-glucanase 3 [Glycine max]
15702	GM_M07_B1_G11_MR	g2864613	BLASTX	143	7e-11	55	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana]
15703	GM_M07_B1_G12_MF	g3142328	BLASTN	791	7e-29	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15704	GM_M07_B1_H05_MF	g507910	BLASTN	342	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15705	GM_M07_B1_H05_MR	g507910	BLASTN	412	5e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence
15706	GM_M07_B1_H07_MF	g905360	BLASTN	381	3e-10	83	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
15707	GM_M07_B1_H07_MR	g507910	BLASTN	365	7e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15708	GM_M09_B1_A07_MF	g3282159	BLASTN	352	7e-09	63	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]
15709	GM_M09_B1_A09_MF	g3021268	BLASTX	169	1e-24	44	(AL022347) putative protein [Arabidopsis thaliana]
15710	GM_M09_B1_A11_MF	g3097320	BLASTN	755	4e-27	70	Glycine max gene for Bd 30K, complete cds
15711	GM_M09_B1_B06_MR	g4063760	BLASTX	344	3e-29	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15712	GM_M09_B1_B08_MF	g3097320	BLASTN	452	2e-13	78	Glycine max gene for Bd 30K, complete cds
15713	GM_M09_B1_B08_MR	g3947735	BLASTX	207	7e-15	37	(AJ009720) NL27 [Solanum tuberosum]
15714	GM_M09_B1_B09_MF	g4063756	BLASTN	481	1e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15715	GM_M09_B1_C02_MR	g1666236	BLASTX	196	1e-14	32	(U76261) unknown [Hordeum vulgare]
15716	GM_M09_B1_C03_MR	g155854	BLASTN	347	6e-09	58	Babesia bigemina antigen (Bbg 1.1) mRNA, 3' end.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15717	GM_M09_B1_C11_MR	g3142328	BLASTN	678	1e-23	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15718	GM_M09_B1_D01_MR	g3834313	BLASTX	316	9e-34	69	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
15719	GM_M09_B1_D04_MF	g2894600	BLASTX	358	9e-31	59	(AL021889) putative protein [Arabidopsis thaliana]
15720	GM_M09_B1_D09_MF	g2522228	BLASTX	152	2e-09	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
15721	GM_M09_B1_D10_MF	g2464905	BLASTX	228	3e-18	59	(Z99708) minor allergen [Arabidopsis thaliana]
15722	GM_M09_B1_D11_MF	g2811226	BLASTX	238	3e-18	86	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
15723	GM_M09_B1_E01_MR	g3080353	BLASTX	165	3e-11	66	(AL022580) cytochrome P450 [Arabidopsis thaliana]
15724	GM_M09_B1_E06_MR	g18559	BLASTN	1621	1e-66	91	G.max gene for catalase
15725	GM_M09_B1_E10_MF	g22102	BLASTN	442	5e-13	63	Zea mays A1 gene for 40.1kd A1 protein (NADPH-dependent reductase).
15726	GM_M09_B1_F01_MF	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15727	GM_M09_B1_F01_MR	g507910	BLASTN	635	4e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15728	GM_M09_B1_F07_MR	g3176804	BLASTN	334	6e-09	61	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite, 3' sequence
15729	GM_M09_B1_F09_MF	g130582	BLASTX	319	2e-26	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
15730	GM_M09_B1_G02_MF	g507910	BLASTN	449	1e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence
15731	GM_M09_B1_G02_MR	g507910	BLASTN	412	5e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
15732	GM_M09_B1_G03_MR	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15733	GM_M09_B1_G05_MF	g3097320	BLASTN	671	2e-23	84	Glycine max gene for Bd 30K, complete cds
15734	GM_M09_B1_G05_MR	g100484	BLASTX	251	1e-19	50	hypothetical protein - garden snapdragon
15735	GM_M09_B1_G07_MR	g2995405	BLASTX	293	4e-24	58	(Y12432) polyprotein [Ananas comosus]
15736	GM_M09_B1_G08_MF	g1707644	BLASTX	179	2e-12	37	(X99514) mexE [Pseudomonas aeruginosa]
15737	GM_M09_B1_G09_MR	g2982257	BLASTX	144	8e-12	77	(AF051211) probable calcium dependent protein kinase [Picea mariana]
15738	GM_M09_B1_G11_MF	g3738114	BLASTN	373	8e-10	64	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
15739	GM_M09_B1_H01_MR	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15740	GM_M09_B1_H08_MR	g3135274	BLASTX	218	2e-16	56	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]
15741	GM_M09_B1_H11_MF	g18559	BLASTN	658	8e-23	70	G.max gene for catalase
15742	GM_M10_A1_A09_MR	g3645899	BLASTX	216	1e-15	52	(U68408) 5' end not determined experimentally [Zea mays]
15743	GM_M10_A1_B05_MR	g3777526	BLASTN	552	6e-18	86	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
15744	GM_M10_A1_B09_MR	g4063760	BLASTX	179	5e-13	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15745	GM_M10_A1_C09_MR	g507910	BLASTN	566	6e-19	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15746	GM_M10_A1_C10_MR	g3785999	BLASTX	175	5e-15	84	(AC005499) putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]
15747	GM_M10_A1_D03_MR	g1076763	BLASTX	153	1e-11	44	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
15748	GM_M10_A1_D07_MR	g3142328	BLASTN	499	1e-15	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15749	GM_M10_A1_D08_MR	g3033389	BLASTX	147	5e-15	39	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15750	GM_M10_A1_F03_MR	g2129618	BLASTX	193	3e-13	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15751	GM_M10_A1_F06_MR	g4063756	BLASTN	350	9e-09	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15752	GM_M10_A1_G01_MR	g3097320	BLASTN	1281	5e-51	81	Glycine max gene for Bd 30K, complete cds
15753	GM_M10_A1_G04_MR	g4092471	BLASTN	401	4e-11	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
15754	GM_M10_A2_A02_MF	g226407	BLASTX	246	1e-18	64	retrotransposon del1-46 [Lilium henryi]
15755	GM_M10_A2_B03_MF	g2408029	BLASTX	187	9e-13	66	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
15756	GM_M10_A2_B05_MF	g3283026	BLASTX	164	9e-12	39	putative transposase [Arabidopsis thaliana]
15757	GM_M10_A2_B09_MF	g3834317	BLASTX	331	6e-29	91	(AC005679) Similar to CDC16 protein gb U18291 (CDC16Hs) from Homo sapiens. [Arabidopsis thaliana]
15758	GM_M10_A2_C09_MF	g507910	BLASTN	603	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15759	GM_M10_A2_E01_MF	g3930515	BLASTX	122	2e-13	47	(AF059674) putative gag protein [Nicotiana tabacum]
15760	GM_M10_A2_E02_MF	g507910	BLASTN	540	8e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15761	GM_M10_A2_E09_MF	g4092471	BLASTN	457	1e-13	71	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
15762	GM_M10_A2_F01_MF	g1666236	BLASTX	148	3e-09	31	(U76261) unknown [Hordeum vulgare]
15763	GM_M10_A2_F04_MF	g1272349	BLASTX	247	1e-19	50	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
15764	GM_M10_A2_F05_MF	g3097320	BLASTN	520	2e-16	77	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
15765	GM_M10_A2_F07_MF	g3687234	BLASTX	170	1e-10	42	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15766	GM_M10_A2_F10_MF	g4063760	BLASTX	432	1e-38	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15767	GM_M10_A2_G01_MF	g3097320	BLASTN	460	8e-14	71	Glycine max gene for Bd 30K, complete cds
15768	GM_M10_A2_H02_MF	g730526	BLASTX	242	6e-36	90	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana gi 404166 (X75162) BBC1 protein [Arabidopsis thaliana]
15769	GM_M10_A2_H05_MF	g1769898	BLASTX	213	1e-15	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15770	GM_M10_A2_H08_MF	g2865427	BLASTX	170	1e-10	38	(AF039372) polyprotein [Arabidopsis thaliana]
15771	GM_M10_A2_H12_MF	g2522227	BLASTX	222	1e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15772	GM_M10_B1_A06_MF	g2764526	BLASTN	355	5e-09	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
15773	GM_M10_B1_A07_MF	g3097320	BLASTN	601	9e-22	76	Glycine max gene for Bd 30K, complete cds
15774	GM_M10_B1_B01_MF	g3645899	BLASTX	369	5e-32	51	(U68408) 5' end not determined experimentally [Zea mays]
15775	GM_M10_B1_B03_MF	g99922	BLASTX	316	2e-37	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15776	GM_M10_B1_B05_MF	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15777	GM_M10_B1_B10_MF	g507910	BLASTN	533	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15778	GM_M10_B1_B10_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15779	GM_M10_B1_B11_MF	g2586082	BLASTX	206	2e-25	58	(U72725) retrofit [Oryza longistaminata]
15780	GM_M10_B1_C02_MR	g1666236	BLASTX	128	5e-09	37	(U76261) unknown [Hordeum vulgare]
15781	GM_M10_B1_C11_MR	g2129618	BLASTX	204	2e-14	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15782	GM_M10_B1_D09_MF	g2335061	BLASTN	423	4e-12	60	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
15783	GM_M10_B1_D09_MR	g3510505	BLASTX	172	9e-14	35	(AF030881) pol polyprotein [Fugu rubripes]
15784	GM_M10_B1_D10_MR	g2995405	BLASTX	346	1e-29	50	(Y12432) polyprotein [Ananas comosus]
15785	GM_M10_B1_E01_MF	g3097320	BLASTN	336	1e-15	83	Glycine max gene for Bd 30K, complete cds
15786	GM_M10_B1_E03_MR	g320569	BLASTX	226	4e-18	50	transposon TNT1 - Arabidopsis thaliana (fragment)
15787	GM_M10_B1_E05_MR	g173088	BLASTX	180	1e-11	35	has homology to retroviral pol genes; ORF2 TYB3-2 (5' end of coding region not precisely determined)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15788	GM_M10_B1_E10_MR	g13767	BLASTN	431	2e-13	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
15789	GM_M10_B1_E11_MF	g2129618	BLASTX	200	5e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15790	GM_M10_B1_F01_MF	g3142328	BLASTN	649	2e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15791	GM_M10_B1_F02_MR	g2522227	BLASTX	154	5e-10	39	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15792	GM_M10_B1_F05_MF	g3142328	BLASTN	1772	1e-73	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15793	GM_M10_B1_F05_MR	g507910	BLASTN	647	1e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
15794	GM_M10_B1_F07_MR	g3845287	BLASTN	357	4e-09	60	Plasmodium falciparum chromosome 2, section 57 of 73 of the complete sequence
15795	GM_M10_B1_F11_MF	g2129618	BLASTX	160	9e-10	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15796	GM_M10_B1_F12_MR	g3319372	BLASTX	257	1e-21	42	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
15797	GM_M10_B1_G03_MF	g4063760	BLASTX	360	6e-31	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15798	GM_M10_B1_G06_MF	g3599418	BLASTN	391	1e-10	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15799	GM_M10_B1_H04_MR	g2462058	BLASTX	156	2e-21	38	(Y13389) reverse transcriptase [Antirrhinum majus]
15800	GM_M10_B1_H06_MF	g2801423	BLASTN	474	2e-14	68	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
15801	GM_M10_B1_H11_MR	g905361	BLASTX	739	2e-72	97	(U22103) gag-protease polyprotein [Glycine max]
15802	GM_M10_B1_H12_MF	g4063760	BLASTX	430	2e-38	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15803	GM_M10_B2_A03_MF	g3097320	BLASTN	448	3e-13	72	Glycine max gene for Bd 30K, complete cds
15804	GM_M10_B2_A05_MR	g4063760	BLASTX	232	3e-17	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15805	GM_M10_B2_A06_MF	g4063756	BLASTN	530	7e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15806	GM_M10_B2_A09_MF	g2443320	BLASTX	242	3e-18	42	(D85597) polyprotein [Oryza australiensis]
15807	GM_M10_B2_A09_MR	g1769898	BLASTX	208	3e-15	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15808	GM_M10_B2_B08_MF	g170288	BLASTN	517	2e-16	67	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma1) gene, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15809	GM_M10_B2_B09_MR	g905361	BLASTX	515	1e-48	97	(U22103) gag-protease polyprotein [Glycine max]
15810	GM_M10_B2_C02_MR	g3599418	BLASTN	405	3e-11	65	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15811	GM_M10_B2_C11_MF	g3097320	BLASTN	362	2e-09	80	Glycine max gene for Bd 30K, complete cds
15812	GM_M10_B2_D04_MR	g507910	BLASTN	460	4e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15813	GM_M10_B2_D07_MF	g170606	BLASTN	782	6e-29	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
15814	GM_M10_B2_D08_MR	g128405	BLASTX	258	1e-21	65	NODULIN 21 (N-21) gi 99942 pir S08632 nodulin-21 - soybean gi 18694 (X16488) nodulin-21 (AA 1-201) [Glycine max]
15815	GM_M10_B2_D11_MF	g3695294	BLASTN	430	2e-12	85	Glycine max nodule-specific glutamine synthetase gene, complete cds
15816	GM_M10_B2_E06_MR	g3097320	BLASTN	367	1e-09	69	Glycine max gene for Bd 30K, complete cds
15817	GM_M10_B2_E07_MR	g18559	BLASTN	800	3e-29	76	G.max gene for catalase
15818	GM_M10_B2_E08_MR	g100226	BLASTX	207	5e-15	37	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]
15819	GM_M10_B2_E09_MR	g2522228	BLASTX	189	2e-13	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
15820	GM_M10_B2_E12_MR	g3142328	BLASTN	935	2e-35	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15821	GM_M10_B2_F01_MR	g2109275	BLASTX	158	3e-09	38	(U97106) downy mildew resistance protein RPP5 [Arabidopsis thaliana]
15822	GM_M10_B2_F02_MF	g100484	BLASTX	134	1e-10	37	hypothetical protein - garden snapdragon
15823	GM_M10_B2_F04_MR	g1769898	BLASTX	154	2e-09	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15824	GM_M10_B2_F05_MR	g2497540	BLASTX	241	3e-19	47	PYRUVATE KINASE, CHLOROPLAST ISOZYME G
15825	GM_M10_B2_G01_MR	g3063459	BLASTX	176	2e-11	69	(AC003981) F22O13.21 [Arabidopsis thaliana]
15826	GM_M10_B2_G02_MF	g18559	BLASTN	356	4e-09	73	G.max gene for catalase
15827	GM_M10_B2_G03_MR	g3831448	BLASTN	785	2e-28	76	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]
15828	GM_M10_B2_G06_MF	g2995405	BLASTX	443	4e-40	61	(Y12432) polyprotein [Ananas comosus]
15829	GM_M10_B2_G07_MR	g1769898	BLASTX	312	2e-26	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15830	GM_M10_B2_G11_MF	g3273122	BLASTN	359	3e-09	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-53, complete sequence [Plasmodium falciparum]
15831	GM_M10_B2_G12_MR	g3650035	BLASTX	233	2e-17	45	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
15832	GM_M10_B2_H02_MF	g3097320	BLASTN	1165	1e-45	84	Glycine max gene for Bd 30K, complete cds
15833	GM_M10_B2_H04_MR	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15834	GM_M10_B2_H09_MF	g4063760	BLASTX	280	2e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15835	GM_M10_B2_H09_MR	g507910	BLASTN	684	3e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15836	GM_M10_B2_H11_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15837	GM_M10_B2_H11_MR	g507910	BLASTN	518	8e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
15838	GM_M13_A1_A07_MF	g3142328	BLASTN	1355	2e-54	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15839	GM_M13_A1_A09_MR	g3746069	BLASTX	243	2e-18	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
15840	GM_M13_A1_A11_MR	g3738114	BLASTN	594	8e-20	67	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
15841	GM_M13_A1_B01_MF	g507910	BLASTN	350	3e-09	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15842	GM_M13_A1_B01_MR	g3142379	BLASTX	213	5e-16	55	(AF053008) envelope-like [Glycine max]
15843	GM_M13_A1_B02_MF	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15844	GM_M13_A1_B05_MF	g2522228	BLASTX	222	4e-17	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
15845	GM_M13_A1_B06_MF	g507910	BLASTN	502	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
15846	GM_M13_A1_B06_MR	g4063760	BLASTX	427	4e-38	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15847	GM_M13_A1_B08_MF	g3645899	BLASTX	286	4e-23	56	(U68408) 5' end not determined experimentally [Zea mays]
15848	GM_M13_A1_B10_MF	g3513747	BLASTX	307	4e-25	53	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15849	GM_M13_A1_C01_MR	g4115365	BLASTX	111	1e-10	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
15850	GM_M13_A1_C03_MR	g4050011	BLASTN	584	2e-19	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
15851	GM_M13_A1_C10_MF	g3777527	BLASTX	119	4e-10	39	(AF053008) gag-pol polyprotein [Glycine max]
15852	GM_M13_A1_D02_MF	g1431738	BLASTN	528	5e-17	88	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
15853	GM_M13_A1_D04_MF	g3319351	BLASTX	211	5e-15	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
15854	GM_M13_A1_D09_MF	g3695395	BLASTX	284	2e-23	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
15855	GM_M13_A1_D09_MR	g2462134	BLASTX	194	8e-14	37	(Y13368) reverse transcriptase [Beta vulgaris]
15856	GM_M13_A1_D12_MF	g507910	BLASTN	402	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15857	GM_M13_A1_D12_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15858	GM_M13_A1_E02_MF	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15859	GM_M13_A1_E04_MR	g3142328	BLASTN	1020	3e-39	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
15860	GM_M13_A1_E10_MF	g3513747	BLASTX	230	9e-19	45	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15861	GM_M13_A1_F01_MR	g18559	BLASTN	329	4e-10	78	G.max gene for catalase
15862	GM_M13_A1_F02_MR	g2522228	BLASTX	119	8e-14	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
15863	GM_M13_A1_F03_MF	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15864	GM_M13_A1_F03_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15865	GM_M13_A1_F04_MF	g3152629	BLASTN	361	3e-09	62	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
15866	GM_M13_A1_F12_MF	g2443320	BLASTX	231	4e-17	38	(D85597) polyprotein [Oryza australiensis]
15867	GM_M13_A1_G01_MR	g3142379	BLASTX	280	2e-23	63	(AF053008) envelope-like [Glycine max]
15868	GM_M13_A1_G10_MF	g4063760	BLASTX	199	9e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15869	GM_M13_A1_G10_MR	g4038056	BLASTX	298	2e-24	53	(AC005897) putative transposon [Arabidopsis thaliana]
15870	GM_M13_A1_G11_MF	g3063445	BLASTX	169	1e-10	36	(AC003981) F22O13.7 [Arabidopsis thaliana]
15871	GM_M13_A1_H02_MF	g3738133	BLASTN	442	6e-13	63	Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence [Homo sapiens]
15872	GM_M13_A1_H06_MF	g4038056	BLASTX	203	2e-14	37	(AC005897) putative transposon [Arabidopsis thaliana]
15873	GM_M13_A1_H08_MF	g3777527	BLASTX	709	5e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
15874	GM_M13_A1_H08_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15875	GM_M13_A2_A08_MR	g944837	BLASTN	358	3e-09	65	P.elliotii DNA for repeat region
15876	GM_M13_A2_A09_MF	g2578038	BLASTN	396	7e-11	65	Human DNA sequence from PAC 106H14 on chromosome Xq21.1-21.33. Contains STS
15877	GM_M13_A2_A10_MF	g507910	BLASTN	404	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15878	GM_M13_A2_A10_MR	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15879	GM_M13_A2_B02_MF	g3142328	BLASTN	1351	2e-54	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15880	GM_M13_A2_B02_MR	g507910	BLASTN	376	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15881	GM_M13_A2_B07_MF	g3097320	BLASTN	739	2e-26	78	Glycine max gene for Bd 30K, complete cds
15882	GM_M13_A2_B10_MR	g1785699	BLASTX	170	4e-12	42	(Y08501) orf145a [Arabidopsis thaliana]
15883	GM_M13_A2_C10_MR	g4126312	BLASTN	349	1e-08	62	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
15884	GM_M13_A2_D02_MF	g3777527	BLASTX	511	7e-47	94	(AF053008) gag-pol polyprotein [Glycine max]
15885	GM_M13_A2_D04_MF	g1769897	BLASTX	107	8e-12	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15886	GM_M13_A2_D12_MR	g507910	BLASTN	466	2e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15887	GM_M13_A2_F01_MR	g421955	BLASTX	142	2e-12	55	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15888	GM_M13_A2_F05_MR	g3097320	BLASTN	637	8e-22	77	Glycine max gene for Bd 30K, complete cds
15889	GM_M13_A2_F06_MF	g2500026	BLASTX	354	1e-31	70	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) gi 1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana]
15890	GM_M13_A2_F10_MR	g905361	BLASTX	244	5e-19	72	(U22103) gag-protease polyprotein [Glycine max]
15891	GM_M13_A2_G02_MF	g1142701	BLASTN	1021	8e-40	83	Glycine max satellite STR120-A.3.
15892	GM_M13_A2_G03_MR	g1813979	BLASTX	249	2e-20	52	(Y10860) hypothetical protein [Musa acuminata]
15893	GM_M13_A2_G05_MF	g4063760	BLASTX	505	2e-46	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15894	GM_M13_A2_G07_MR	g2981130	BLASTN	396	7e-11	67	Populus balsamifera subsp. trichocarpa AGAMOUS homolog (PTAG1) gene, complete cds
15895	GM_M13_A2_G10_MF	g549100	BLASTX	456	2e-41	95	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1071 IN TRANSPOSON TN5271 >gi 95495 pir A41290 probable transposase (IS1071) - Alcaligenes sp. transposon Tn5271 >gi 141982 (M65135) transposase [Alcaligenes sp.]
15896	GM_M13_A2_H03_MF	g1769897	BLASTX	329	2e-28	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15897	GM_M13_A2_H07_MR	g3142328	BLASTN	604	2e-20	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15898	GM_M13_A2_H10_MR	g3645899	BLASTX	110	6e-14	38	(U68408) 5' end not determined experimentally [Zea mays]
15899	GM_M13_B1_A02_MF	g3176791	BLASTN	443	8e-14	65	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
15900	GM_M13_B1_A04_MF	g2832901	BLASTN	1190	6e-47	79	Cajanus cajan copia-like retrotransposon,Panzee
15901	GM_M13_B1_A08_MF	g3789709	BLASTN	442	6e-13	64	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
15902	GM_M13_B1_B02_MR	g454847	BLASTN	489	4e-15	77	Glycine max ribosomal protein S11 gene, complete cds
15903	GM_M13_B1_B04_MF	g4063760	BLASTX	176	2e-11	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15904	GM_M13_B1_B05_MR	g18559	BLASTN	389	1e-10	72	G.max gene for catalase
15905	GM_M13_B1_B09_MR	g18683	BLASTN	475	1e-14	66	G.max N-20t gene
15906	GM_M13_B1_B10_MF	g2244793	BLASTX	500	2e-45	73	(Z97336) TMV resistance protein homolog [Arabidopsis thaliana]
15907	GM_M13_B1_B12_MF	g522302	BLASTX	193	4e-13	45	(L35053) endonuclease [Magnaporthe grisea]
15908	GM_M13_B1_C01_MR	g4056480	BLASTX	254	5e-21	65	(AC005896) putative adenylate kinase [Arabidopsis thaliana]
15909	GM_M13_B1_C03_MF	g2995405	BLASTX	261	7e-36	61	(Y12432) polyprotein [Ananas comosus]
15910	GM_M13_B1_C04_MR	g2995405	BLASTX	369	4e-32	50	(Y12432) polyprotein [Ananas comosus]
15911	GM_M13_B1_C05_MR	g3021268	BLASTX	273	1e-21	57	(AL022347) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15912	GM_M13_B1_C08_MF	g4063756	BLASTN	441	7e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15913	GM_M13_B1_C12_MR	g507910	BLASTN	513	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15914	GM_M13_B1_D04_MR	g4063756	BLASTN	387	2e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15915	GM_M13_B1_D07_MR	g400531	BLASTN	610	1e-20	71	V.sativa mRNA for NADPH-ferrihemoprotein reductase.
15916	GM_M13_B1_D11_MR	g3643604	BLASTX	314	4e-26	57	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
15917	GM_M13_B1_D12_MF	g18559	BLASTN	352	6e-09	71	G.max gene for catalase
15918	GM_M13_B1_E02_MF	g1769898	BLASTX	126	2e-11	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15919	GM_M13_B1_E03_MR	g3924609	BLASTX	189	1e-12	36	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
15920	GM_M13_B1_E08_MF	g18559	BLASTN	546	1e-17	73	G.max gene for catalase
15921	GM_M13_B1_F01_MF	g3513747	BLASTX	315	6e-26	53	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15922	GM_M13_B1_F07_MF	g13767	BLASTN	374	9e-11	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
15923	GM_M13_B1_F11_MF	g3176788	BLASTN	345	2e-09	63	Homo sapiens allele 8 fragile site locus (FRA10B) minisatellite sequence
15924	GM_M13_B1_G01_MF	g3323609	BLASTX	175	4e-12	57	(AF064093) KE04p [Homo sapiens]
15925	GM_M13_B1_G03_MF	g3319362	BLASTX	231	2e-17	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15926	GM_M13_B1_G06_MF	g2160161	BLASTX	164	2e-10	31	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]
15927	GM_M13_B1_G11_MF	g1142702	BLASTN	510	1e-16	78	Glycine max satellite STR120-A.4.
15928	GM_M13_B1_H01_MF	g1871190	BLASTX	311	5e-27	51	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
15929	GM_M13_B1_H03_MR	g2522230	BLASTX	355	1e-31	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15930	GM_M13_B1_H04_MR	g3402671	BLASTN	640	7e-22	72	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]
15931	GM_M13_B1_H07_MF	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15932	GM_M13_B1_H07_MR	g507910	BLASTN	618	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15933	GM_M13_B1_H10_MF	g507910	BLASTN	379	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15934	GM_M13_B1_H11_MF	g4063760	BLASTX	274	8e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15935	GM_M13_B2_A06_MR	g4063760	BLASTX	406	8e-36	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15936	GM_M13_B2_B10_MF	g3777527	BLASTX	205	3e-14	90	(AF053008) gag-pol polyprotein [Glycine max]
15937	GM_M13_B2_C10_MR	g2326264	BLASTN	376	5e-10	68	Arabidopsis thaliana DNA for CCT alpha/TCP-1, complete cds.
15938	GM_M13_B2_C12_MR	g13768	BLASTN	334	5e-09	60	Torulopsis glabrata mitochondrial DNA for tRNA-Thr,-His and -Glu upstream of cytochrome b gene >gi 343951 gb M11856 YSLMTIG01 Yeast (T.glabrata) mitochondrial DNA between L rRNA and cytochrome b genes.
15939	GM_M13_B2_D02_MR	g2995405	BLASTX	243	1e-18	42	(Y12432) polyprotein [Ananas comosus]
15940	GM_M13_B2_D07_MR	g2995405	BLASTX	279	2e-22	60	(Y12432) polyprotein [Ananas comosus]
15941	GM_M13_B2_D11_MR	g3777527	BLASTX	652	6e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
15942	GM_M13_B2_E06_MR	g3097320	BLASTN	536	3e-17	72	Glycine max gene for Bd 30K, complete cds
15943	GM_M13_B2_E10_MR	g1769897	BLASTX	166	7e-11	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15944	GM_M13_B2_F07_MR	g3935164	BLASTX	234	2e-19	53	(AC004557) F17L21.7 [Arabidopsis thaliana]
15945	GM_M13_B2_F11_MR	g226407	BLASTX	170	1e-10	33	retrotransposon del1-46 [Lilium henryi]
15946	GM_M13_B2_G01_MR	g320569	BLASTX	215	7e-17	50	transposon TNT1 - Arabidopsis thaliana (fragment)
15947	GM_M13_B2_G02_MR	g4063760	BLASTX	276	5e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15948	GM_M13_B2_G03_MR	g3645899	BLASTX	306	3e-25	47	(U68408) 5' end not determined experimentally [Zea mays]
15949	GM_M13_B2_G08_MR	g3142379	BLASTX	154	1e-09	44	(AF053008) envelope-like [Glycine max]
15950	GM_M13_B2_H03_MR	g1769897	BLASTX	164	1e-10	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15951	GM_M14_A1_B08_MF	g2626751	BLASTN	386	2e-10	62	Triticum aestivum retrotransposon Tar1, partial sequence.
15952	GM_M14_A1_B09_MR	g4092470	BLASTN	355	5e-09	63	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
15953	GM_M14_A1_D07_MF	g170605	BLASTN	354	3e-09	66	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
15954	GM_M14_A1_F01_MF	g3777527	BLASTX	297	5e-24	69	(AF053008) gag-pol polyprotein [Glycine max]
15955	GM_M14_A1_F12_MF	g1769897	BLASTX	189	3e-13	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15956	GM_M14_A1_G05_MR	g1840106	BLASTN	413	2e-12	68	Human fragile site locus (FRA16B) minisatellite repeat
15957	GM_M14_A1_G10_MF	g225242	BLASTX	245	9e-19	80	ORF 1708 [Nicotiana tabacum]
15958	GM_M14_A1_G12_MF	g905361	BLASTX	429	2e-39	93	(U22103) gag-protease polyprotein [Glycine max]
15959	GM_M14_A1_H04_MF	g18559	BLASTN	325	1e-14	75	G.max gene for catalase
15960	GM_M14_A2_A03_MF	g3142379	BLASTX	390	2e-35	68	(AF053008) envelope-like [Glycine max]
15961	GM_M14_A2_A03_MR	g3097320	BLASTN	728	6e-26	77	Glycine max gene for Bd 30K, complete cds
15962	GM_M14_A2_A08_MR	g3097320	BLASTN	847	3e-31	74	Glycine max gene for Bd 30K, complete cds
15963	GM_M14_A2_A09_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15964	GM_M14_A2_A10_MR	g3777527	BLASTX	378	7e-55	97	(AF053008) gag-pol polyprotein [Glycine max]
15965	GM_M14_A2_B04_MF	g1946265	BLASTX	139	4e-15	77	(Y11414) myb [Oryza sativa]
15966	GM_M14_A2_B05_MF	g1946265	BLASTX	114	6e-12	80	(Y11414) myb [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15967	GM_M14_A2_B07_MF	g3777527	BLASTX	556	1e-51	93	(AF053008) gag-pol polyprotein [Glycine max]
15968	GM_M14_A2_B07_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15969	GM_M14_A2_B10_MF	g3461840	BLASTX	270	3e-21	41	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
15970	GM_M14_A2_C02_MR	g507910	BLASTN	587	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15971	GM_M14_A2_C06_MF	g507910	BLASTN	641	2e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15972	GM_M14_A2_C07_MF	g2499465	BLASTX	145	9e-12	49	PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) gi 1166373 (L49175) C4 photosynthetic phosphoenolpyruvate carboxylase [Amaranthus hypochondriacus] gi 1181197 gnl PID e211616 (Z68125) C4 photosynthetic phosphoenolpyruvate carboxylase [Amaranthus hypochondriacus]
15973	GM_M14_A2_D03_MR	g3142328	BLASTN	843	3e-31	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15974	GM_M14_A2_D05_MR	g1076763	BLASTX	111	7e-12	42	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
15975	GM_M14_A2_D06_MF	g3868800	BLASTX	201	4e-14	77	(AB013603) topoisomerase III beta [Mus musculus]
15976	GM_M14_A2_D06_MR	g587603	BLASTN	371	8e-10	63	P.falciparum gene for beta subunit RNA polymerase
15977	GM_M14_A2_D08_MF	g4063760	BLASTX	234	3e-24	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15978	GM_M14_A2_D11_MR	g2194136	BLASTX	185	3e-12	37	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
15979	GM_M14_A2_E01_MR	g18559	BLASTN	823	3e-30	77	G.max gene for catalase
15980	GM_M14_A2_E02_MR	g18559	BLASTN	909	3e-34	73	G.max gene for catalase
15981	GM_M14_A2_E04_MF	g4033838	BLASTX	277	7e-23	69	(Y18550) sigma-like factor [Arabidopsis thaliana]
15982	GM_M14_A2_E04_MR	g2443320	BLASTX	174	5e-11	33	(D85597) polyprotein [Oryza australiensis]
15983	GM_M14_A2_E05_MF	g1402883	BLASTX	148	7e-17	50	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
15984	GM_M14_A2_E05_MR	g3645899	BLASTX	186	1e-15	40	(U68408) 5' end not determined experimentally [Zea mays]
15985	GM_M14_A2_E11_MF	g2443320	BLASTX	186	4e-14	43	(D85597) polyprotein [Oryza australiensis]
15986	GM_M14_A2_F05_MF	g3142328	BLASTN	649	2e-22	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15987	GM_M14_A2_F12_MR	g3777527	BLASTX	138	3e-16	44	(AF053008) gag-pol polyprotein [Glycine max]
15988	GM_M14_A2_G05_MR	g3777527	BLASTX	595	8e-56	98	(AF053008) gag-pol polyprotein [Glycine max]
15989	GM_M14_A2_G07_MR	g3421096	BLASTX	112	2e-10	91	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana]
15990	GM_M14_A2_G09_MF	g507910	BLASTN	452	8e-14	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15991	GM_M14_A2_G11_MR	g2129618	BLASTX	192	4e-13	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15992	GM_M14_A2_H03_MF	g1769898	BLASTX	308	6e-26	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15993	GM_M14_A2_H03_MR	g556344	BLASTN	482	8e-16	78	Pisum sativum histone H1 (H1-41) mRNA, complete cds.
15994	GM_M14_A2_H04_MF	g3777527	BLASTX	556	1e-51	95	(AF053008) gag-pol polyprotein [Glycine max]
15995	GM_M14_A2_H07_MR	g2522227	BLASTX	216	5e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15996	GM_M14_A2_H12_MF	g2252863	BLASTX	161	3e-10	54	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]
15997	GM_M14_B2_A01_MF	g3402703	BLASTX	200	8e-15	80	(AC004261) hypothetical protein [Arabidopsis thaliana]
15998	GM_M14_B2_A01_MR	g3779030	BLASTX	222	1e-17	33	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
15999	GM_M14_B2_A03_MF	g1666236	BLASTX	145	7e-09	32	(U76261) unknown [Hordeum vulgare]
16000	GM_M14_B2_A04_MR	g629693	BLASTX	165	6e-11	32	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16001	GM_M14_B2_A05_MR	g3688808	BLASTX	148	9e-09	52	(AF084104) AcsA [Bacillus firmus]
16002	GM_M14_B2_A08_MF	g18559	BLASTN	1065	3e-41	75	G.max gene for catalase
16003	GM_M14_B2_A10_MF	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16004	GM_M14_B2_B02_MF	g1514643	BLASTX	166	3e-16	75	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
16005	GM_M14_B2_B06_MF	g4063760	BLASTX	438	3e-39	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16006	GM_M14_B2_B06_MR	g3777527	BLASTX	326	4e-27	46	(AF053008) gag-pol polyprotein [Glycine max]
16007	GM_M14_B2_B07_MF	g2586083	BLASTX	295	4e-24	49	(U72725) receptor kinase-like protein [Oryza longistaminata]
16008	GM_M14_B2_B07_MR	g3777527	BLASTX	185	4e-12	35	(AF053008) gag-pol polyprotein [Glycine max]
16009	GM_M14_B2_B09_MR	g100484	BLASTX	303	3e-25	57	hypothetical protein - garden snapdragon
16010	GM_M14_B2_B11_MF	g2462134	BLASTX	208	2e-15	35	(Y13368) reverse transcriptase [Beta vulgaris]
16011	GM_M14_B2_B12_MF	g3169169	BLASTN	399	6e-11	80	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]
16012	GM_M14_B2_C05_MF	g3176798	BLASTN	395	1e-11	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
16013	GM_M14_B2_C08_MF	g3097320	BLASTN	993	6e-38	78	Glycine max gene for Bd 30K, complete cds
16014	GM_M14_B2_C08_MR	g3142328	BLASTN	537	2e-27	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16015	GM_M14_B2_D02_MF	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16016	GM_M14_B2_D02_MR	g4063760	BLASTX	478	2e-43	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16017	GM_M14_B2_D06_MR	g2605619	BLASTX	179	4e-13	65	(D88618) OSMYB2 [Oryza sativa]
16018	GM_M14_B2_D07_MF	g507910	BLASTN	586	7e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16019	GM_M14_B2_D11_MF	g730558	BLASTX	182	2e-13	65	60S RIBOSOMAL PROTEIN L34 gi 1076636 pir S48027 ribosomal protein L34 - common tobacco gi 2129964 pir S48028 ribosomal protein L34.e, cytosolic - common tobacco gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] gi 436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]
16020	GM_M14_B2_D11_MR	g3757516	BLASTX	108	2e-10	47	(AC005167) putative TMV resistance protein [Arabidopsis thaliana]
16021	GM_M14_B2_E05_MR	g507910	BLASTN	587	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16022	GM_M14_B2_E06_MR	g3779026	BLASTX	272	2e-21	45	(AC005171) putative retrotransposon [Arabidopsis thaliana]
16023	GM_M14_B2_E08_MR	g2522230	BLASTX	189	4e-14	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16024	GM_M14_B2_E09_MF	g3097320	BLASTN	434	1e-12	72	Glycine max gene for Bd 30K, complete cds
16025	GM_M14_B2_F03_MF	g1142701	BLASTN	1220	8e-49	82	Glycine max satellite STR120-A.3.
16026	GM_M14_B2_F05_MF	g905361	BLASTX	141	4e-10	26	(U22103) gag-protease polyprotein [Glycine max]
16027	GM_M14_B2_F05_MR	g3097320	BLASTN	886	4e-33	74	Glycine max gene for Bd 30K, complete cds
16028	GM_M14_B2_F06_MF	g1666236	BLASTX	150	2e-09	26	(U76261) unknown [Hordeum vulgare]
16029	GM_M14_B2_F12_MF	g3319362	BLASTX	384	1e-33	51	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16030	GM_M14_B2_G03_MR	g3721856	BLASTX	96	1e-10	72	(AB014057) beta-Amyrin Synthase [Panax ginseng]
16031	GM_M14_B2_G06_MR	g505129	BLASTN	463	5e-14	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16032	GM_M14_B2_G12_MF	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16033	GM_M14_B2_G12_MR	g507910	BLASTN	382	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16034	GM_M14_B2_H01_MF	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16035	GM_M14_B2_H01_MR	g507910	BLASTN	593	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16036	GM_M14_B2_H02_MR	g2842477	BLASTX	151	4e-09	74	(AL021749) copper-binding protein-like [Arabidopsis thaliana]
16037	GM_M14_B2_H03_MF	g2995405	BLASTX	451	5e-41	63	(Y12432) polyprotein [Ananas comosus]
16038	GM_M14_B2_H04_MF	g1666236	BLASTX	185	2e-13	28	(U76261) unknown [Hordeum vulgare]
16039	GM_M14_B2_H06_MF	g2827621	BLASTX	168	1e-10	45	(AL021636) putative protein [Arabidopsis thaliana]
16040	GM_M14_B2_H06_MR	g2864611	BLASTX	149	4e-09	57	(AL021811) putative protein [Arabidopsis thaliana]
16041	GM_M14_B2_H07_MR	g2708743	BLASTX	154	7e-09	35	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16042	GM_M14_B2_H08_MR	g99721	BLASTX	381	4e-33	54	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
16043	GM_M14_B2_H10_MR	g3522952	BLASTX	166	1e-11	73	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16044	GM_M15_A1_A02_MR	g2129618	BLASTX	166	2e-10	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16045	GM_M15_A1_B01_MR	g4063760	BLASTX	400	3e-46	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16046	GM_M15_A1_B03_MF	g3953461	BLASTX	155	1e-09	58	(AC002328) F20N2.6 [Arabidopsis thaliana]
16047	GM_M15_A1_B05_MR	g4063760	BLASTX	263	1e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16048	GM_M15_A1_B08_MF	g18559	BLASTN	1107	3e-43	84	G.max gene for catalase
16049	GM_M15_A1_C01_MF	g2769655	BLASTN	395	8e-11	63	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
16050	GM_M15_A1_C02_MF	g4063760	BLASTX	398	5e-35	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16051	GM_M15_A1_C03_MR	g4063760	BLASTX	248	5e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16052	GM_M15_A1_C06_MR	g629693	BLASTX	97	3e-11	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16053	GM_M15_A1_C07_MF	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16054	GM_M15_A1_C07_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16055	GM_M15_A1_C10_MR	g14227	BLASTN	414	2e-12	63	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
16056	GM_M15_A1_D02_MR	g2443320	BLASTX	224	5e-27	48	(D85597) polyprotein [Oryza australiensis]
16057	GM_M15_A1_D04_MF	g3201625	BLASTX	152	9e-10	46	(AC004669) hypothetical protein [Arabidopsis thaliana]
16058	GM_M15_A1_D04_MR	g3445210	BLASTX	406	3e-37	51	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
16059	GM_M15_A1_D05_MF	g1142701	BLASTN	263	6e-20	76	Glycine max satellite STR120-A.3.
16060	GM_M15_A1_D07_MR	g3142328	BLASTN	961	1e-36	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16061	GM_M15_A1_D10_MR	g3367519	BLASTX	253	1e-27	57	(AC004392) Contains similarity to gb U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana]
16062	GM_M15_A1_D12_MF	g170606	BLASTN	664	2e-23	65	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
16063	GM_M15_A1_D12_MR	g2811226	BLASTX	310	4e-26	65	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
16064	GM_M15_A1_E05_MR	g255578	BLASTN	929	6e-36	95	small auxin up RNA gene cluster: orf X10A [Glycine max=soybeans, cv. Wayne, Genomic, 666 nt]
16065	GM_M15_A1_E10_MR	g3142328	BLASTN	1952	8e-82	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
16066	GM_M15_A1_F02_MR	g2522227	BLASTX	223	1e-17	36	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16067	GM_M15_A1_F04_MR	g4063760	BLASTX	542	2e-50	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16068	GM_M15_A1_F09_MR	g1769898	BLASTX	340	2e-29	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16069	GM_M15_A1_G04_MF	g507910	BLASTN	380	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16070	GM_M15_A1_G04_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16071	GM_M15_A1_G05_MR	g2739369	BLASTX	334	4e-29	66	(AC002505) putative pectinesterase [Arabidopsis thaliana]
16072	GM_M15_A1_G09_MR	g343344	BLASTN	455	5e-18	81	Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes.
16073	GM_M15_A1_G10_MR	g1769898	BLASTX	452	5e-42	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16074	GM_M15_A1_H03_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16075	GM_M15_A1_H06_MR	g1769898	BLASTX	177	2e-24	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16076	GM_M15_A2_A02_MF	g1076668	BLASTX	656	1e-63	96	NADH dehydrogenase (EC 1.6.99.3) - potato gi 639834 (X83999) NADH dehydrogenase [Solanum tuberosum]
16077	GM_M15_A2_A05_MR	g2522230	BLASTX	306	2e-26	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16078	GM_M15_A2_A07_MF	g728695	BLASTX	245	5e-25	86	(Z48618) DNA helicase type protein [Saccharomyces cerevisiae]
16079	GM_M15_A2_A07_MR	g3645899	BLASTX	365	1e-31	53	(U68408) 5' end not determined experimentally [Zea mays]
16080	GM_M15_A2_A08_MR	g2811226	BLASTX	252	7e-20	89	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
16081	GM_M15_A2_A11_MF	g18559	BLASTN	888	3e-33	77	G.max gene for catalase
16082	GM_M15_A2_B01_MR	g905361	BLASTX	589	6e-59	84	(U22103) gag-protease polyprotein [Glycine max]
16083	GM_M15_A2_B04_MF	g2708743	BLASTX	154	7e-09	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16084	GM_M15_A2_B06_MF	g130582	BLASTX	243	1e-19	43	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16085	GM_M15_A2_B07_MR	g507910	BLASTN	538	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
16086	GM_M15_A2_B12_MR	g992916	BLASTN	631	2e-21	76	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
16087	GM_M15_A2_C07_MR	g4006831	BLASTX	158	2e-09	36	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
16088	GM_M15_A2_C08_MF	g4063760	BLASTX	371	4e-32	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
16089	GM_M15_A2_C09_MR	g3142328	BLASTN	793	6e-29	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16090	GM_M15_A2_C11_MR	g1769898	BLASTX	377	2e-33	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16091	GM_M15_A2_C12_MF	g3777527	BLASTX	609	3e-57	98	(AF053008) gag-pol polyprotein [Glycine max]
16092	GM_M15_A2_C12_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16093	GM_M15_A2_D01_MF	g4063760	BLASTX	380	5e-33	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16094	GM_M15_A2_D02_MF	g100484	BLASTX	354	9e-31	60	hypothetical protein - garden snapdragon
16095	GM_M15_A2_D05_MR	g2827992	BLASTX	509	5e-48	65	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]
16096	GM_M15_A2_D08_MR	g2462134	BLASTX	195	6e-14	39	(Y13368) reverse transcriptase [Beta vulgaris]
16097	GM_M15_A2_D10_MR	g4063770	BLASTX	182	3e-12	38	(AB004906) transposase [Ipomoea purpurea]
16098	GM_M15_A2_E01_MR	g2708743	BLASTX	246	1e-18	35	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16099	GM_M15_A2_E05_MF	g507910	BLASTN	354	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
16100	GM_M15_A2_E05_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16101	GM_M15_A2_E06_MF	g2443320	BLASTX	166	3e-10	35	(D85597) polyprotein [Oryza australiensis]
16102	GM_M15_A2_E09_MF	g3777527	BLASTX	301	4e-42	76	(AF053008) gag-pol polyprotein [Glycine max]
16103	GM_M15_A2_E12_MF	g2708743	BLASTX	154	7e-09	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16104	GM_M15_A2_F01_MR	g2121303	BLASTN	376	6e-10	62	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
16105	GM_M15_A2_F02_MF	g2244802	BLASTX	355	3e-30	54	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
16106	GM_M15_A2_F09_MF	g4063760	BLASTX	349	9e-30	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16107	GM_M15_A2_F10_MF	g2244802	BLASTX	382	4e-33	56	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
16108	GM_M15_A2_G01_MF	g3930515	BLASTX	166	7e-11	32	(AF059674) putative gag protein [Nicotiana tabacum]
16109	GM_M15_A2_G05_MR	g3645899	BLASTX	233	5e-28	52	(U68408) 5' end not determined experimentally [Zea mays]
16110	GM_M15_A2_G09_MR	g507910	BLASTN	350	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16111	GM_M15_A2_G10_MR	g2522228	BLASTX	274	4e-23	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
16112	GM_M15_A2_H01_MF	g4063760	BLASTX	210	6e-15	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16113	GM_M15_A2_H01_MR	g4063760	BLASTX	198	1e-15	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16114	GM_M15_A2_H04_MR	g3287270	BLASTX	164	6e-10	45	(Y09533) involved in starch metabalism [Solanum tuberosum]
16115	GM_M15_A2_H08_MF	g2656024	BLASTN	366	2e-09	60	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16116	GM_M15_A2_H10_MR	g2194124	BLASTX	194	4e-14	62	(AC002062) Similar to Glycine metalloendoproteinase (gb U63725). [Arabidopsis thaliana]
16117	GM_M15_A2_H11_MF	g3582067	BLASTN	383	4e-11	72	Rattus norvegicus repeat; map end-D8Wox18
16118	GM_M15_A2_H11_MR	g2194136	BLASTX	185	3e-12	39	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
16119	GM_M15_B1_A05_MR	g4063760	BLASTX	265	7e-21	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16120	GM_M15_B1_A07_MR	g2522230	BLASTX	185	9e-14	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16121	GM_M15_B1_B04_MR	g1402881	BLASTX	266	3e-23	43	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
16122	GM_M15_B1_B06_MR	g4063760	BLASTX	250	2e-35	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16123	GM_M15_B1_C03_MR	g99922	BLASTX	551	5e-59	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
16124	GM_M15_B1_C04_MR	g2829611	BLASTX	144	6e-09	47	HEMK PROTEIN HOMOLOG >gi 1653158 gnl PID d1018807 (D90911) protoporphyrinogen oxidase [Synechocystis sp.]
16125	GM_M15_B1_C12_MR	g3184508	BLASTN	453	2e-13	66	Homo sapiens chromosome 17, clone HRPC41C23, complete sequence [Homo sapiens]
16126	GM_M15_B1_D05_MR	g18559	BLASTN	477	1e-14	66	G.max gene for catalase
16127	GM_M15_B1_D09_MR	g3738114	BLASTN	357	4e-09	62	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
16128	GM_M15_B1_E01_MR	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence
16129	GM_M15_B1_E04_MR	g1326016	BLASTX	157	4e-19	34	TY3-2 orfB
16130	GM_M15_B1_E08_MR	g3097320	BLASTN	411	1e-11	73	Glycine max gene for Bd 30K, complete cds
16131	GM_M15_B1_E09_MR	g478218	BLASTX	220	2e-17	60	reverse transcriptase (copia-like retrotransposon) - maize (fragment) gi 168449 (M94482) reverse transcriptase [Zea mays]
16132	GM_M15_B1_F01_MR	g4056482	BLASTX	233	3e-17	58	(AC005896) putative ABC transporter [Arabidopsis thaliana]
16133	GM_M15_B1_F03_MR	g1769898	BLASTX	385	2e-34	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16134	GM_M15_B1_G01_MR	g2194136	BLASTX	192	6e-13	33	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
16135	GM_M15_B1_H05_MR	g2367392	BLASTX	177	1e-11	30	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]
16136	GM_M15_B1_H10_MR	g18559	BLASTN	364	2e-09	73	G.max gene for catalase
16137	GM_M15_B1_H11_MR	g2583130	BLASTX	107	7e-09	53	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
16138	GM_M15_B2_A03_MR	g3142328	BLASTN	985	1e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16139	GM_M15_B2_A09_MR	g3645899	BLASTX	209	3e-17	43	(U68408) 5' end not determined experimentally [Zea mays]
16140	GM_M15_B2_A12_MF	g3142328	BLASTN	763	1e-27	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16141	GM_M15_B2_B02_MF	g3426334	BLASTN	362	2e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
16142	GM_M15_B2_B04_MR	g2605911	BLASTX	208	8e-22	86	(AF029258) plasma membrane H+-ATPase [Kosteletzkya virginica]
16143	GM_M15_B2_B05_MF	g3386621	BLASTX	208	2e-18	71	(AC004665) unknown protein [Arabidopsis thaliana]
16144	GM_M15_B2_B07_MF	g2443320	BLASTX	348	1e-29	53	(D85597) polyprotein [Oryza australiensis]
16145	GM_M15_B2_B07_MR	g3779030	BLASTX	171	3e-12	32	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
16146	GM_M15_B2_B11_MR	g2462134	BLASTX	155	1e-09	44	(Y13368) reverse transcriptase [Beta vulgaris]
16147	GM_M15_B2_C01_MF	g4038056	BLASTX	360	4e-31	52	(AC005897) putative transposon [Arabidopsis thaliana]
16148	GM_M15_B2_C02_MR	g18559	BLASTN	1097	1e-42	77	G.max gene for catalase
16149	GM_M15_B2_C08_MF	g18559	BLASTN	797	4e-29	73	G.max gene for catalase
16150	GM_M15_B2_C09_MR	g3549678	BLASTX	155	2e-09	87	(AL031394) putative aspartate--tRNA ligase [Arabidopsis thaliana]
16151	GM_M15_B2_C12_MF	g905361	BLASTX	429	2e-39	95	(U22103) gag-protease polyprotein [Glycine max]
16152	GM_M15_B2_D01_MF	g3810596	BLASTX	194	2e-13	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16153	GM_M15_B2_D01_MR	g2981494	BLASTX	116	6e-10	62	(AF053473) kinesin heavy chain [Mus musculus]
16154	GM_M15_B2_D04_MF	g3930515	BLASTX	121	4e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
16155	GM_M15_B2_D04_MR	g2129709	BLASTX	306	4e-25	46	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
16156	GM_M15_B2_D05_MF	g3142328	BLASTN	1676	4e-69	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16157	GM_M15_B2_D06_MR	g629693	BLASTX	160	3e-19	69	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16158	GM_M15_B2_D10_MR	g507910	BLASTN	420	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16159	GM_M15_B2_D11_MF	g3930515	BLASTX	100	7e-09	42	(AF059674) putative gag protein [Nicotiana tabacum]
16160	GM_M15_B2_D11_MR	g4038056	BLASTX	325	2e-27	48	(AC005897) putative transposon [Arabidopsis thaliana]
16161	GM_M15_B2_E01_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16162	GM_M15_B2_E01_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16163	GM_M15_B2_E02_MR	g4038056	BLASTX	400	2e-35	54	(AC005897) putative transposon [Arabidopsis thaliana]
16164	GM_M15_B2_E03_MF	g3777527	BLASTX	232	4e-17	40	(AF053008) gag-pol polyprotein [Glycine max]
16165	GM_M15_B2_E06_MF	g100484	BLASTX	214	1e-15	44	hypothetical protein - garden snapdragon
16166	GM_M15_B2_E10_MF	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16167	GM_M15_B2_E11_MR	g4038056	BLASTX	372	2e-32	52	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16168	GM_M15_B2_E12_MF	g3645899	BLASTX	293	7e-28	64	(U68408) 5' end not determined experimentally [Zea mays]
16169	GM_M15_B2_F04_MF	g1769897	BLASTX	168	6e-11	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16170	GM_M15_B2_F05_MR	g3650039	BLASTX	311	3e-26	46	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16171	GM_M15_B2_F07_MF	g3695395	BLASTX	97	3e-13	39	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
16172	GM_M15_B2_F08_MR	g100484	BLASTX	364	7e-32	53	hypothetical protein - garden snapdragon
16173	GM_M15_B2_F10_MF	g2429543	BLASTX	170	1e-10	38	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
16174	GM_M15_B2_G05_MF	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16175	GM_M15_B2_G05_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16176	GM_M15_B2_G06_MR	g3645899	BLASTX	217	5e-32	60	(U68408) 5' end not determined experimentally [Zea mays]
16177	GM_M15_B2_G07_MF	g18559	BLASTN	380	3e-10	71	G.max gene for catalase
16178	GM_M15_B2_G07_MR	g2995405	BLASTX	283	5e-25	43	(Y12432) polyprotein [Ananas comosus]
16179	GM_M15_B2_G12_MF	g3935164	BLASTX	379	9e-33	52	(AC004557) F17L21.7 [Arabidopsis thaliana]
16180	GM_M15_B2_H08_MF	g507910	BLASTN	475	7e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16181	GM_M15_B2_H08_MR	g507910	BLASTN	547	4e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16182	GM_M15_B2_H09_MR	g2114242	BLASTN	378	5e-10	65	Human (lambda) DNA for immunoglobulin light chain
16183	GM_M15_B2_H10_MF	g507910	BLASTN	364	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16184	GM_M15_B2_H10_MR	g905361	BLASTX	677	7e-66	94	(U22103) gag-protease polyprotein [Glycine max]
16185	GM_M16_A1_A07_MR	g2275207	BLASTX	295	2e-25	52	(AC002337) hypothetical protein [Arabidopsis thaliana]
16186	GM_M16_A1_A11_MF	g2522227	BLASTX	164	4e-11	46	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16187	GM_M16_A1_B01_MF	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16188	GM_M16_A1_B01_MR	g3777527	BLASTX	709	5e-68	97	(AF053008) gag-pol polyprotein [Glycine max]
16189	GM_M16_A1_B05_MR	g2506938	BLASTX	171	4e-17	62	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST
16190	GM_M16_A1_B07_MR	g2995405	BLASTX	307	2e-25	52	(Y12432) polyprotein [Ananas comosus]
16191	GM_M16_A1_C01_MR	g507910	BLASTN	587	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16192	GM_M16_A1_C03_MR	g4063760	BLASTX	238	6e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16193	GM_M16_A1_C08_MR	g454847	BLASTN	377	4e-10	69	Glycine max ribosomal protein S11 gene, complete cds
16194	GM_M16_A1_C09_MR	g4063760	BLASTX	500	7e-46	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16195	GM_M16_A1_D08_MR	g3650039	BLASTX	280	7e-23	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16196	GM_M16_A1_D10_MF	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16197	GM_M16_A1_D10_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16198	GM_M16_A1_D12_MF	g507910	BLASTN	662	3e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
16199	GM_M16_A1_D12_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16200	GM_M16_A1_E02_MF	g2522228	BLASTX	97	9e-10	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
16201	GM_M16_A1_E03_MF	g3142328	BLASTN	428	2e-12	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16202	GM_M16_A1_E05_MR	g2344891	BLASTX	167	6e-11	37	(AC002388) hypothetical protein [Arabidopsis thaliana]
16203	GM_M16_A1_E06_MF	g3885341	BLASTX	149	2e-10	32	(AC005623) unknown protein [Arabidopsis thaliana]
16204	GM_M16_A1_E10_MF	g2618704	BLASTX	170	3e-11	83	(AC002510) putative thioredoxin reductase [Arabidopsis thaliana]
16205	GM_M16_A1_E12_MR	g507910	BLASTN	406	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16206	GM_M16_A1_G02_MF	g3869069	BLASTN	636	1e-21	68	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
16207	GM_M16_A1_G10_MR	g4038056	BLASTX	201	3e-30	58	(AC005897) putative transposon [Arabidopsis thaliana]
16208	GM_M16_A1_G12_MF	g218269	BLASTX	364	1e-32	85	(D12839) reverse transcriptase [Glycine max]
16209	GM_M16_A1_G12_MR	g2462056	BLASTX	284	3e-24	49	(Y13388) reverse transcriptase [Antirrhinum majus]
16210	GM_M16_A1_H02_MR	g3142328	BLASTN	527	7e-17	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16211	GM_M16_A1_H03_MF	g4063756	BLASTN	468	4e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16212	GM_M16_A1_H03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16213	GM_M16_A1_H05_MF	g3449327	BLASTN	378	5e-10	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
16214	GM_M16_A1_H05_MR	g1737492	BLASTX	147	1e-10	62	(U81318) poly(A)-binding protein [Triticum aestivum]
16215	GM_M16_A1_H08_MF	g3319362	BLASTX	266	5e-21	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16216	GM_M16_A1_H09_MR	g4038056	BLASTX	393	1e-34	54	(AC005897) putative transposon [Arabidopsis thaliana]
16217	GM_M16_A1_H10_MR	g3930515	BLASTX	121	4e-13	47	(AF059674) putative gag protein [Nicotiana tabacum]
16218	GM_M16_A1_H11_MF	g2191130	BLASTX	162	3e-10	40	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]
16219	GM_M16_A2_A04_MF	g1708710	BLASTX	272	6e-23	45	(U60069) 11.pep [Solanum tuberosum]
16220	GM_M16_A2_A04_MR	g2244866	BLASTX	187	3e-12	41	(Z97337) hypothetical protein [Arabidopsis thaliana]
16221	GM_M16_A2_A07_MR	g507910	BLASTN	575	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16222	GM_M16_A2_A10_MF	g2129618	BLASTX	179	8e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16223	GM_M16_A2_A10_MR	g629693	BLASTX	287	1e-27	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16224	GM_M16_A2_A11_MF	g507910	BLASTN	475	7e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16225	GM_M16_A2_B04_MR	g2570066	BLASTN	259	4e-11	78	Pisum sativum mRNA for second sucrose synthase.
16226	GM_M16_A2_B06_MR	g1236949	BLASTX	354	1e-41	83	(U50075) lipoxygenase L-5 [Glycine max]
16227	GM_M16_A2_B09_MR	g3930515	BLASTX	105	5e-09	47	(AF059674) putative gag protein [Nicotiana tabacum]
16228	GM_M16_A2_B10_MF	g130582	BLASTX	353	4e-30	60	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16229	GM_M16_A2_B10_MR	g4063760	BLASTX	376	1e-32	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16230	GM_M16_A2_B12_MF	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16231	GM_M16_A2_C02_MF	g130582	BLASTX	297	4e-24	53	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16232	GM_M16_A2_C05_MF	g4038056	BLASTX	305	3e-25	50	(AC005897) putative transposon [Arabidopsis thaliana]
16233	GM_M16_A2_C07_MF	g3777527	BLASTX	599	3e-56	95	(AF053008) gag-pol polyprotein [Glycine max]
16234	GM_M16_A2_C07_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16235	GM_M16_A2_C12_MR	g3142328	BLASTN	1678	3e-69	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16236	GM_M16_A2_D02_MR	g1666236	BLASTX	200	5e-15	30	(U76261) unknown [Hordeum vulgare]
16237	GM_M16_A2_D04_MR	g507910	BLASTN	601	1e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
16238	GM_M16_A2_D07_MR	g3142328	BLASTN	973	4e-37	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16239	GM_M16_A2_D11_MR	g2809243	BLASTX	150	5e-10	59	(AC002560) F21B7.12 [Arabidopsis thaliana]
16240	GM_M16_A2_D12_MF	g4038056	BLASTX	351	3e-30	55	(AC005897) putative transposon [Arabidopsis thaliana]
16241	GM_M16_A2_E01_MF	g2801423	BLASTN	383	3e-10	65	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
16242	GM_M16_A2_E04_MF	g18559	BLASTN	885	4e-33	76	G.max gene for catalase
16243	GM_M16_A2_E06_MF	g3935141	BLASTX	159	4e-10	56	(AC005106) T25N20.5 [Arabidopsis thaliana]
16244	GM_M16_A2_E08_MR	g2995405	BLASTX	212	2e-15	44	(Y12432) polyprotein [Ananas comosus]
16245	GM_M16_A2_E12_MF	g2914706	BLASTX	135	4e-16	55	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
16246	GM_M16_A2_F01_MF	g2443320	BLASTX	242	3e-18	42	(D85597) polyprotein [Oryza australiensis]
16247	GM_M16_A2_F02_MF	g3063469	BLASTX	182	5e-12	47	(AC003981) F22O13.31 [Arabidopsis thaliana]
16248	GM_M16_A2_F03_MF	g3599418	BLASTN	512	3e-16	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
16249	GM_M16_A2_F04_MR	g3176673	BLASTX	110	4e-15	77	(AC003671) Similar to serine/threonine kinase gb Y12531 from Brassica oleracea. [Arabidopsis thaliana]
16250	GM_M16_A2_F06_MF	g3142328	BLASTN	672	2e-23	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16251	GM_M16_A2_F07_MF	g2708743	BLASTX	154	7e-09	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16252	GM_M16_A2_F10_MR	g2655098	BLASTX	283	2e-23	73	(AF023472) peptide transporter [Hordeum vulgare]
16253	GM_M16_A2_F11_MF	g2522226	BLASTN	568	9e-19	64	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
16254	GM_M16_A2_G01_MR	g2522227	BLASTX	210	2e-16	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16255	GM_M16_A2_G02_MF	g1769898	BLASTX	284	2e-23	75	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16256	GM_M16_A2_G05_MF	g3287696	BLASTX	309	8e-26	46	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
16257	GM_M16_A2_G12_MF	g3777527	BLASTX	595	8e-56	97	(AF053008) gag-pol polyprotein [Glycine max]
16258	GM_M16_A2_H02_MF	g1769898	BLASTX	132	8e-11	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16259	GM_M16_A2_H05_MF	g4063760	BLASTX	162	7e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16260	GM_M16_A2_H07_MF	g100484	BLASTX	355	7e-31	60	hypothetical protein - garden snapdragon
16261	GM_M16_A2_H09_MR	g1853970	BLASTX	268	2e-21	62	(D88122) CPRD46 protein [Vigna unguiculata]
16262	GM_M16_B1_A05_MR	g3510505	BLASTX	266	7e-21	39	(AF030881) pol polyprotein [Fugu rubripes]
16263	GM_M16_B1_B01_MR	g130592	BLASTX	184	2e-12	40	ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE ; ENDONUCLEASE; REVERSE TRANSCRIPTASE] >gi 75491 pir QQCV5 hypothetical protein 5 - cauliflower mosaic virus (strains Strasbourg, CM1841 and D/H) >gi 58826 (V00141) reading frame (V) [Cauliflower mosaic virus]
16264	GM_M16_B1_B11_MR	g3776007	BLASTX	103	7e-09	53	(AJ010467) RNA helicase [Arabidopsis thaliana]
16265	GM_M16_B1_C04_MR	g2924257	BLASTN	398	6e-11	66	Tobacco chloroplast genome DNA
16266	GM_M16_B1_C08_MR	g1666236	BLASTX	179	1e-12	30	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16267	GM_M16_B1_C11_MR	g3650039	BLASTX	235	5e-18	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16268	GM_M16_B1_D02_MR	g2827535	BLASTX	246	4e-20	51	(AL021633) hypothetical protein [Arabidopsis thaliana]
16269	GM_M16_B1_D11_MR	g3021268	BLASTX	369	7e-32	54	(AL022347) putative protein [Arabidopsis thaliana]
16270	GM_M16_B1_E01_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16271	GM_M16_B1_E03_MR	g507910	BLASTN	620	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence
16272	GM_M16_B1_F01_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16273	GM_M16_B1_F07_MR	g2129709	BLASTX	171	1e-10	36	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
16274	GM_M16_B1_G02_MR	g3142328	BLASTN	984	1e-37	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16275	GM_M16_B1_G06_MR	g507910	BLASTN	394	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16276	GM_M16_B1_G07_MR	g3947839	BLASTN	558	4e-18	66	Human DNA sequence from clone 569D19 on chromosome 22q13.1. Contains a novel gene similar to mouse Ras, Dexamethasone-induced 1 (Ras-related protein, RASD1, DEXRAS1) and the last exon of the MB gene for Myoglobin. Cont...
16277	GM_M16_B1_H03_MR	g3777527	BLASTX	593	1e-55	94	(AF053008) gag-pol polyprotein [Glycine max]
16278	GM_M16_B1_H06_MR	g3930515	BLASTX	125	2e-13	50	(AF059674) putative gag protein [Nicotiana tabacum]
16279	GM_M16_B1_H07_MR	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16280	GM_M16_B2_A04_MF	g507910	BLASTN	379	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16281	GM_M16_B2_A04_MR	g507910	BLASTN	352	3e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16282	GM_M16_B2_A07_MR	g3386620	BLASTX	346	4e-30	58	(AC004665) hypothetical protein [Arabidopsis thaliana]
16283	GM_M16_B2_A11_MR	g4063760	BLASTX	329	2e-35	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16284	GM_M16_B2_B02_MF	g4063770	BLASTX	126	7e-11	35	(AB004906) transposase [Ipomoea purpurea]
16285	GM_M16_B2_B06_MR	g629693	BLASTX	181	3e-16	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16286	GM_M16_B2_C02_MR	g3142328	BLASTN	1143	7e-45	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16287	GM_M16_B2_C05_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16288	GM_M16_B2_C09_MF	g507910	BLASTN	442	2e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16289	GM_M16_B2_C09_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16290	GM_M16_B2_C10_MR	g3283026	BLASTX	270	1e-21	40	putative transposase [Arabidopsis thaliana]
16291	GM_M16_B2_C12_MF	g3777527	BLASTX	276	8e-22	44	(AF053008) gag-pol polyprotein [Glycine max]
16292	GM_M16_B2_D02_MF	g4063760	BLASTX	192	5e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16293	GM_M16_B2_D05_MF	g629693	BLASTX	374	9e-34	53	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16294	GM_M16_B2_D05_MR	g3377834	BLASTX	151	6e-09	29	(AF075598) No definition line found [Arabidopsis thaliana]
16295	GM_M16_B2_E05_MF	g905361	BLASTX	124	3e-10	32	(U22103) gag-protease polyprotein [Glycine max]
16296	GM_M16_B2_E05_MR	g13563	BLASTN	388	1e-10	64	Yeast mitochondrial aap1 gene for ATPase subunit 8
16297	GM_M16_B2_E06_MR	g3510505	BLASTX	135	1e-12	34	(AF030881) pol polyprotein [Fugu rubripes]
16298	GM_M16_B2_E12_MR	g2827715	BLASTX	240	3e-18	40	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
16299	GM_M16_B2_F03_MR	g2194136	BLASTX	259	4e-20	39	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
16300	GM_M16_B2_F06_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16301	GM_M16_B2_F09_MF	g3645899	BLASTX	197	8e-18	47	(U68408) 5' end not determined experimentally [Zea mays]
16302	GM_M16_B2_F10_MR	g3777527	BLASTX	684	3e-65	94	(AF053008) gag-pol polyprotein [Glycine max]
16303	GM_M16_B2_G04_MF	g18559	BLASTN	1549	3e-63	90	G.max gene for catalase
16304	GM_M16_B2_G04_MR	g2708743	BLASTX	123	6e-11	33	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16305	GM_M16_B2_G05_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16306	GM_M16_B2_G06_MF	g3810596	BLASTX	129	1e-13	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16307	GM_M16_B2_G06_MR	g18559	BLASTN	990	7e-38	76	G.max gene for catalase
16308	GM_M16_B2_G07_MF	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16309	GM_M16_B2_G10_MR	g18559	BLASTN	1201	2e-47	86	G.max gene for catalase
16310	GM_M16_B2_G11_MR	g3810596	BLASTX	215	1e-15	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16311	GM_M16_B2_H01_MR	g3810596	BLASTX	320	7e-28	54	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16312	GM_M16_B2_H02_MF	g4115559	BLASTX	251	4e-20	41	(AB013596) UDP-glucose:anthocysnin 5-O-glucosyltransferase [Perilla frutescens]
16313	GM_M16_B2_H02_MR	g2522230	BLASTX	304	3e-26	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16314	GM_M16_B2_H11_MF	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16315	GM_M16_B2_H11_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16316	GM_M17_A1_B01_MF	g719291	BLASTX	404	2e-35	59	(U19134) unknown [Arabidopsis thaliana] gi 1095007 prf 2107236A SABRE gene [Arabidopsis thaliana]
16317	GM_M17_A1_B02_MF	g2145358	BLASTX	161	4e-21	68	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16318	GM_M17_A1_C03_MF	g3777527	BLASTX	236	2e-17	37	(AF053008) gag-pol polyprotein [Glycine max]
16319	GM_M17_A1_C04_MF	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16320	GM_M17_A1_C10_MF	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16321	GM_M17_A1_D02_MF	g3510347	BLASTN	441	7e-13	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
16322	GM_M17_A1_D06_MF	g2815245	BLASTN	400	5e-18	80	C.arietinum mRNA for class I type 2 metallothionein (clone: CanMT-2)
16323	GM_M17_A1_D10_MF	g1142702	BLASTN	457	4e-14	74	Glycine max satellite STR120-A.4.
16324	GM_M17_A1_D12_MF	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16325	GM_M17_A1_E06_MF	g3097320	BLASTN	483	8e-15	73	Glycine max gene for Bd 30K, complete cds
16326	GM_M17_A1_E07_MF	g2351062	BLASTN	729	7e-26	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20
16327	GM_M17_A1_E12_MF	g4063760	BLASTX	225	1e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16328	GM_M17_A1_F01_MF	g719291	BLASTX	445	6e-40	63	(U19134) unknown [Arabidopsis thaliana] gi 1095007 prf 2107236A SABRE gene [Arabidopsis thaliana]
16329	GM_M17_A1_F02_MF	g130582	BLASTX	391	3e-34	60	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16330	GM_M17_A1_F03_MF	g3777527	BLASTX	234	2e-42	71	(AF053008) gag-pol polyprotein [Glycine max]
16331	GM_M17_A1_G02_MF	g3777527	BLASTX	655	3e-62	98	(AF053008) gag-pol polyprotein [Glycine max]
16332	GM_M17_A1_G03_MF	g507910	BLASTN	412	5e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16333	GM_M17_A1_G05_MF	g3097320	BLASTN	424	4e-12	67	Glycine max gene for Bd 30K, complete cds
16334	GM_M17_A1_G07_MF	g3935148	BLASTX	220	2e-19	59	(AC005106) T25N20.12 [Arabidopsis thaliana]
16335	GM_M17_A1_G09_MF	g2264320	BLASTN	419	7e-12	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
16336	GM_M17_A1_G10_MF	g3249098	BLASTX	225	4e-18	44	(AC003114) ESTs gb T04610, gb N38459, gb T45174, gb R30481 and gb N64971 come from this gene. [Arabidopsis thaliana]
16337	GM_M17_A1_H07_MF	g1370171	BLASTN	591	1e-20	77	L.japonicus mRNA for small GTP-binding protein, RAB1X.
16338	GM_M17_A1_H08_MF	g4063756	BLASTN	461	9e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16339	GM_M17_A2_A01_MF	g2995405	BLASTX	145	4e-10	37	(Y12432) polyprotein [Ananas comosus]
16340	GM_M17_A2_A07_MR	g2995405	BLASTX	258	3e-24	54	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16341	GM_M17_A2_A09_MR	g3142328	BLASTN	1138	1e-44	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16342	GM_M17_A2_A10_MR	g3281850	BLASTX	276	1e-22	94	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
16343	GM_M17_A2_A11_MR	g3510264	BLASTX	378	4e-34	55	(AC005310) hypothetical protein, 5' partial [Arabidopsis thaliana]
16344	GM_M17_A2_B03_MR	g2769655	BLASTN	463	7e-14	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
16345	GM_M17_A2_B05_MR	g4063760	BLASTX	198	1e-13	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16346	GM_M17_A2_B06_MF	g2443357	BLASTX	294	7e-28	70	(AB004293) SigB [Arabidopsis thaliana] gi 2597831 gnl PID e1169752 (Y15362) sigma factor [Arabidopsis thaliana] gi 2879922 gnl PID d1025747 (AB004820) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] gi 3063440 (AC003981) F22O13.2 [Arabidopsis thaliana]
16347	GM_M17_A2_B08_MF	g507910	BLASTN	498	7e-16	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16348	GM_M17_A2_B11_MF	g507910	BLASTN	738	1e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
16349	GM_M17_A2_B11_MR	g507910	BLASTN	588	6e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
16350	GM_M17_A2_B12_MF	g1066857	BLASTX	258	4e-42	87	(L48995) acetyl-CoA carboxylase [Glycine max]
16351	GM_M17_A2_C01_MF	g2769655	BLASTN	381	4e-10	66	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
16352	GM_M17_A2_C01_MR	g2792208	BLASTX	217	4e-17	44	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
16353	GM_M17_A2_C05_MF	g100484	BLASTX	364	7e-32	61	hypothetical protein - garden snapdragon
16354	GM_M17_A2_C08_MR	g3746069	BLASTX	173	6e-11	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
16355	GM_M17_A2_C09_MR	g100484	BLASTX	260	1e-27	55	hypothetical protein - garden snapdragon
16356	GM_M17_A2_C10_MR	g2764526	BLASTN	466	5e-14	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
16357	GM_M17_A2_D02_MR	g2582971	BLASTX	164	7e-18	66	(D83711) TKRP125 [Nicotiana tabacum]
16358	GM_M17_A2_D04_MF	g3947439	BLASTX	151	6e-09	26	(AC005034) gc-rich sequence dna-binding factor [Homo sapiens]
16359	GM_M17_A2_D06_MF	g3097320	BLASTN	1123	8e-44	80	Glycine max gene for Bd 30K, complete cds
16360	GM_M17_A2_D09_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16361	GM_M17_A2_D09_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16362	GM_M17_A2_D10_MF	g130582	BLASTX	366	2e-31	53	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16363	GM_M17_A2_E04_MR	g2914758	BLASTN	361	3e-09	63	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
16364	GM_M17_A2_E05_MF	g507910	BLASTN	547	4e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
16365	GM_M17_A2_E05_MR	g905361	BLASTX	528	4e-50	78	(U22103) gag-protease polyprotein [Glycine max]
16366	GM_M17_A2_E07_MR	g130582	BLASTX	381	4e-33	60	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16367	GM_M17_A2_E08_MF	g1666236	BLASTX	169	1e-11	30	(U76261) unknown [Hordeum vulgare]
16368	GM_M17_A2_E10_MF	g3142328	BLASTN	1688	1e-69	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16369	GM_M17_A2_E11_MF	g3142328	BLASTN	651	2e-22	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16370	GM_M17_A2_F01_MF	g2316016	BLASTX	239	7e-18	75	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
16371	GM_M17_A2_F05_MR	g131754	BLASTX	144	2e-09	49	PPLZ02 PROTEIN gi 99973 pir S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine gi 19507 (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]
16372	GM_M17_A2_F08_MR	g1663551	BLASTX	216	5e-17	39	(U55810) disease resistance protein homolog [Glycine max]
16373	GM_M17_A2_G02_MR	g507910	BLASTN	486	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16374	GM_M17_A2_G03_MF	g2213598	BLASTX	200	1e-13	34	(AC000348) T7N9.18 [Arabidopsis thaliana]
16375	GM_M17_A2_G03_MR	g3970928	BLASTN	320	2e-09	62	Homo sapiens chromosome 19, cosmid F14319, complete sequence [Homo sapiens]
16376	GM_M17_A2_G04_MR	g1663537	BLASTX	131	2e-16	46	(U55803) disease resistance protein homolog [Glycine max]
16377	GM_M17_A2_G11_MF	g3777527	BLASTX	192	7e-13	38	(AF053008) gag-pol polyprotein [Glycine max]
16378	GM_M17_A2_H02_MR	g507910	BLASTN	486	2e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16379	GM_M17_A2_H04_MF	g507910	BLASTN	556	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
16380	GM_M17_A2_H10_MF	g18695	BLASTN	449	2e-13	76	Soybean nodulin 22 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16381	GM_M17_B1_A05_MR	g1297184	BLASTN	482	1e-14	66	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, complete cds.
16382	GM_M17_B1_A08_MF	g2760167	BLASTN	479	1e-14	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]
16383	GM_M17_B1_A09_MF	g3645899	BLASTX	206	6e-24	50	(U68408) 5' end not determined experimentally [Zea mays]
16384	GM_M17_B1_B02_MF	g18559	BLASTN	814	7e-30	73	G.max gene for catalase
16385	GM_M17_B1_B03_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16386	GM_M17_B1_B04_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16387	GM_M17_B1_B08_MF	g1066857	BLASTX	228	4e-36	89	(L48995) acetyl-CoA carboxylase [Glycine max]
16388	GM_M17_B1_C12_MR	g4063760	BLASTX	366	1e-31	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16389	GM_M17_B1_E01_MF	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16390	GM_M17_B1_E01_MR	g905361	BLASTX	329	3e-28	77	(U22103) gag-protease polyprotein [Glycine max]
16391	GM_M17_B1_E02_MF	g2654868	BLASTX	177	3e-20	83	(AF015301) RbohAp108 [Arabidopsis thaliana]
16392	GM_M17_B1_E02_MR	g2979574	BLASTN	465	6e-14	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
16393	GM_M17_B1_E03_MF	g4063760	BLASTX	294	7e-24	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16394	GM_M17_B1_E04_MR	g4063760	BLASTX	164	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16395	GM_M17_B1_E09_MF	g18559	BLASTN	648	2e-22	72	G.max gene for catalase
16396	GM_M17_B1_E12_MF	g2655227	BLASTN	509	3e-16	74	Zea mays Ty3/gypsy-type retrotransposon reverse transcriptase/integrase polyprotein pseudogene, partial sequence.
16397	GM_M17_B1_F01_MF	g18559	BLASTN	952	4e-36	77	G.max gene for catalase
16398	GM_M17_B1_F04_MF	g4063760	BLASTX	237	8e-18	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16399	GM_M17_B1_F06_MF	g905361	BLASTX	183	2e-12	35	(U22103) gag-protease polyprotein [Glycine max]
16400	GM_M17_B1_F06_MR	g99922	BLASTX	298	7e-34	59	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA), pid:e150225 [Glycine max]
16401	GM_M17_B1_F07_MF	g2245104	BLASTX	199	8e-19	39	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
16402	GM_M17_B1_F07_MR	g2129618	BLASTX	226	8e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16403	GM_M17_B1_F09_MR	g170606	BLASTN	438	5e-13	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
16404	GM_M17_B1_F11_MR	g2979597	BLASTN	388	2e-10	63	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
16405	GM_M17_B1_G12_MF	g3377813	BLASTX	224	7e-18	69	(AF076275) No definition line found [Arabidopsis thaliana]
16406	GM_M17_B2_A01_MF	g3935157	BLASTX	269	9e-29	75	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16407	GM_M17_B2_A02_MF	g3142328	BLASTN	435	1e-12	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16408	GM_M17_B2_A04_MR	g905361	BLASTX	287	1e-23	71	(U22103) gag-protease polyprotein [Glycine max]
16409	GM_M17_B2_A06_MF	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16410	GM_M17_B2_A06_MR	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16411	GM_M17_B2_A08_MF	g1663537	BLASTX	333	2e-29	54	(U55803) disease resistance protein homolog [Glycine max]
16412	GM_M17_B2_A12_MF	g905361	BLASTX	498	7e-47	91	(U22103) gag-protease polyprotein [Glycine max]
16413	GM_M17_B2_A12_MR	g3142328	BLASTN	977	3e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16414	GM_M17_B2_B05_MR	g18695	BLASTN	427	2e-12	71	Soybean nodulin 22 gene
16415	GM_M17_B2_B10_MF	g3319362	BLASTX	332	4e-28	52	(AF077408) contains similarity to reverse transcriptase (Pfam. rvt.hmm, score 19.29) [Arabidopsis thaliana]
16416	GM_M17_B2_B12_MR	g629693	BLASTX	139	9e-12	48	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16417	GM_M17_B2_C05_MF	g507910	BLASTN	571	3e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
16418	GM_M17_B2_C05_MR	g4092471	BLASTN	493	3e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
16419	GM_M17_B2_C06_MR	g18559	BLASTN	1171	4e-46	81	G.max gene for catalase
16420	GM_M17_B2_C09_MR	g3378224	BLASTX	334	2e-29	73	(AJ001213) reverse transcriptase [Lycopersicon chilense]
16421	GM_M17_B2_D01_MR	g3777527	BLASTX	207	7e-17	33	(AF053008) gag-pol polyprotein [Glycine max]
16422	GM_M17_B2_D03_MF	g3142328	BLASTN	1013	6e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16423	GM_M17_B2_D03_MR	g3097320	BLASTN	664	5e-23	78	Glycine max gene for Bd 30K, complete cds
16424	GM_M17_B2_D05_MF	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16425	GM_M17_B2_D05_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16426	GM_M17_B2_E04_MF	g3142328	BLASTN	890	2e-33	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16427	GM_M17_B2_E04_MR	g2864621	BLASTX	163	1e-10	33	hypothetical protein [Arabidopsis thaliana]
16428	GM_M17_B2_E11_MF	g2252823	BLASTN	364	2e-09	66	Arabidopsis thaliana BAC IG005I10
16429	GM_M17_B2_E12_MF	g18559	BLASTN	527	7e-17	86	G.max gene for catalase
16430	GM_M17_B2_F07_MR	g3097320	BLASTN	1312	2e-52	81	Glycine max gene for Bd 30K, complete cds
16431	GM_M17_B2_F10_MR	g4115912	BLASTN	350	9e-09	64	Arabidopsis thaliana BAC F3H7
16432	GM_M17_B2_F12_MF	g3845074	BLASTN	406	3e-11	63	Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence
16433	GM_M17_B2_G04_MF	g4063760	BLASTX	427	4e-38	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16434	GM_M17_B2_G05_MF	g3142328	BLASTN	1777	8e-74	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16435	GM_M17_B2_G06_MR	g905361	BLASTX	684	1e-66	95	(U22103) gag-protease polyprotein [Glycine max]
16436	GM_M17_B2_G07_MF	g2995405	BLASTX	296	2e-24	56	(Y12432) polyprotein [Ananas comosus]
16437	GM_M17_B2_G10_MR	g507910	BLASTN	442	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16438	GM_M17_B2_G11_MF	g507910	BLASTN	442	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16439	GM_M17_B2_H01_MF	g3599418	BLASTN	356	4e-09	70	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
16440	GM_M17_B2_H03_MF	g3645899	BLASTX	146	1e-13	41	(U68408) 5' end not determined experimentally [Zea mays]
16441	GM_M17_B2_H09_MR	g2995405	BLASTX	374	1e-32	57	(Y12432) polyprotein [Ananas comosus]
16442	GM_M18_A1_A02_MF	g18559	BLASTN	879	8e-33	77	G.max gene for catalase
16443	GM_M18_A1_A02_MR	g2642158	BLASTX	179	2e-12	44	(AC003000) hypothetical protein [Arabidopsis thaliana]
16444	GM_M18_A1_A05_MR	g3142328	BLASTN	661	6e-23	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16445	GM_M18_A1_A07_MF	g13774	BLASTN	363	1e-09	63	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
16446	GM_M18_A1_A09_MR	g131754	BLASTX	150	5e-10	49	PPLZ02 PROTEIN gi 99973 pir S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine gi 19507 (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]
16447	GM_M18_A1_A10_MF	g4038056	BLASTX	222	2e-16	41	(AC005897) putative transposon [Arabidopsis thaliana]
16448	GM_M18_A1_A12_MR	g1142701	BLASTN	1358	5e-55	86	Glycine max satellite STR120-A.3.
16449	GM_M18_A1_B01_MR	g3097320	BLASTN	983	2e-37	76	Glycine max gene for Bd 30K, complete cds
16450	GM_M18_A1_B05_MR	g20861	BLASTN	362	2e-09	66	P.sativum retrotransposon
16451	GM_M18_A1_B07_MR	g4006827	BLASTX	301	4e-25	52	(AC005970) subtilisin-like protease [Arabidopsis thaliana]
16452	GM_M18_A1_C02_MR	g1167523	BLASTX	109	1e-11	35	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16453	GM_M18_A1_D01_MF	g1871182	BLASTX	189	4e-22	64	(U90439) phospholipase D isolog [Arabidopsis thaliana]
16454	GM_M18_A1_D05_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16455	GM_M18_A1_D10_MR	g3319351	BLASTX	415	1e-36	65	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16456	GM_M18_A1_D11_MF	g421960	BLASTX	161	3e-11	91	small nuclear ribonucleoprotein U2B" - potato gi 169589 (M72892) spliceosomal protein [Solanum tuberosum]
16457	GM_M18_A1_D11_MR	g100226	BLASTX	243	6e-19	44	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16458	GM_M18_A1_E08_MF	g2702273	BLASTX	150	5e-17	59	(AC003033) carrot B2 protein-like [Arabidopsis thaliana]
16459	GM_M18_A1_F06_MF	g4063770	BLASTX	178	9e-12	41	(AB004906) transposase [Ipomoea purpurea]
16460	GM_M18_A1_F07_MR	g1142701	BLASTN	1235	2e-49	85	Glycine max satellite STR120-A.3.
16461	GM_M18_A1_F08_MF	g4096078	BLASTN	362	3e-09	70	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]
16462	GM_M18_A1_F08_MR	g4063760	BLASTX	235	1e-18	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16463	GM_M18_A1_G08_MR	g131150	BLASTX	140	1e-15	66	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 gi 81515 pir S00445 photosystem I protein A2 - spinach chloroplast gi 12271 (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia oleracea] gi 225422 prf 1303218B gene psaB [Spinacia oleracea]
16464	GM_M18_A1_G11_MR	g1769898	BLASTX	368	2e-32	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16465	GM_M18_A1_H04_MF	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16466	GM_M18_A1_H07_MR	g2995405	BLASTX	524	6e-49	69	(Y12432) polyprotein [Ananas comosus]
16467	GM_M18_A1_H09_MR	g18559	BLASTN	709	4e-25	72	G.max gene for catalase
16468	GM_M18_A1_H10_MR	g2443320	BLASTX	305	5e-25	50	(D85597) polyprotein [Oryza australiensis]
16469	GM_M18_A1_H11_MR	g99729	BLASTX	138	2e-14	40	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
16470	GM_M18_A2_A02_MR	g131754	BLASTX	150	5e-10	49	PPLZ02 PROTEIN gi 99973 pir S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine gi 19507 (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]
16471	GM_M18_A2_B02_MR	g2462058	BLASTX	335	1e-29	48	(Y13389) reverse transcriptase [Antirrhinum majus]
16472	GM_M18_A2_B04_MF	g3097320	BLASTN	1002	2e-38	77	Glycine max gene for Bd 30K, complete cds
16473	GM_M18_A2_B09_MR	g3097320	BLASTN	579	4e-19	77	Glycine max gene for Bd 30K, complete cds
16474	GM_M18_A2_B10_MR	g905361	BLASTX	185	1e-12	30	(U22103) gag-protease polyprotein [Glycine max]
16475	GM_M18_A2_B12_MR	g4063760	BLASTX	287	4e-23	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16476	GM_M18_A2_C03_MF	g1066857	BLASTX	239	6e-35	97	(L48995) acetyl-CoA carboxylase [Glycine max]
16477	GM_M18_A2_C10_MF	g4063760	BLASTX	208	9e-15	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16478	GM_M18_A2_C10_MR	g4038056	BLASTX	202	3e-14	53	(AC005897) putative transposon [Arabidopsis thaliana]
16479	GM_M18_A2_C12_MR	g507910	BLASTN	394	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16480	GM_M18_A2_D05_MR	g1666236	BLASTX	212	2e-16	34	(U76261) unknown [Hordeum vulgare]
16481	GM_M18_A2_D06_MR	g3142328	BLASTN	1736	6e-72	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16482	GM_M18_A2_D10_MR	g3688600	BLASTX	107	2e-12	84	(AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16483	GM_M18_A2_E03_MR	g18559	BLASTN	976	3e-37	77	G.max gene for catalase
16484	GM_M18_A2_E04_MF	g3645899	BLASTX	138	3e-09	60	(U68408) 5' end not determined experimentally [Zea mays]
16485	GM_M18_A2_E04_MR	g2129618	BLASTX	256	5e-20	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16486	GM_M18_A2_E10_MR	g3548808	BLASTX	439	1e-40	61	(AC005313) unknown protein [Arabidopsis thaliana]
16487	GM_M18_A2_E11_MF	g507910	BLASTN	569	4e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16488	GM_M18_A2_F01_MF	g4063760	BLASTX	221	3e-17	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16489	GM_M18_A2_F02_MF	g3645899	BLASTX	334	3e-28	53	(U68408) 5' end not determined experimentally [Zea mays]
16490	GM_M18_A2_F04_MF	g1944188	BLASTN	625	9e-22	71	Soybean DNA for nodulin 35, partial cds
16491	GM_M18_A2_F06_MF	g1066857	BLASTX	215	2e-26	93	(L48995) acetyl-CoA carboxylase [Glycine max]
16492	GM_M18_A2_G02_MF	g3097320	BLASTN	530	6e-17	74	Glycine max gene for Bd 30K, complete cds
16493	GM_M18_A2_G04_MR	g18559	BLASTN	727	6e-26	86	G.max gene for catalase
16494	GM_M18_A2_G05_MF	g4038056	BLASTX	294	4e-24	54	(AC005897) putative transposon [Arabidopsis thaliana]
16495	GM_M18_A2_G06_MR	g2995405	BLASTX	236	2e-31	46	(Y12432) polyprotein [Ananas comosus]
16496	GM_M18_A2_G07_MF	g1431738	BLASTN	654	9e-23	75	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
16497	GM_M18_A2_G09_MF	g1769898	BLASTX	399	5e-36	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16498	GM_M18_A2_G11_MR	g2605909	BLASTX	162	4e-14	80	(AF029257) plasma membrane H+-ATPase [Kosteletzkya virginica]
16499	GM_M18_A2_G12_MR	g3777527	BLASTX	689	7e-66	97	(AF053008) gag-pol polyprotein [Glycine max]
16500	GM_M18_A2_H02_MR	g3776579	BLASTX	156	5e-09	64	(AC005388) Strong similarity to F22O13.22 gi 3063460 myosin homolog from A. thaliana BAC gb AC003981. [Arabidopsis thaliana]
16501	GM_M18_A2_H06_MR	g1813704	BLASTX	275	7e-22	43	(U82559) aldehyde oxidase 1 homolog [Lycopersicon esculentum]
16502	GM_M18_A2_H07_MR	g2088652	BLASTX	324	2e-28	78	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] gi 2351376 (U54561) eIF3-p47 homolog; homolog of human translation initiation factor eIF3 p47 subunit [Arabidopsis thaliana]
16503	GM_M18_A2_H11_MF	g3097320	BLASTN	703	8e-25	73	Glycine max gene for Bd 30K, complete cds
16504	GM_M18_A2_H12_MR	g3777527	BLASTX	687	1e-65	97	(AF053008) gag-pol polyprotein [Glycine max]
16505	GM_M18_B1_A02_MR	g3599418	BLASTN	988	8e-38	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
16506	GM_M18_B1_A03_MR	g2129618	BLASTX	198	8e-14	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16507	GM_M18_B1_A10_MF	g3445238	BLASTX	239	2e-19	63	(AL022347) putative protein [Arabidopsis thaliana] gi 3451059 gnl PID e1316746 (AL031326) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16508	GM_M18_B1_A10_MR	g3913067	BLASTX	199	5e-15	55	ALTERNATIVE OXIDASE 2 PRECURSOR >gi 1946336 (U87906) alternative oxidase [Glycine max]
16509	GM_M18_B1_B01_MF	g3142328	BLASTN	534	2e-33	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16510	GM_M18_B1_B03_MR	g507910	BLASTN	557	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16511	GM_M18_B1_B04_MF	g99729	BLASTX	212	2e-26	49	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
16512	GM_M18_B1_B05_MF	g4063760	BLASTX	166	6e-14	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16513	GM_M18_B1_B05_MR	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
16514	GM_M18_B1_B06_MF	g1170606	BLASTX	167	5e-21	68	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize gi 3114421 pdb 1ZAK A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) Atp:amp-Phosphotransferase, Transferase Mol_id: 1; Molecule: Adenylate Kinase; Chain: A, B; Ec: 2.7.4.3; Biological_u... gi 3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) Atp:amp-Phosphotransferase, Transferase Mol_id: 1; Molecule: Adenylate Kinase; Chain: A, B, Ec: 2.7.4.3; Biological_u...
16515	GM_M18_B1_B07_MF	g2626751	BLASTN	387	1e-19	63	Triticum aestivum retrotransposon Tar1, partial sequence.
16516	GM_M18_B1_B07_MR	g3695393	BLASTX	102	1e-09	47	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]
16517	GM_M18_B1_B08_MF	g3758836	BLASTN	349	1e-08	71	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
16518	GM_M18_B1_C02_MF	g3845268	BLASTN	374	7e-10	64	Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence
16519	GM_M18_B1_C07_MF	g343022	BLASTN	620	4e-21	80	Pea chloroplast photosystem II gene encoding the D2 and 44kd chlorophyll a-binding proteins, complete cds.
16520	GM_M18_B1_C07_MR	g3645899	BLASTX	333	4e-28	58	(U68408) 5' end not determined experimentally [Zea mays]
16521	GM_M18_B1_C08_MF	g2244749	BLASTX	211	1e-15	74	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
16522	GM_M18_B1_C09_MF	g2121303	BLASTN	473	3e-14	67	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
16523	GM_M18_B1_C12_MF	g3777527	BLASTX	507	2e-46	85	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16524	GM_M18_B1_D03_MR	g507910	BLASTN	602	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16525	GM_M18_B1_D04_MF	g3142328	BLASTN	983	1e-37	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16526	GM_M18_B1_D05_MR	g18695	BLASTN	377	4e-10	68	Soybean nodulin 22 gene
16527	GM_M18_B1_D08_MR	g18559	BLASTN	923	8e-35	74	G.max gene for catalase
16528	GM_M18_B1_D10_MF	g4063756	BLASTN	441	7e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16529	GM_M18_B1_D10_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16530	GM_M18_B1_D11_MF	g3269288	BLASTX	351	3e-31	70	(AL030978) putative protein [Arabidopsis thaliana]
16531	GM_M18_B1_E02_MF	g3097320	BLASTN	582	3e-19	73	Glycine max gene for Bd 30K, complete cds
16532	GM_M18_B1_E06_MF	g2129698	BLASTX	98	4e-15	70	protein kinase ATN1 (EC 2 7 1.-) - Arabidopsis thaliana gi 1054633 (X92728) protein kinase [Arabidopsis thaliana]
16533	GM_M18_B1_E07_MR	g905361	BLASTX	226	4e-17	41	(U22103) gag-protease polyprotein [Glycine max]
16534	GM_M18_B1_E10_MR	g3252807	BLASTX	239	2e-18	60	(AC004705) hypothetical protein [Arabidopsis thaliana]
16535	GM_M18_B1_F05_MF	g4063760	BLASTX	396	8e-35	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16536	GM_M18_B1_F07_MF	g3097320	BLASTN	874	2e-32	79	Glycine max gene for Bd 30K, complete cds
16537	GM_M18_B1_G01_MR	g2522227	BLASTX	213	1e-16	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16538	GM_M18_B1_G09_MF	g1346387	BLASTX	188	2e-13	87	KNOTTED-LIKE HOMEOBOX PROTEIN 3 gi 1045042 (X92392) KNAT3 homeobox protein [Arabidopsis thaliana]
16539	GM_M18_B1_G10_MF	g3097320	BLASTN	378	4e-10	72	Glycine max gene for Bd 30K, complete cds
16540	GM_M18_B1_G10_MR	g3645899	BLASTX	205	1e-23	51	(U68408) 5' end not determined experimentally [Zea mays]
16541	GM_M18_B1_G11_MF	g3947735	BLASTX	268	2e-21	49	(AJ009720) NL27 [Solanum tuberosum]
16542	GM_M18_B1_G12_MR	g4050011	BLASTN	436	1e-12	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
16543	GM_M18_B1_H01_MF	g1750376	BLASTX	201	5e-14	75	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]
16544	GM_M18_B1_H03_MR	g2443320	BLASTX	241	9e-20	43	(D85597) polyprotein [Oryza australiensis]
16545	GM_M18_B1_H08_MF	g4038056	BLASTX	331	4e-28	51	(AC005897) putative transposon [Arabidopsis thaliana]
16546	GM_M18_B2_A02_MF	g2129618	BLASTX	200	5e-14	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16547	GM_M18_B2_A03_MR	g1769897	BLASTX	158	2e-20	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16548	GM_M18_B2_A05_MF	g18559	BLASTN	605	7e-26	75	G.max gene for catalase
16549	GM_M18_B2_A06_MF	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16550	GM_M18_B2_A07_MR	g2129618	BLASTX	156	2e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16551	GM_M18_B2_A08_MR	g2252864	BLASTX	174	6e-12	55	(AF013294) Similar to receptor kinase [Arabidopsis thaliana]
16552	GM_M18_B2_B04_MF	g4038056	BLASTX	300	9e-25	46	(AC005897) putative transposon [Arabidopsis thaliana]
16553	GM_M18_B2_B07_MR	g2522226	BLASTN	509	4e-16	65	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
16554	GM_M18_B2_B12_MF	g2213632	BLASTX	179	2e-12	53	(AC000103) F21J9.24 [Arabidopsis thaliana]
16555	GM_M18_B2_C03_MF	g2497574	BLASTX	173	2e-12	41	THYMIDINE KINASE, MITOCHONDRIAL >gi 1905969 (U77088) thymidine kinase 2 [Homo sapiens]
16556	GM_M18_B2_C06_MR	g226407	BLASTX	177	3e-11	32	retrotransposon del1-46 [Lilium henryi]
16557	GM_M18_B2_C09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16558	GM_M18_B2_C11_MR	g3097836	BLASTN	418	8e-12	66	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
16559	GM_M18_B2_D05_MR	g2618698	BLASTX	128	1e-12	81	(AC002510) unknown protein [Arabidopsis thaliana]
16560	GM_M18_B2_D11_MF	g507910	BLASTN	430	8e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16561	GM_M18_B2_F01_MF	g3319362	BLASTX	229	4e-17	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16562	GM_M18_B2_F10_MR	g3142328	BLASTN	993	5e-38	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16563	GM_M18_B2_F11_MR	g1171046	BLASTX	156	1e-10	60	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493) metallothionein-like protein [Trifolium repens]
16564	GM_M18_B2_F12_MF	g3645899	BLASTX	235	3e-34	57	(U68408) 5' end not determined experimentally [Zea mays]
16565	GM_M18_B2_G02_MF	g18559	BLASTN	729	5e-26	77	G.max gene for catalase
16566	GM_M18_B2_G04_MR	g2522228	BLASTX	235	3e-36	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
16567	GM_M18_B2_G05_MR	g18559	BLASTN	410	1e-11	67	G.max gene for catalase
16568	GM_M18_B2_G06_MR	g3894201	BLASTX	240	1e-19	80	(AC005662) phosphatidylinositol-4-phosphate-5-kinase, 5' partial [Arabidopsis thaliana]
16569	GM_M18_B2_G12_MR	g3142328	BLASTN	1984	3e-83	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16570	GM_M18_B2_H01_MR	g3097320	BLASTN	1178	3e-46	82	Glycine max gene for Bd 30K, complete cds
16571	GM_M18_B2_H02_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16572	GM_M18_B2_H02_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16573	GM_M18_B2_H04_MF	g3097320	BLASTN	445	4e-13	72	Glycine max gene for Bd 30K, complete cds
16574	GM_M18_B2_H04_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16575	GM_M18_B2_H05_MF	g507910	BLASTN	374	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16576	GM_M18_B2_H07_MF	g294042	BLASTN	423	4e-12	65	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
16577	GM_M18_B2_H10_MR	g18559	BLASTN	1074	1e-41	76	G.max gene for catalase
16578	GM_M18_B2_H11_MF	g507910	BLASTN	367	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16579	GM_M18_B2_H11_MR	g4063760	BLASTX	393	2e-34	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16580	GM_M18_B2_H12_MR	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16581	GM_M19_A1_A07_MR	g905361	BLASTX	176	1e-11	30	(U22103) gag-protease polyprotein [Glycine max]
16582	GM_M19_A1_A12_MR	g169313	BLASTN	354	5e-09	58	Phaseolus vulgaris arcelin (arc) gene, complete cds.
16583	GM_M19_A1_B02_MF	g3445210	BLASTX	115	9e-14	57	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
16584	GM_M19_A1_B05_MF	g4063760	BLASTX	490	8e-45	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16585	GM_M19_A1_B05_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
16586	GM_M19_A1_B09_MF	g4063760	BLASTX	209	6e-16	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16587	GM_M19_A1_B10_MF	g4063760	BLASTX	275	7e-22	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16588	GM_M19_A1_B10_MR	g3046855	BLASTN	352	7e-09	71	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]
16589	GM_M19_A1_B11_MF	g342964	BLASTN	346	2e-09	59	paramecium species 5.311 mt dna dimer: replication init. region.
16590	GM_M19_A1_C03_MR	g905361	BLASTX	193	2e-13	30	(U22103) gag-protease polyprotein [Glycine max]
16591	GM_M19_A1_C05_MF	g3777527	BLASTX	672	4e-64	97	(AF053008) gag-pol polyprotein [Glycine max]
16592	GM_M19_A1_C06_MR	g3033389	BLASTX	233	1e-17	38	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16593	GM_M19_A1_C10_MF	g1769897	BLASTX	341	5e-33	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16594	GM_M19_A1_D02_MR	g3415116	BLASTN	367	1e-09	69	Arabidopsis thaliana villin 3 (VLN3) mRNA, complete cds
16595	GM_M19_A1_D03_MR	g1769898	BLASTX	387	1e-34	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16596	GM_M19_A1_D05_MF	g343801	BLASTN	304	5e-11	60	Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 5' flank.
16597	GM_M19_A1_D07_MF	g4063760	BLASTX	207	2e-16	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16598	GM_M19_A1_D08_MF	g531389	BLASTX	297	4e-24	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
16599	GM_M19_A1_D08_MR	g4038037	BLASTX	233	2e-17	35	(AC005936) hypothetical protein [Arabidopsis thaliana]
16600	GM_M19_A1_E01_MF	g505129	BLASTN	354	5e-09	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16601	GM_M19_A1_E05_MR	g2522228	BLASTX	445	3e-41	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
16602	GM_M19_A1_E07_MF	g905361	BLASTX	269	1e-21	64	(U22103) gag-protease polyprotein [Glycine max]
16603	GM_M19_A1_E07_MR	g3777527	BLASTX	555	2e-51	84	(AF053008) gag-pol polyprotein [Glycine max]
16604	GM_M19_A1_E09_MR	g4063760	BLASTX	354	3e-33	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16605	GM_M19_A1_E12_MF	g2522228	BLASTX	190	1e-13	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
16606	GM_M19_A1_E12_MR	g2244802	BLASTX	389	7e-34	50	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
16607	GM_M19_A1_F05_MF	g992916	BLASTN	384	3e-10	71	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
16608	GM_M19_A1_F06_MF	g3097320	BLASTN	1084	5e-42	83	Glycine max gene for Bd 30K, complete cds
16609	GM_M19_A1_F08_MF	g3810596	BLASTX	209	5e-15	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16610	GM_M19_A1_F11_MF	g3319345	BLASTX	159	1e-09	33	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
16611	GM_M19_A1_G04_MF	g3297823	BLASTX	182	4e-12	53	(AL031032) putative protein [Arabidopsis thaliana]
16612	GM_M19_A1_G05_MR	g3319351	BLASTX	305	5e-25	42	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16613	GM_M19_A1_G06_MR	g1142701	BLASTN	263	9e-20	76	Glycine max satellite STR120-A.3.
16614	GM_M19_A1_G09_MF	g4063760	BLASTX	252	2e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16615	GM_M19_A1_G11_MR	g3142328	BLASTN	1262	3e-50	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16616	GM_M19_A1_H01_MR	g3319351	BLASTX	311	1e-25	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16617	GM_M19_A1_H04_MF	g18683	BLASTN	393	8e-11	69	G.max N-20t gene
16618	GM_M19_A1_H04_MR	g100484	BLASTX	386	3e-34	55	hypothetical protein - garden snapdragon
16619	GM_M19_A1_H05_MR	g4063770	BLASTX	230	9e-29	54	(AB004906) transposase [Ipomoea purpurea]
16620	GM_M19_A1_H06_MF	g3894387	BLASTX	216	9e-16	46	(AF053995) Hcr2-0B [Lycopersicon esculentum]
16621	GM_M19_A1_H07_MF	g3283026	BLASTX	109	9e-19	38	putative transposase [Arabidopsis thaliana]
16622	GM_M19_A1_H10_MF	g2462056	BLASTX	285	3e-24	49	(Y13388) reverse transcriptase [Antirrhinum majus]
16623	GM_M19_A1_H10_MR	g18768	BLASTN	509	1e-16	66	Soybean Tgm6 transposable element 3' end
16624	GM_M19_A1_H11_MR	g3097320	BLASTN	469	3e-14	71	Glycine max gene for Bd 30K, complete cds
16625	GM_M19_A2_A03_MF	g170080	BLASTN	424	3e-12	70	Soybean seed lectin gene transposable element tgm1.
16626	GM_M19_A2_A07_MR	g2995405	BLASTX	302	5e-25	44	(Y12432) polyprotein [Ananas comosus]
16627	GM_M19_A2_A08_MR	g2995405	BLASTX	297	2e-24	45	(Y12432) polyprotein [Ananas comosus]
16628	GM_M19_A2_A11_MF	g4063760	BLASTX	376	1e-32	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16629	GM_M19_A2_B02_MF	g1707020	BLASTX	185	9e-15	36	(U78721) hypothetical protein [Arabidopsis thaliana]
16630	GM_M19_A2_B07_MF	g1931642	BLASTX	397	9e-36	61	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
16631	GM_M19_A2_B07_MR	g2501850	BLASTX	173	1e-11	91	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
16632	GM_M19_A2_C01_MF	g3860247	BLASTX	249	3e-29	95	(AC005824) unknown protein [Arabidopsis thaliana]

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16633	GM_M19_A2_C01_MR	g2586082	BLASTX	259	9e-33	57	(U72725) retrofit [Oryza longistaminata]
16634	GM_M19_A2_C08_MR	g18559	BLASTN	939	2e-35	74	G.max gene for catalase
16635	GM_M19_A2_D03_MF	g2522226	BLASTN	447	3e-13	62	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
16636	GM_M19_A2_D04_MR	g2522228	BLASTX	492	3e-46	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
16637	GM_M19_A2_D05_MR	g3033389	BLASTX	225	1e-16	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16638	GM_M19_A2_D06_MF	g2264320	BLASTN	496	2e-15	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
16639	GM_M19_A2_D07_MF	g18559	BLASTN	329	3e-10	70	G.max gene for catalase
16640	GM_M19_A2_D12_MF	g2114040	BLASTN	372	2e-10	69	Vigna vexillata DNA for TY1-copia-like retrotransposable element
16641	GM_M19_A2_E06_MF	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence
16642	GM_M19_A2_E07_MF	g3142328	BLASTN	882	5e-33	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16643	GM_M19_A2_F02_MR	g18559	BLASTN	1030	1e-39	75	G.max gene for catalase
16644	GM_M19_A2_F03_MF	g2764526	BLASTN	375	6e-10	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
16645	GM_M19_A2_F03_MR	g100484	BLASTX	264	4e-21	49	hypothetical protein - garden snapdragon
16646	GM_M19_A2_F04_MF	g3449326	BLASTN	429	2e-12	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]
16647	GM_M19_A2_F05_MF	g2522228	BLASTX	458	1e-42	69	(AB007466) reverse transcriptase-like protein [Vicia faba]
16648	GM_M19_A2_F06_MF	g1431738	BLASTN	564	1e-18	79	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
16649	GM_M19_A2_F10_MF	g2462828	BLASTX	358	9e-31	57	(AF000657) hypothetical protein [Arabidopsis thaliana]
16650	GM_M19_A2_F11_MF	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence
16651	GM_M19_A2_F11_MR	g507910	BLASTN	380	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16652	GM_M19_A2_G01_MR	g3319351	BLASTX	328	2e-27	48	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16653	GM_M19_A2_G03_MF	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16654	GM_M19_A2_G03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16655	GM_M19_A2_G04_MR	g1769898	BLASTX	125	9e-10	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16656	GM_M19_A2_G06_MF	g2317901	BLASTX	141	5e-21	72	(U89959) Similar to vesicle transport protein, PIR Accession Number A55931 [Arabidopsis thaliana]
16657	GM_M19_A2_G11_MR	g3777527	BLASTX	253	3e-23	47	(AF053008) gag-pol polyprotein [Glycine max]
16658	GM_M19_A2_H02_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence
16659	GM_M19_A2_H02_MR	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16660	GM_M19_A2_H05_MF	g1142703	BLASTN	301	1e-17	77	Glycine max satellite STR120-B.1.
16661	GM_M19_B1_A03_MR	g508826	BLASTN	470	3e-14	67	Drosophila melanogaster Oregon-R mitochondrial A+T region.
16662	GM_M19_B1_A10_MF	g4115365	BLASTX	215	6e-25	48	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
16663	GM_M19_B1_B01_MR	g3142328	BLASTN	1614	2e-66	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16664	GM_M19_B1_B04_MF	g1167523	BLASTX	257	2e-21	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16665	GM_M19_B1_B09_MF	g1769898	BLASTX	186	8e-13	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16666	GM_M19_B1_B12_MF	g505129	BLASTN	357	3e-09	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16667	GM_M19_B1_C01_MF	g100226	BLASTX	173	2e-25	79	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]
16668	GM_M19_B1_C08_MF	g4063770	BLASTX	179	7e-12	39	(AB004906) transposase [Ipomoea purpurea]
16669	GM_M19_B1_C09_MR	g1769898	BLASTX	372	5e-33	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16670	GM_M19_B1_C12_MF	g3688193	BLASTX	112	5e-11	67	(AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]
16671	GM_M19_B1_D01_MF	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
16672	GM_M19_B1_D04_MR	g3894387	BLASTX	240	3e-18	40	(AF053995) Her2-0B [Lycopersicon esculentum]
16673	GM_M19_B1_D06_MF	g3005576	BLASTX	167	6e-11	57	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]
16674	GM_M19_B1_D07_MR	g2995405	BLASTX	286	3e-23	53	(Y12432) polyprotein [Ananas comosus]
16675	GM_M19_B1_D10_MR	g3142328	BLASTN	1960	3e-82	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16676	GM_M19_B1_E01_MR	g3097320	BLASTN	458	1e-13	71	Glycine max gene for Bd 30K, complete cds
16677	GM_M19_B1_E02_MR	g1490417	BLASTX	405	6e-36	57	(U45025) 89B helicase [Drosophila melanogaster]
16678	GM_M19_B1_E03_MR	g3142328	BLASTN	498	1e-15	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16679	GM_M19_B1_E05_MR	g4063756	BLASTN	519	2e-16	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16680	GM_M19_B1_E07_MR	g170605	BLASTN	402	2e-11	60	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
16681	GM_M19_B1_E08_MR	g475598	BLASTX	444	8e-44	88	(U08382) BiP isoform C [Glycine max]
16682	GM_M19_B1_E10_MR	g4063760	BLASTX	289	2e-23	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16683	GM_M19_B1_E11_MR	g3142328	BLASTN	1627	6e-67	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16684	GM_M19_B1_F03_MR	g2980806	BLASTX	205	3e-21	62	(AL022197) putative protein [Arabidopsis thaliana]

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16685	GM_M19_B1_F04_MF	g1769899	BLASTX	320	5e-28	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16686	GM_M19_B1_F04_MR	g2827715	BLASTX	290	1e-23	44	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
16687	GM_M19_B1_F05_MR	g2708743	BLASTX	269	4e-21	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16688	GM_M19_B1_F07_MR	g3645899	BLASTX	315	3e-26	53	(U68408) 5' end not determined experimentally [Zea mays]
16689	GM_M19_B1_F11_MR	g1142703	BLASTN	283	2e-15	77	Glycine max satellite STR120-B.1.
16690	GM_M19_B1_G04_MF	g3386533	BLASTN	1555	8e-64	97	Glycine max mariner element Soymar1 transposase gene, complete cds
16691	GM_M19_B1_G07_MR	g1769897	BLASTX	189	2e-26	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16692	GM_M19_B1_G09_MF	g507910	BLASTN	345	6e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16693	GM_M19_B1_H03_MR	g2979597	BLASTN	431	2e-12	61	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
16694	GM_M19_B1_H05_MR	g3319351	BLASTX	297	4e-24	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16695	GM_M19_B1_H10_MR	g18559	BLASTN	613	5e-23	73	G.max gene for catalase
16696	GM_M19_B1_H12_MF	g3329366	BLASTX	378	6e-34	56	(AF031243) nodule-specific protein Nlj70 [Lotus japonicus]
16697	GM_M19_B2_A02_MR	g3930515	BLASTX	89	9e-09	40	(AF059674) putative gag protein [Nicotiana tabacum]
16698	GM_M19_B2_A03_MF	g3135269	BLASTX	131	3e-11	55	(AC003058) unknown protein [Arabidopsis thaliana]
16699	GM_M19_B2_A03_MR	g3097836	BLASTN	618	7e-21	68	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
16700	GM_M19_B2_A04_MR	g1769898	BLASTX	250	6e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16701	GM_M19_B2_A05_MR	g3097320	BLASTN	437	9e-13	70	Glycine max gene for Bd 30K, complete cds
16702	GM_M19_B2_A06_MR	g170606	BLASTN	770	2e-28	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
16703	GM_M19_B2_A08_MF	g1769898	BLASTX	300	4e-25	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16704	GM_M19_B2_A08_MR	g905361	BLASTX	197	6e-14	32	(U22103) gag-protease polyprotein [Glycine max]
16705	GM_M19_B2_A10_MR	g2104945	BLASTN	520	1e-16	64	Glycine max copia-like retrotransposon Tgmr, complete sequence
16706	GM_M19_B2_B02_MF	g99922	BLASTX	489	6e-46	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
16707	GM_M19_B2_B05_MF	g4063760	BLASTX	238	6e-18	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16708	GM_M19_B2_B05_MR	g2129618	BLASTX	206	1e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16709	GM_M19_B2_B06_MF	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16710	GM_M19_B2_B06_MR	g507910	BLASTN	358	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16711	GM_M19_B2_B07_MF	g4063760	BLASTX	217	1e-15	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16712	GM_M19_B2_B12_MR	g3786000	BLASTX	178	5e-12	47	(AC005499) hypothetical protein [Arabidopsis thaliana]
16713	GM_M19_B2_C01_MR	g18559	BLASTN	1011	8e-39	75	G.max gene for catalase
16714	GM_M19_B2_C02_MF	g99922	BLASTX	327	3e-42	83	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
16715	GM_M19_B2_C02_MR	g2160694	BLASTX	202	1e-14	75	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
16716	GM_M19_B2_C03_MR	g2996647	BLASTN	446	4e-13	62	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
16717	GM_M19_B2_C04_MF	g2129618	BLASTX	232	2e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16718	GM_M19_B2_C11_MF	g2463654	BLASTN	476	2e-14	66	Petunia vein clearing virus, complete genome
16719	GM_M19_B2_D01_MR	g2921211	BLASTX	158	3e-17	93	(AF026149) beta-ketoacyl-ACP synthase II [Perilla frutescens]
16720	GM_M19_B2_D02_MR	g18559	BLASTN	1024	2e-39	71	G.max gene for catalase
16721	GM_M19_B2_D04_MR	g3193292	BLASTX	111	2e-17	87	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]
16722	GM_M19_B2_D05_MR	g3513747	BLASTX	380	7e-33	53	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
16723	GM_M19_B2_D12_MR	g507910	BLASTN	638	3e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16724	GM_M19_B2_E02_MF	g2522230	BLASTX	268	1e-22	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16725	GM_M19_B2_E02_MR	g18559	BLASTN	755	3e-27	74	G.max gene for catalase
16726	GM_M19_B2_E03_MF	g13096	BLASTN	354	5e-09	60	Leishmania tarentolae maxicircle DNA fragment
16727	GM_M19_B2_E05_MR	g4038056	BLASTX	235	2e-33	54	(AC005897) putative transposon [Arabidopsis thaliana]
16728	GM_M19_B2_E08_MF	g2995405	BLASTX	199	2e-26	59	(Y12432) polyprotein [Ananas comosus]
16729	GM_M19_B2_E09_MR	g4063760	BLASTX	302	3e-26	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16730	GM_M19_B2_E10_MF	g3777527	BLASTX	184	5e-13	75	(AF053008) gag-pol polyprotein [Glycine max]
16731	GM_M19_B2_E12_MF	g4092471	BLASTN	428	3e-12	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
16732	GM_M19_B2_F06_MR	g2529665	BLASTX	179	2e-15	62	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]
16733	GM_M19_B2_G01_MF	g3097320	BLASTN	1217	4e-48	81	Glycine max gene for Bd 30K, complete cds
16734	GM_M19_B2_G02_MF	g2995405	BLASTX	459	7e-42	68	(Y12432) polyprotein [Ananas comosus]
16735	GM_M19_B2_G04_MF	g507910	BLASTN	380	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16736	GM_M19_B2_G04_MR	g507910	BLASTN	360	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16737	GM_M19_B2_G11_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16738	GM_M19_B2_H01_MR	g1755162	BLASTX	323	2e-28	57	(U75192) germin-like protein [Arabidopsis thaliana]
16739	GM_M19_B2_H02_MF	g507910	BLASTN	379	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16740	GM_M19_B2_H02_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16741	GM_M19_B2_H03_MR	g4063760	BLASTX	263	1e-20	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16742	GM_M19_B2_H06_MF	g3695395	BLASTX	235	5e-18	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
16743	GM_M19_B2_H10_MR	g3337395	BLASTN	420	6e-12	60	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
16744	GM_M19_B2_H11_MR	g3449334	BLASTN	318	3e-11	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
16745	GM_M19_B2_H12_MF	g4063760	BLASTX	229	6e-17	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16746	GM_M20_A1_A02_MF	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16747	GM_M20_A1_A02_MR	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16748	GM_M20_A1_A06_MF	g2804155	BLASTN	399	6e-11	66	Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat
16749	GM_M20_A1_A10_MF	g4063760	BLASTX	264	9e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16750	GM_M20_A1_B04_MF	g1666236	BLASTX	187	1e-13	30	(U76261) unknown [Hordeum vulgare]
16751	GM_M20_A1_B05_MF	g2522228	BLASTX	488	8e-46	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
16752	GM_M20_A1_B11_MF	g3142328	BLASTN	472	2e-14	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16753	GM_M20_A1_B11_MR	g3777527	BLASTX	483	2e-44	94	(AF053008) gag-pol polyprotein [Glycine max]
16754	GM_M20_A1_C05_MF	g507910	BLASTN	414	4e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16755	GM_M20_A1_C06_MF	g3319351	BLASTX	308	3e-25	57	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16756	GM_M20_A1_C08_MF	g2842493	BLASTX	167	7e-16	86	(AL021749) predicted protein [Arabidopsis thaliana]
16757	GM_M20_A1_C08_MR	g2522228	BLASTX	423	6e-39	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
16758	GM_M20_A1_D04_MF	g13096	BLASTN	394	7e-11	61	Leishmania tarentolae maxicircle DNA fragment
16759	GM_M20_A1_D06_MF	g507910	BLASTN	451	9e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16760	GM_M20_A1_D07_MR	g505129	BLASTN	351	7e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16761	GM_M20_A1_D08_MF	g2673914	BLASTX	186	6e-13	46	(AC002561) hypothetical protein [Arabidopsis thaliana]
16762	GM_M20_A1_D09_MF	g3142328	BLASTN	803	2e-29	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16763	GM_M20_A1_D11_MF	g3033389	BLASTX	189	8e-13	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16764	GM_M20_A1_D11_MR	g3894387	BLASTX	206	1e-14	40	(AF053995) Hcr2-0B [Lycopersicon esculentum]
16765	GM_M20_A1_E06_MF	g1171583	BLASTN	243	6e-09	68	P.falciparum complete gene map of plastid-like DNA (IR-A)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16766	GM_M20_A1_E10_MR	g18559	BLASTN	361	3e-09	67	G.max gene for catalase
16767	GM_M20_A1_E11_MR	g124226	BLASTX	171	9e-15	100	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) gi 100278 pir S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco gi 19702 (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]
16768	GM_M20_A1_E12_MR	g4063760	BLASTX	437	4e-39	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16769	GM_M20_A1_F07_MR	g3097320	BLASTN	560	3e-18	74	Glycine max gene for Bd 30K, complete cds
16770	GM_M20_A1_F09_MF	g1769897	BLASTX	219	2e-16	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16771	GM_M20_A1_F10_MF	g3097320	BLASTN	975	4e-37	79	Glycine max gene for Bd 30K, complete cds
16772	GM_M20_A1_G05_MF	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16773	GM_M20_A1_G07_MR	g1709919	BLASTX	564	5e-54	78	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) gi 439105 (L23834) glutamine phosphoribosylpyrophosphate amidotransferase [Vigna aconitifolia]
16774	GM_M20_A1_G08_MR	g2133292	BLASTX	167	3e-10	29	pol polyprotein homolog - fungus (Fusarium oxysporum) retrotransposon skippy gi 510697 (L34658) pol polyprotein [Fusarium oxysporum]
16775	GM_M20_A1_H04_MR	g3822225	BLASTX	131	1e-16	61	(AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]
16776	GM_M20_A1_H05_MR	g3645899	BLASTX	195	2e-13	43	(U68408) 5' end not determined experimentally [Zea mays]
16777	GM_M20_A1_H07_MF	g100484	BLASTX	313	3e-26	51	hypothetical protein - garden snapdragon
16778	GM_M20_A1_H09_MF	g18559	BLASTN	954	3e-36	77	G.max gene for catalase
16779	GM_M20_A1_H09_MR	g3777527	BLASTX	698	8e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
16780	GM_M20_A1_H10_MR	g3142328	BLASTN	577	4e-19	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16781	GM_M20_A1_H11_MR	g3924609	BLASTX	175	4e-11	47	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
16782	GM_M20_A2_A01_MR	g2129618	BLASTX	250	2e-19	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16783	GM_M20_A2_A02_MF	g3810596	BLASTX	151	8e-09	29	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16784	GM_M20_A2_A03_MR	g3142379	BLASTX	228	1e-17	58	(AF053008) envelope-like [Glycine max]
16785	GM_M20_A2_A06_MF	g3142328	BLASTN	984	4e-62	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16786	GM_M20_A2_A09_MF	g3097320	BLASTN	1008	1e-38	81	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
16787	GM_M20_A2_A10_MF	g2462134	BLASTX	170	2e-13	37	(Y13368) reverse transcriptase [Beta vulgaris]
16788	GM_M20_A2_A12_MF	g3892061	BLASTX	150	5e-09	27	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
16789	GM_M20_A2_B01_MR	g3687234	BLASTX	185	3e-12	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
16790	GM_M20_A2_B04_MF	g4038056	BLASTX	254	1e-29	49	(AC005897) putative transposon [Arabidopsis thaliana]
16791	GM_M20_A2_B06_MR	g3777527	BLASTX	191	4e-17	42	(AF053008) gag-pol polyprotein [Glycine max]
16792	GM_M20_A2_B07_MF	g3142328	BLASTN	359	3e-09	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16793	GM_M20_A2_B10_MF	g2129618	BLASTX	216	1e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16794	GM_M20_A2_B12_MF	g2245104	BLASTX	234	2e-17	37	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
16795	GM_M20_A2_C08_MF	g2253569	BLASTN	379	6e-11	67	Plasmodium falciparum microsatellite TA99 sequence
16796	GM_M20_A2_C09_MF	g18559	BLASTN	330	2e-11	71	G.max gene for catalase
16797	GM_M20_A2_C10_MR	g3063456	BLASTX	152	3e-09	41	(AC003981) F22O13.18 [Arabidopsis thaliana]
16798	GM_M20_A2_C12_MF	g3250687	BLASTX	264	4e-22	46	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
16799	GM_M20_A2_C12_MR	g2979540	BLASTN	564	2e-18	67	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]
16800	GM_M20_A2_D01_MR	g155854	BLASTN	447	1e-13	61	Babesia bigemina antigen (Bbg 1.1) mRNA, 3' end.
16801	GM_M20_A2_D04_MR	g2996647	BLASTN	476	2e-14	65	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
16802	GM_M20_A2_D05_MF	g3063438	BLASTN	367	1e-09	69	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
16803	GM_M20_A2_D07_MR	g2996647	BLASTN	462	8e-14	63	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
16804	GM_M20_A2_E02_MF	g3097320	BLASTN	648	3e-22	74	Glycine max gene for Bd 30K, complete cds
16805	GM_M20_A2_E02_MR	g3777527	BLASTX	151	5e-11	47	(AF053008) gag-pol polyprotein [Glycine max]
16806	GM_M20_A2_E03_MF	g18559	BLASTN	428	1e-17	69	G.max gene for catalase
16807	GM_M20_A2_F02_MF	g496384	BLASTN	483	5e-15	75	Tobacco mRNA for protein kinase NPK5, complete cds
16808	GM_M20_A2_F06_MR	g3915613	BLASTX	106	9e-09	38	PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B)
16809	GM_M20_A2_F11_MF	g2995405	BLASTX	416	3e-37	60	(Y12432) polyprotein [Ananas comosus]
16810	GM_M20_A2_F11_MR	g2995405	BLASTX	242	1e-18	45	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16811	GM_M20_A2_G01_MF	g478809	BLASTX	270	3e-22	40	protein kinase 6 (EC 2.7.1 -) - soybean gi 170047 (M67449) protein kinase [Glycine max] gi 444789 prf 1908223A protein kinase [Glycine max]
16812	GM_M20_A2_G01_MR	g3779024	BLASTX	223	9e-29	61	(AC005171) unknown protein [Arabidopsis thaliana]
16813	GM_M20_A2_G02_MR	g3426334	BLASTN	517	2e-16	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
16814	GM_M20_A2_G09_MR	g3540206	BLASTX	405	1e-35	52	(AC004260) Hypothetical protein [Arabidopsis thaliana]
16815	GM_M20_A2_G10_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16816	GM_M20_A2_H03_MR	g1771194	BLASTN	417	8e-12	77	L.japonicus gene encoding RING finger protein
16817	GM_M20_A2_H04_MF	g3142328	BLASTN	1853	3e-77	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16818	GM_M20_A2_H04_MR	g3845281	BLASTN	405	3e-11	64	Plasmodium falciparum chromosome 2, section 56 of 73 of the complete sequence
16819	GM_M20_A2_H09_MR	g3702323	BLASTX	604	4e-58	86	(AC005397) unknown protein [Arabidopsis thaliana]
16820	GM_M20_A2_H10_MF	g1769898	BLASTX	231	1e-17	39	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16821	GM_M20_A2_H11_MR	g1666236	BLASTX	177	7e-16	28	(U76261) unknown [Hordeum vulgare]
16822	GM_M20_A2_H12_MF	g3249105	BLASTX	237	1e-18	62	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
16823	GM_M20_B1_A02_MR	g3097320	BLASTN	1275	1e-50	79	Glycine max gene for Bd 30K, complete cds
16824	GM_M20_B1_A11_MF	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16825	GM_M20_B1_A11_MR	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16826	GM_M20_B1_A12_MR	g1129068	BLASTX	176	2e-24	91	malate dehydrogenase; EC 1.1.1.40, malic enzyme
16827	GM_M20_B1_B04_MF	g3063438	BLASTN	367	1e-09	69	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
16828	GM_M20_B1_B07_MF	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16829	GM_M20_B1_B07_MR	g507910	BLASTN	362	9e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16830	GM_M20_B1_C03_MF	g3319362	BLASTX	235	1e-17	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16831	GM_M20_B1_C05_MF	g1769899	BLASTX	153	3e-10	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16832	GM_M20_B1_C06_MR	g13773	BLASTN	415	2e-12	64	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
16833	GM_M20_B1_C07_MR	g3935164	BLASTX	94	5e-09	36	(AC004557) F17L21.7 [Arabidopsis thaliana]
16834	GM_M20_B1_C08_MF	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16835	GM_M20_B1_C08_MR	g4063760	BLASTX	142	3e-10	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
16836	GM_M20_B1_C10_MF	g1769899	BLASTX	192	2e-14	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16837	GM_M20_B1_C10_MR	g2462134	BLASTX	270	4e-22	38	(Y13368) reverse transcriptase [Beta vulgaris]
16838	GM_M20_B1_D03_MR	g1514643	BLASTX	145	8e-16	58	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
16839	GM_M20_B1_D04_MF	g12212	BLASTN	1209	2e-52	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
16840	GM_M20_B1_D04_MR	g2734643	BLASTX	369	4e-52	66	(U48738) ribosomal protein subunit 2 [Agalinis sp.]
16841	GM_M20_B1_D10_MF	g1167523	BLASTX	157	3e-09	33	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16842	GM_M20_B1_D10_MR	g2443320	BLASTX	211	5e-15	38	(D85597) polyprotein [Oryza australiensis]
16843	GM_M20_B1_E03_MR	g3142328	BLASTN	1293	1e-51	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16844	GM_M20_B1_E04_MR	g3142328	BLASTN	1268	2e-50	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16845	GM_M20_B1_E07_MF	g992916	BLASTN	427	1e-20	76	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
16846	GM_M20_B1_E08_MF	g3097320	BLASTN	732	4e-26	81	Glycine max gene for Bd 30K, complete cds
16847	GM_M20_B1_E09_MF	g2760325	BLASTX	220	9e-17	66	(AC002130) F1N21.10 [Arabidopsis thaliana]
16848	GM_M20_B1_E10_MF	g18559	BLASTN	381	3e-10	80	G.max gene for catalase
16849	GM_M20_B1_E11_MR	g2995405	BLASTX	226	8e-17	52	(Y12432) polyprotein [Ananas comosus]
16850	GM_M20_B1_E12_MF	g2281101	BLASTX	233	8e-18	51	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]
16851	GM_M20_B1_F01_MR	g18559	BLASTN	951	4e-36	73	G.max gene for catalase
16852	GM_M20_B1_F02_MF	g3097320	BLASTN	430	2e-12	71	Glycine max gene for Bd 30K, complete cds
16853	GM_M20_B1_F02_MR	g4038056	BLASTX	310	8e-26	50	(AC005897) putative transposon [Arabidopsis thaliana]
16854	GM_M20_B1_F03_MF	g3063438	BLASTN	364	2e-09	72	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
16855	GM_M20_B1_F04_MF	g18559	BLASTN	623	2e-31	81	G.max gene for catalase
16856	GM_M20_B1_F07_MR	g3142328	BLASTN	580	3e-19	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16857	GM_M20_B1_F10_MF	g603890	BLASTX	183	1e-13	57	(Z46949) pathogenesis-related protein PR-6 type [Sambucus nigra]
16858	GM_M20_B1_F12_MF	g81857	BLASTX	111	4e-17	64	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) gi 19658 (X63872) translationally controlled tumor protein [Medicago sativa]
16859	GM_M20_B1_G03_MR	g160698	BLASTN	363	3e-10	58	P.berghei telomeric repeat region subfragment a DNA.
16860	GM_M20_B1_G05_MR	g3097320	BLASTN	386	2e-10	61	Glycine max gene for Bd 30K, complete cds
16861	GM_M20_B1_H03_MF	g3287695	BLASTX	191	5e-13	45	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16862	GM_M20_B1_H04_MF	g3377834	BLASTX	150	7e-09	30	(AF075598) No definition line found [Arabidopsis thaliana]
16863	GM_M20_B1_H07_MR	g100484	BLASTX	171	4e-11	40	hypothetical protein - garden snapdragon
16864	GM_M20_B1_H11_MR	g3645899	BLASTX	199	8e-18	42	(U68408) 5' end not determined experimentally [Zea mays]
16865	GM_M20_B2_A04_MF	g2522228	BLASTX	419	2e-38	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
16866	GM_M20_B2_A08_MR	g3075392	BLASTX	227	9e-18	69	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]
16867	GM_M20_B2_A11_MR	g2098713	BLASTX	336	2e-29	67	(U82977) pectinesterase [Citrus sinensis]
16868	GM_M20_B2_A12_MF	g2879886	BLASTN	346	9e-09	67	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
16869	GM_M20_B2_B02_MF	g313723	BLASTN	372	6e-10	79	P.sativum hemC mRNA for hydroxymethylbilane synthase
16870	GM_M20_B2_B02_MR	g2970554	BLASTN	613	1e-20	71	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
16871	GM_M20_B2_B03_MF	g3056587	BLASTX	147	8e-10	70	(AC004255) T1F9.8 [Arabidopsis thaliana]
16872	GM_M20_B2_B05_MR	g2995405	BLASTX	387	4e-34	53	(Y12432) polyprotein [Ananas comosus]
16873	GM_M20_B2_B06_MR	g2995405	BLASTX	235	1e-24	45	(Y12432) polyprotein [Ananas comosus]
16874	GM_M20_B2_B09_MR	g18559	BLASTN	352	6e-09	67	G.max gene for catalase
16875	GM_M20_B2_B10_MF	g1666096	BLASTX	284	3e-24	70	(Y09113) dioxygenase [Marah macrocarpa]
16876	GM_M20_B2_B12_MF	g22490	BLASTX	189	4e-14	39	(X01380) ORF1 [Zea mays]
16877	GM_M20_B2_C05_MF	g3142328	BLASTN	370	1e-09	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16878	GM_M20_B2_C10_MR	g2462134	BLASTX	130	3e-14	53	(Y13368) reverse transcriptase [Beta vulgaris]
16879	GM_M20_B2_C12_MR	g505129	BLASTN	395	7e-11	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16880	GM_M20_B2_D01_MF	g2760325	BLASTX	210	7e-18	78	(AC002130) F1N21.10 [Arabidopsis thaliana]
16881	GM_M20_B2_D02_MF	g1142703	BLASTN	276	2e-14	76	Glycine max satellite STR120-B.1.
16882	GM_M20_B2_D02_MR	g2522230	BLASTX	285	3e-24	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16883	GM_M20_B2_D03_MF	g4092470	BLASTN	365	2e-09	60	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
16884	GM_M20_B2_D04_MR	g1360613	BLASTX	161	5e-10	34	(X97304) ORF V gene product [Strawberry vein banding virus]
16885	GM_M20_B2_D06_MF	g99755	BLASTX	300	3e-27	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
16886	GM_M20_B2_D11_MR	g2264313	BLASTN	417	8e-12	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]
16887	GM_M20_B2_E09_MR	g4063760	BLASTX	488	1e-44	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16888	GM_M20_B2_E10_MR	g100484	BLASTX	330	4e-28	50	hypothetical protein - garden snapdragon
16889	GM_M20_B2_E12_MR	g3461840	BLASTX	184	5e-12	36	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
16890	GM_M20_B2_F03_MF	g507910	BLASTN	607	8e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16891	GM_M20_B2_F03_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence
16892	GM_M20_B2_F04_MR	g559262	BLASTN	253	8e-09	62	Saccharomyces cerevisiae mitochondrion transfer RNA-Thr2 (tRNA-Thr2); transfer RNA-Cys (tRNA-Cys); transfer RNA-His (tRNA-His) genes.
16893	GM_M20_B2_F06_MF	g3820757	BLASTN	417	4e-12	64	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
16894	GM_M20_B2_F07_MR	g2129618	BLASTX	259	3e-20	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16895	GM_M20_B2_F09_MR	g4063760	BLASTX	513	3e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16896	GM_M20_B2_G01_MF	g3097320	BLASTN	801	2e-37	76	Glycine max gene for Bd 30K, complete cds
16897	GM_M20_B2_G02_MR	g4038056	BLASTX	397	4e-35	49	(AC005897) putative transposon [Arabidopsis thaliana]
16898	GM_M20_B2_G08_MR	g3805846	BLASTX	314	9e-26	79	(AL031986) DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain [Arabidopsis thaliana]
16899	GM_M20_B2_G12_MF	g1944188	BLASTN	475	9e-15	75	Soybean DNA for nodulin 35, partial cds
16900	GM_M20_B2_H04_MR	g3176680	BLASTX	337	3e-29	44	(AC003671) Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb U63373. EST gb AA404878 comes from this gene. [Arabidopsis thaliana]
16901	GM_M20_B2_H09_MF	g2129618	BLASTX	203	2e-14	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16902	GM_M20_B2_H10_MR	g3334667	BLASTX	204	6e-15	38	(Y10493) putative cytochrome P450 [Glycine max]
16903	GM_M20_B2_H12_MR	g3777527	BLASTX	322	1e-26	72	(AF053008) gag-pol polyprotein [Glycine max]
16904	GM_M21_A1_A03_MF	g4063756	BLASTN	440	8e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16905	GM_M21_A1_A03_MR	g507910	BLASTN	424	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16906	GM_M21_A1_A08_MF	g4063770	BLASTX	191	4e-13	36	(AB004906) transposase [Ipomoea purpurea]
16907	GM_M21_A1_A10_MF	g2811226	BLASTX	266	2e-21	92	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
16908	GM_M21_A1_A10_MR	g20044	BLASTN	375	6e-10	61	Tobacco DNA for retroviral-like transposon Tnt 1-94
16909	GM_M21_A1_B01_MR	g2443320	BLASTX	389	6e-34	52	(D85597) polyprotein [Oryza australiensis]
16910	GM_M21_A1_B05_MF	g4038056	BLASTX	179	2e-26	53	(AC005897) putative transposon [Arabidopsis thaliana]
16911	GM_M21_A1_B05_MR	g3695395	BLASTX	208	9e-17	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16912	GM_M21_A1_B08_MF	g507910	BLASTN	380	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16913	GM_M21_A1_B08_MR	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16914	GM_M21_A1_B09_MR	g2979597	BLASTN	376	6e-10	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
16915	GM_M21_A1_B10_MF	g4063760	BLASTX	496	2e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16916	GM_M21_A1_B10_MR	g2522230	BLASTX	262	7e-22	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16917	GM_M21_A1_B12_MR	g18559	BLASTN	554	4e-18	68	G.max gene for catalase
16918	GM_M21_A1_C01_MR	g2501460	BLASTX	155	2e-18	66	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
16919	GM_M21_A1_C02_MF	g4038594	BLASTX	329	1e-28	79	(AJ222798) DET1 protein [Lycopersicon esculentum]
16920	GM_M21_A1_C03_MR	g3834451	BLASTX	319	6e-28	59	(AF072732) polygalacturonase 7 [Lycopersicon esculentum]
16921	GM_M21_A1_C10_MR	g130405	BLASTX	295	4e-24	45	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
16922	GM_M21_A1_C11_MR	g3695385	BLASTX	265	4e-22	45	(AF096370) similar to Medicago truncatula MtN21 (GB:Y15293) [Arabidopsis thaliana]
16923	GM_M21_A1_C12_MF	g3033389	BLASTX	154	4e-09	32	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16924	GM_M21_A1_C12_MR	g3033389	BLASTX	276	3e-22	45	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16925	GM_M21_A1_D03_MF	g3021343	BLASTN	742	1e-27	74	Cicer arietinum mRNA for hypothetical protein homologous to EST B23019
16926	GM_M21_A1_D03_MR	g2085783	BLASTN	391	1e-10	62	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
16927	GM_M21_A1_D06_MF	g2245087	BLASTX	167	1e-11	40	(Z97343) hypothetical protein [Arabidopsis thaliana]
16928	GM_M21_A1_D08_MF	g18559	BLASTN	382	3e-10	71	G.max gene for catalase
16929	GM_M21_A1_D08_MR	g2443320	BLASTX	381	4e-33	51	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16930	GM_M21_A1_D09_MR	g1167523	BLASTX	348	1e-29	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16931	GM_M21_A1_D11_MF	g3650039	BLASTX	227	4e-17	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16932	GM_M21_A1_E08_MF	g3738114	BLASTN	406	3e-11	64	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
16933	GM_M21_A1_E10_MR	g3650039	BLASTX	179	6e-12	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16934	GM_M21_A1_F04_MF	g4092471	BLASTN	367	1e-09	60	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
16935	GM_M21_A1_F06_MF	g478148	BLASTX	423	6e-39	91	reverse transcriptase (copia-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
16936	GM_M21_A1_F07_MF	g2443320	BLASTX	123	9e-16	49	(D85597) polyprotein [Oryza australiensis]
16937	GM_M21_A1_F08_MR	g3687234	BLASTX	167	2e-10	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
16938	GM_M21_A1_F09_MR	g4050011	BLASTN	399	5e-11	70	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
16939	GM_M21_A1_F11_MF	g3650039	BLASTX	203	1e-14	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16940	GM_M21_A1_G05_MR	g2642431	BLASTX	224	2e-16	58	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
16941	GM_M21_A1_G06_MF	g4063760	BLASTX	267	5e-21	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16942	GM_M21_A1_G12_MR	g4063760	BLASTX	443	8e-40	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16943	GM_M21_A1_H03_MR	g170080	BLASTN	1058	5e-41	86	Soybean seed lectin gene transposable element tgm1.
16944	GM_M21_A2_A02_MF	g3142328	BLASTN	538	3e-24	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16945	GM_M21_A2_A02_MR	g1621467	BLASTX	625	2e-60	86	(U73106) laccase [Liriodendron tulipifera]
16946	GM_M21_A2_A03_MF	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
16947	GM_M21_A2_A03_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16948	GM_M21_A2_A07_MF	g1769898	BLASTX	237	2e-25	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16949	GM_M21_A2_A08_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16950	GM_M21_A2_B01_MF	g2443878	BLASTX	150	5e-10	62	(AC002294) Unknown protein [Arabidopsis thaliana]
16951	GM_M21_A2_B03_MF	g3777527	BLASTX	269	4e-28	54	(AF053008) gag-pol polyprotein [Glycine max]
16952	GM_M21_A2_B03_MR	g968986	BLASTN	365	1e-09	73	Glycine max ferritin gene, nuclear gene encoding chloroplast protein, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
16953	GM_M21_A2_B04_MF	g2522228	BLASTX	376	6e-34	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
16954	GM_M21_A2_B09_MF	g905361	BLASTX	418	4e-38	92	(U22103) gag-protease polyprotein [Glycine max]
16955	GM_M21_A2_C02_MR	g226407	BLASTX	343	5e-29	50	retrotransposon del1-46 [Lilium henryi]
16956	GM_M21_A2_C03_MF	g2129618	BLASTX	162	6e-10	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16957	GM_M21_A2_C03_MR	g905361	BLASTX	200	3e-14	37	(U22103) gag-protease polyprotein [Glycine max]
16958	GM_M21_A2_D02_MR	g3777527	BLASTX	236	1e-17	37	(AF053008) gag-pol polyprotein [Glycine max]
16959	GM_M21_A2_D04_MF	g2244803	BLASTX	232	1e-18	38	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
16960	GM_M21_A2_D10_MR	g3142328	BLASTN	1202	2e-47	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16961	GM_M21_A2_E07_MF	g1173187	BLASTX	209	2e-27	93	40S RIBOSOMAL PROTEIN S23 (S12) gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry gi 643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]
16962	GM_M21_A2_F01_MR	g3097320	BLASTN	1159	2e-45	79	Glycine max gene for Bd 30K, complete cds
16963	GM_M21_A2_F02_MR	g3510344	BLASTN	357	4e-09	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
16964	GM_M21_A2_F07_MR	g1167523	BLASTX	358	1e-30	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16965	GM_M21_A2_F08_MR	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16966	GM_M21_A2_F10_MR	g2088662	BLASTX	255	3e-21	61	(AF002109) unknown protein [Arabidopsis thaliana]
16967	GM_M21_A2_G02_MF	g3549672	BLASTX	154	1e-09	93	(AL031394) putative protein [Arabidopsis thaliana]
16968	GM_M21_A2_G02_MR	g1346261	BLASTX	335	3e-29	50	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) gi 1015319 gnl PID d1011751 (D67088) glutamyl-tRNA reductase [Cucumis sativus]
16969	GM_M21_A2_G03_MR	g3386611	BLASTX	136	5e-13	50	(AC004665) unknown protein [Arabidopsis thaliana]
16970	GM_M21_A2_G04_MF	g3142328	BLASTN	944	8e-36	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16971	GM_M21_A2_G06_MR	g3097320	BLASTN	1163	1e-45	81	Glycine max gene for Bd 30K, complete cds
16972	GM_M21_A2_G07_MR	g3426334	BLASTN	514	3e-16	62	Pisum sativum pectin methylesterase (repme1) gene, complete cds
16973	GM_M21_A2_G10_MR	g3549664	BLASTX	156	2e-09	50	(AL031394) putative protein [Arabidopsis thaliana]
16974	GM_M21_A2_G11_MR	g3142328	BLASTN	1974	7e-83	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16975	GM_M21_A2_H02_MF	g840618	BLASTN	349	6e-09	66	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16976	GM_M21_A2_H03_MR	g3142328	BLASTN	1328	3e-53	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16977	GM_M21_A2_H06_MR	g2979567	BLASTN	422	5e-12	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence [Homo sapiens]
16978	GM_M21_A2_H09_MF	g100484	BLASTX	270	1e-31	59	hypothetical protein - garden snapdragon
16979	GM_M21_A2_H09_MR	g1769898	BLASTX	218	3e-28	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16980	GM_M21_B1_A05_MR	g1769897	BLASTX	229	1e-21	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16981	GM_M21_B1_A09_MF	g14227	BLASTN	356	1e-09	68	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
16982	GM_M21_B1_A10_MF	g130582	BLASTX	420	3e-37	65	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16983	GM_M21_B1_A11_MR	g3097320	BLASTN	1003	2e-38	82	Glycine max gene for Bd 30K, complete cds
16984	GM_M21_B1_A12_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16985	GM_M21_B1_B02_MR	g2618683	BLASTN	553	6e-18	67	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]
16986	GM_M21_B1_B04_MF	g2656030	BLASTN	705	8e-25	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
16987	GM_M21_B1_B05_MF	g100484	BLASTX	312	3e-26	49	hypothetical protein - garden snapdragon
16988	GM_M21_B1_B06_MF	g1703380	BLASTX	146	7e-15	100	ADP-RIBOSYLATION FACTOR gi 1132483 gnl PID d1005135 (D17760) ADP-ribosylation factor [Oryza sativa]
16989	GM_M21_B1_B06_MR	g3702341	BLASTX	166	6e-12	56	(AC005397) hypothetical protein [Arabidopsis thaliana]
16990	GM_M21_B1_B10_MR	g18559	BLASTN	1071	2e-41	77	G.max gene for catalase
16991	GM_M21_B1_B12_MR	g2500354	BLASTX	330	4e-29	64	60S RIBOSOMAL PROTEIN L10 (EQM) gi 1902894 gnl PID d1020219 (AB001891) QM family protein [Solanum melongena]
16992	GM_M21_B1_C01_MF	g3777527	BLASTX	197	2e-13	33	(AF053008) gag-pol polyprotein [Glycine max]
16993	GM_M21_B1_C01_MR	g3142328	BLASTN	1703	2e-70	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16994	GM_M21_B1_C05_MF	g3193221	BLASTN	392	1e-10	79	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
16995	GM_M21_B1_C09_MF	g4063760	BLASTX	178	1e-11	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16996	GM_M21_B1_C09_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16997	GM_M21_B1_C12_MF	g1769899	BLASTX	116	1e-16	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16998	GM_M21_B1_D02_MR	g3273387	BLASTN	375	7e-10	62	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
16999	GM_M21_B1_D06_MF	g1762436	BLASTX	172	1e-11	64	(U60277) acyl-acyl carrier protein desaturase [Asclepias syriaca]
17000	GM_M21_B1_D06_MR	g100484	BLASTX	361	2e-33	61	hypothetical protein - garden snapdragon
17001	GM_M21_B1_D08_MF	g2541876	BLASTX	253	3e-20	49	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
17002	GM_M21_B1_D12_MF	g3193221	BLASTN	383	3e-10	78	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
17003	GM_M21_B1_E02_MR	g18559	BLASTN	988	9e-38	76	G.max gene for catalase
17004	GM_M21_B1_E11_MF	g2522228	BLASTX	191	1e-16	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
17005	GM_M21_B1_F03_MF	g3777527	BLASTX	556	1e-51	93	(AF053008) gag-pol polyprotein [Glycine max]
17006	GM_M21_B1_F11_MR	g2347190	BLASTX	163	4e-10	37	(AC002338) Na/H antiporter isolog [Arabidopsis thaliana] gi 3150398 (AC004165) putative Na/H antiporter [Arabidopsis thaliana]
17007	GM_M21_B1_F12_MR	g170029	BLASTN	420	5e-12	83	Glycine max cv. Dare nodulin 26 gene fragment.
17008	GM_M21_B1_G04_MR	g905361	BLASTX	196	8e-14	33	(U22103) gag-protease polyprotein [Glycine max]
17009	GM_M21_B1_G05_MF	g4050011	BLASTN	500	1e-15	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
17010	GM_M21_B1_G07_MF	g3021552	BLASTN	435	1e-12	77	Pisum sativum gdcT gene
17011	GM_M21_B1_G08_MF	g629693	BLASTX	346	9e-31	49	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
17012	GM_M21_B1_G08_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17013	GM_M21_B1_G09_MF	g1769897	BLASTX	133	9e-09	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17014	GM_M21_B1_H03_MR	g507910	BLASTN	581	1e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17015	GM_M21_B1_H04_MF	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17016	GM_M21_B1_H04_MR	g507910	BLASTN	399	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17017	GM_M21_B1_H09_MR	g2760165	BLASTN	356	5e-09	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
17018	GM_M21_B2_A02_MF	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17019	GM_M21_B2_A02_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17020	GM_M21_B2_A07_MF	g507910	BLASTN	418	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17021	GM_M21_B2_A07_MR	g905361	BLASTX	291	4e-24	70	(U22103) gag-protease polyprotein [Glycine max]
17022	GM_M21_B2_A08_MF	g3097320	BLASTN	448	3e-13	72	Glycine max gene for Bd 30K, complete cds
17023	GM_M21_B2_B01_MR	g2995405	BLASTX	297	4e-33	66	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17024	GM_M21_B2_B02_MF	g541967	BLASTX	166	6e-11	77	glycine cleavage system protein T precursor - garden pea >gi 407475 (X74793) T-protein of the glycine decarboxylase complex [Pisum sativum]
17025	GM_M21_B2_B09_MF	g421955	BLASTX	398	3e-36	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17026	GM_M21_B2_B11_MF	g3096920	BLASTX	307	2e-26	45	(AL023094) putative ketoacyl-CoA synthase [Arabidopsis thaliana]
17027	GM_M21_B2_C07_MF	g2245115	BLASTX	156	2e-09	69	(Z97343) unnamed protein product [Arabidopsis thaliana]
17028	GM_M21_B2_C11_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17029	GM_M21_B2_C11_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17030	GM_M21_B2_D02_MR	g3219151	BLASTX	123	1e-11	71	(AB015181) cdc2 related [Mesembryanthemum crystallinum]
17031	GM_M21_B2_D10_MR	g2443320	BLASTX	119	4e-13	38	(D85597) polyprotein [Oryza australiensis]
17032	GM_M21_B2_D11_MF	g2129709	BLASTX	237	9e-18	44	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17033	GM_M21_B2_E01_MF	g3142328	BLASTN	709	4e-25	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17034	GM_M21_B2_E02_MF	g3746069	BLASTX	152	1e-08	28	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
17035	GM_M21_B2_E08_MF	g3810596	BLASTX	319	1e-26	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17036	GM_M21_B2_E10_MF	g99922	BLASTX	350	3e-31	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17037	GM_M21_B2_F01_MF	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
17038	GM_M21_B2_F04_MF	g2522227	BLASTX	198	4e-15	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17039	GM_M21_B2_F11_MF	g3645899	BLASTX	220	2e-25	52	(U68408) 5' end not determined experimentally [Zea mays]
17040	GM_M21_B2_G01_MR	g2895613	BLASTN	348	5e-09	62	Colias alexandra alexandra large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
17041	GM_M21_B2_G02_MR	g3171159	BLASTN	599	5e-20	67	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
17042	GM_M21_B2_G03_MF	g1480927	BLASTN	1392	2e-57	91	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
17043	GM_M21_B2_G03_MR	g2129618	BLASTX	112	3e-13	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17044	GM_M21_B2_G08_MF	g3242717	BLASTX	207	1e-15	92	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17045	GM_M21_B2_G09_MF	g136251	BLASTX	287	4e-24	76	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR gi 99767 pir A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana gi 166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]
17046	GM_M21_B2_G10_MR	g2979597	BLASTN	378	5e-10	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
17047	GM_M21_B2_G11_MR	g3142328	BLASTN	1229	9e-49	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17048	GM_M21_B2_H02_MR	g3097320	BLASTN	1207	1e-47	82	Glycine max gene for Bd 30K, complete cds
17049	GM_M21_B2_H07_MF	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17050	GM_M21_B2_H07_MR	g507910	BLASTN	382	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17051	GM_M22_A1_A09_MF	g2626751	BLASTN	445	4e-13	63	Triticum aestivum retrotransposon Tar1, partial sequence.
17052	GM_M22_A1_A12_MF	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17053	GM_M22_A1_B08_MF	g3319362	BLASTX	180	3e-16	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17054	GM_M22_A1_B09_MF	g12212	BLASTN	1146	1e-50	91	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
17055	GM_M22_A1_B10_MF	g3510347	BLASTN	504	1e-15	70	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
17056	GM_M22_A1_B11_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17057	GM_M22_A1_C02_MF	g3645899	BLASTX	369	5e-32	54	(U68408) 5' end not determined experimentally [Zea mays]
17058	GM_M22_A1_C03_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17059	GM_M22_A1_C04_MF	g3142328	BLASTN	772	5e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17060	GM_M22_A1_C06_MF	g3810596	BLASTX	292	7e-24	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17061	GM_M22_A1_C08_MF	g3142328	BLASTN	975	3e-37	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17062	GM_M22_A1_C09_MF	g3142328	BLASTN	816	5e-30	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17063	GM_M22_A1_C11_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17064	GM_M22_A1_D09_MF	g3548797	BLASTN	425	4e-12	66	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]
17065	GM_M22_A1_D10_MF	g531389	BLASTX	283	1e-22	44	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17066	GM_M22_A1_E01_MF	g3445238	BLASTX	227	3e-18	62	(AL022347) putative protein [Arabidopsis thaliana] gi 3451059 gnl PID e1316746 (AL031326) putative protein [Arabidopsis thaliana]
17067	GM_M22_A1_E02_MF	g507910	BLASTN	549	3e-18	84	Glycine max BSR-101 satellite SB92 genomic sequence.
17068	GM_M22_A1_E07_MF	g4063770	BLASTX	193	5e-20	39	(AB004906) transposase [Ipomoea purpurea]
17069	GM_M22_A1_E12_MF	g20999	BLASTN	296	1e-11	63	P.vulgaris gln-delta gene for plastid-located glutamine synthetase (promotor region)
17070	GM_M22_A1_F02_MF	g507910	BLASTN	376	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17071	GM_M22_A1_F04_MF	g1769898	BLASTX	444	4e-41	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17072	GM_M22_A1_F08_MF	g3687234	BLASTX	193	3e-13	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
17073	GM_M22_A1_G04_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17074	GM_M22_A1_H07_MF	g3097320	BLASTN	1210	9e-48	81	Glycine max gene for Bd 30K, complete cds
17075	GM_M22_A1_H11_MF	g3097320	BLASTN	955	3e-36	78	Glycine max gene for Bd 30K, complete cds
17076	GM_M22_A2_A01_MF	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17077	GM_M22_A2_A04_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17078	GM_M22_A2_A11_MF	g255578	BLASTN	637	1e-22	86	small auxin up RNA gene cluster: orf X10A [Glycine max=soybeans, cv. Wayne, Genomic, 666 nt]
17079	GM_M22_A2_B02_MF	g3142379	BLASTX	243	2e-19	57	(AF053008) envelope-like [Glycine max]
17080	GM_M22_A2_C06_MF	g3097320	BLASTN	621	4e-21	82	Glycine max gene for Bd 30K, complete cds
17081	GM_M22_A2_C10_MF	g1431738	BLASTN	670	2e-23	78	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
17082	GM_M22_A2_F01_MF	g3212863	BLASTX	285	3e-24	80	(AC004005) putative translation initiation factor [Arabidopsis thaliana]
17083	GM_M22_A2_F03_MF	g18559	BLASTN	841	4e-31	73	G.max gene for catalase
17084	GM_M22_A2_F06_MF	g2764526	BLASTN	398	6e-11	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17085	GM_M22_A2_F07_MF	g507910	BLASTN	345	6e-09	67	Glycine max BSR-101 satellite SB92 genomic sequence.
17086	GM_M22_A2_F11_MF	g2522227	BLASTX	218	3e-17	44	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17087	GM_M22_A2_F12_MF	g1769897	BLASTX	183	1e-12	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17088	GM_M22_A2_G06_MF	g2264320	BLASTN	497	2e-15	61	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
17089	GM_M22_A2_G08_MF	g3777527	BLASTX	168	1e-12	35	(AF053008) gag-pol polyprotein [Glycine max]
17090	GM_M22_A2_G11_MF	g1167523	BLASTX	190	9e-13	33	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17091	GM_M22_A2_H02_MF	g1167523	BLASTX	299	6e-26	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17092	GM_M22_A2_H07_MF	g507910	BLASTN	358	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17093	GM_M22_A2_H08_MF	g3645899	BLASTX	334	3e-28	48	(U68408) 5' end not determined experimentally [Zea mays]
17094	GM_M22_B1_A03_MR	g99922	BLASTX	173	9e-21	68	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17095	GM_M22_B1_A04_MF	g18559	BLASTN	483	7e-15	72	G.max gene for catalase
17096	GM_M22_B1_A08_MR	g4038056	BLASTX	389	3e-34	52	(AC005897) putative transposon [Arabidopsis thaliana]
17097	GM_M22_B1_B05_MR	g3645899	BLASTX	441	1e-39	61	(U68408) 5' end not determined experimentally [Zea mays]
17098	GM_M22_B1_B06_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17099	GM_M22_B1_B07_MR	g3142328	BLASTN	791	7e-29	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17100	GM_M22_B1_B12_MR	g3645899	BLASTX	298	2e-24	49	(U68408) 5' end not determined experimentally [Zea mays]
17101	GM_M22_B1_C01_MR	g2522228	BLASTX	433	5e-40	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
17102	GM_M22_B1_C02_MF	g170603	BLASTN	550	6e-19	74	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
17103	GM_M22_B1_C02_MR	g4063760	BLASTX	608	2e-57	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17104	GM_M22_B1_C03_MR	g3513745	BLASTX	164	7e-10	31	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
17105	GM_M22_B1_C04_MR	g1769898	BLASTX	272	4e-22	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17106	GM_M22_B1_C07_MR	g3176776	BLASTN	338	5e-09	67	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 5' sequence
17107	GM_M22_B1_C08_MR	g226407	BLASTX	498	2e-45	62	retrotransposon del1-46 [Lilium henryi]
17108	GM_M22_B1_C11_MR	g3777527	BLASTX	728	5e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
17109	GM_M22_B1_C12_MR	g422418	BLASTX	260	2e-20	41	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
17110	GM_M22_B1_D02_MF	g507910	BLASTN	574	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
17111	GM_M22_B1_D05_MF	g3777527	BLASTX	673	4e-64	94	(AF053008) gag-pol polyprotein [Glycine max]
17112	GM_M22_B1_D06_MF	g4063769	BLASTN	503	9e-16	70	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
17113	GM_M22_B1_D08_MR	g4063760	BLASTX	443	8e-40	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17114	GM_M22_B1_D09_MR	g1769897	BLASTX	251	6e-20	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17115	GM_M22_B1_D10_MR	g905361	BLASTX	184	2e-12	33	(U22103) gag-protease polyprotein [Glycine max]
17116	GM_M22_B1_E07_MF	g507910	BLASTN	366	6e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17117	GM_M22_B1_E07_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17118	GM_M22_B1_E08_MF	g322661	BLASTX	182	2e-13	71	S-receptor kinase-related protein - Chinese kale gi 17919 (Z18862) S-receptor kinase related protein [Brassica oleracea]
17119	GM_M22_B1_E10_MR	g1171591	BLASTN	405	3e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-B)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17120	GM_M22_B1_E12_MF	g4063760	BLASTX	167	8e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17121	GM_M22_B1_F01_MR	g13507	BLASTN	243	2e-10	67	Yeast mitochondrial gene for ATPase (genes oli-2 and oli-4).
17122	GM_M22_B1_F03_MF	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17123	GM_M22_B1_F05_MF	g2129618	BLASTX	221	3e-16	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17124	GM_M22_B1_F09_MF	g13619	BLASTN	412	1e-12	63	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
17125	GM_M22_B1_F10_MF	g3777527	BLASTX	635	4e-60	97	(AF053008) gag-pol polyprotein [Glycine max]
17126	GM_M22_B1_F11_MR	g3097320	BLASTN	745	1e-26	78	Glycine max gene for Bd 30K, complete cds
17127	GM_M22_B1_F12_MF	g4150933	BLASTN	350	9e-09	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
17128	GM_M22_B1_G02_MF	g2129618	BLASTX	161	7e-10	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17129	GM_M22_B1_G03_MF	g2522228	BLASTX	193	1e-31	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
17130	GM_M22_B1_G04_MF	g1617270	BLASTX	193	2e-13	74	(X94624) acyl-CoA synthetase [Brassica napus]
17131	GM_M22_B1_G06_MR	g3377855	BLASTX	227	2e-33	77	(AF076274) contains similarity to reverse tranciptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
17132	GM_M22_B1_G07_MF	g18559	BLASTN	925	6e-35	75	G.max gene for catalase
17133	GM_M22_B1_G08_MF	g905361	BLASTX	435	4e-40	96	(U22103) gag-protease polyprotein [Glycine max]
17134	GM_M22_B1_G09_MF	g4115365	BLASTX	312	1e-25	53	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
17135	GM_M22_B1_G11_MF	g3097320	BLASTN	937	2e-35	81	Glycine max gene for Bd 30K, complete cds
17136	GM_M22_B1_H01_MF	g3777527	BLASTX	182	8e-12	33	(AF053008) gag-pol polyprotein [Glycine max]
17137	GM_M22_B1_H01_MR	g505129	BLASTN	397	5e-11	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17138	GM_M22_B1_H04_MR	g4063760	BLASTX	106	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17139	GM_M22_B1_H06_MR	g3377834	BLASTX	149	9e-09	34	(AF075598) No definition line found [Arabidopsis thaliana]
17140	GM_M22_B1_H08_MF	g4063760	BLASTX	265	9e-21	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17141	GM_M22_B2_A01_MR	g3789709	BLASTN	496	2e-15	68	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
17142	GM_M22_B2_A02_MR	g505129	BLASTN	374	6e-10	67	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17143	GM_M22_B2_A03_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17144	GM_M22_B2_A03_MR	g905361	BLASTX	335	7e-29	84	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17145	GM_M22_B2_A04_MF	g2129618	BLASTX	196	1e-13	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17146	GM_M22_B2_A06_MR	g3097320	BLASTN	484	7e-15	70	Glycine max gene for Bd 30K, complete cds
17147	GM_M22_B2_A10_MF	g3097320	BLASTN	685	6e-24	84	Glycine max gene for Bd 30K, complete cds
17148	GM_M22_B2_A11_MF	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17149	GM_M22_B2_A11_MR	g507910	BLASTN	601	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17150	GM_M22_B2_B01_MF	g4063760	BLASTX	274	8e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17151	GM_M22_B2_B01_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17152	GM_M22_B2_B06_MF	g2708743	BLASTX	93	9e-09	43	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
17153	GM_M22_B2_B06_MR	g1262280	BLASTN	366	1e-09	62	Mesembryanthemum crystallinum Atpv5 gene, promoter region.
17154	GM_M22_B2_B07_MR	g13610	BLASTN	387	9e-11	59	Yeast mitochondrial var1 gene (allele 40.0) a ribosomal protein >gi 343948 gb J01525 YSCMTVAR1 Yeast (S.cerevisiae) mitochondrial var1 gene, 40.0 allele.
17155	GM_M22_B2_B08_MF	g3176768	BLASTN	442	6e-14	64	Homo sapiens allele 1 fragile site locus (FRA10B) minisatellite, 3' sequence
17156	GM_M22_B2_B08_MR	g1515105	BLASTX	214	2e-24	65	(Y07613) heat shock protein 90A [Arabidopsis thaliana]
17157	GM_M22_B2_B09_MF	g340796	BLASTN	402	4e-12	60	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
17158	GM_M22_B2_B09_MR	g2160150	BLASTX	166	1e-12	50	(AC000375) EST gb T43829 comes from this gene. [Arabidopsis thaliana]
17159	GM_M22_B2_B10_MF	g3645899	BLASTX	165	4e-17	43	(U68408) 5' end not determined experimentally [Zea mays]
17160	GM_M22_B2_B12_MR	g1236920	BLASTN	352	6e-09	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
17161	GM_M22_B2_C05_MF	g507910	BLASTN	588	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17162	GM_M22_B2_C10_MF	g505129	BLASTN	338	7e-11	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17163	GM_M22_B2_C12_MR	g2121303	BLASTN	378	5e-10	61	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
17164	GM_M22_B2_D03_MF	g2522228	BLASTX	193	1e-31	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
17165	GM_M22_B2_D04_MF	g3821288	BLASTN	381	1e-10	70	Pisum sativum repeated element highly similar to the BamHI repeated sequence families of Vicia faba
17166	GM_M22_B2_D09_MR	g3176795	BLASTN	381	1e-10	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
17167	GM_M22_B2_D11_MR	g4038056	BLASTX	327	1e-27	51	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17168	GM_M22_B2_E01_MR	g4063756	BLASTN	463	7e-14	61	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17169	GM_M22_B2_E02_MF	g3142328	BLASTN	725	7e-26	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17170	GM_M22_B2_E02_MR	g1785736	BLASTX	151	4e-10	55	(Y08502) orf119 [Arabidopsis thaliana]
17171	GM_M22_B2_E03_MF	g4063760	BLASTX	326	3e-27	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17172	GM_M22_B2_E07_MR	g3777527	BLASTX	233	3e-17	43	(AF053008) gag-pol polyprotein [Glycine max]
17173	GM_M22_B2_E08_MF	g3513747	BLASTX	310	2e-25	45	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17174	GM_M22_B2_E09_MR	g4165194	BLASTX	306	3e-25	41	(AJ009736) Pol protein [Drosophila melanogaster]
17175	GM_M22_B2_E10_MF	g3142328	BLASTN	668	3e-23	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17176	GM_M22_B2_E12_MF	g2462058	BLASTX	321	4e-28	53	(Y13389) reverse transcriptase [Antirrhinum majus]
17177	GM_M22_B2_F01_MF	g170603	BLASTN	559	2e-19	74	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
17178	GM_M22_B2_F01_MR	g4063760	BLASTX	575	1e-56	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17179	GM_M22_B2_F04_MF	g2995179	BLASTN	445	5e-13	64	Homo sapiens DNA sequence from PAC 262D12 on chromosome q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIK...
17180	GM_M22_B2_F04_MR	g4063760	BLASTX	202	4e-14	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17181	GM_M22_B2_F05_MF	g2879886	BLASTN	399	4e-11	66	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
17182	GM_M22_B2_F12_MF	g3777526	BLASTN	745	1e-26	93	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
17183	GM_M22_B2_F12_MR	g3777527	BLASTX	206	1e-18	42	(AF053008) gag-pol polyprotein [Glycine max]
17184	GM_M22_B2_G03_MF	g2129618	BLASTX	252	1e-19	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17185	GM_M22_B2_G04_MR	g505129	BLASTN	358	3e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17186	GM_M22_B2_G08_MR	g18559	BLASTN	379	4e-10	63	G.max gene for catalase
17187	GM_M22_B2_G09_MR	g1076286	BLASTX	527	4e-50	80	amidophosphoribosyltransferase - Arabidopsis thaliana gi 469193 gnl PID d1006574 (D28868) amidophosphoribosyltransferase [Arabidopsis thaliana]
17188	GM_M22_B2_G11_MF	g4140712	BLASTX	383	1e-34	60	(AF110183) putative integrase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17189	GM_M22_B2_G12_MR	g3645899	BLASTX	287	3e-23	51	(U68408) 5' end not determined experimentally [Zea mays]
17190	GM_M22_B2_H05_MF	g2244915	BLASTX	170	8e-11	39	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
17191	GM_M22_B2_H06_MR	g2244915	BLASTX	202	3e-14	34	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
17192	GM_M22_B2_H09_MF	g1666236	BLASTX	178	1e-12	29	(U76261) unknown [Hordeum vulgare]
17193	GM_M22_B2_H12_MR	g3985952	BLASTN	544	2e-17	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]
17194	GM_M23_A1_A01_MF	g2522230	BLASTX	183	2e-13	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17195	GM_M23_A1_A02_MF	g99922	BLASTX	567	3e-54	85	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17196	GM_M23_A1_A04_MR	g2879886	BLASTN	431	1e-12	60	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
17197	GM_M23_A1_A08_MF	g3688328	BLASTX	281	7e-24	54	(AJ228325) reverse transcriptase [Ginkgo biloba]
17198	GM_M23_A1_A08_MR	g2213607	BLASTX	140	2e-22	59	(AC000103) F21J9.1 [Arabidopsis thaliana]
17199	GM_M23_A1_A09_MF	g2522227	BLASTX	172	4e-12	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17200	GM_M23_A1_A09_MR	g18695	BLASTN	702	4e-25	87	Soybean nodulin 22 gene
17201	GM_M23_A1_A10_MF	g2827705	BLASTX	193	1e-13	38	(AL021684) predicted protein [Arabidopsis thaliana]
17202	GM_M23_A1_A11_MF	g18559	BLASTN	830	1e-30	77	G.max gene for catalase
17203	GM_M23_A1_A11_MR	g2443320	BLASTX	281	2e-22	46	(D85597) polyprotein [Oryza australiensis]
17204	GM_M23_A1_B04_MF	g2879886	BLASTN	379	3e-10	62	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
17205	GM_M23_A1_B04_MR	g1762933	BLASTX	160	4e-11	49	(U66263) tumor-related protein [Nicotiana tabacum]
17206	GM_M23_A1_B06_MF	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17207	GM_M23_A1_B06_MR	g507910	BLASTN	489	2e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17208	GM_M23_A1_B08_MF	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17209	GM_M23_A1_B08_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17210	GM_M23_A1_B11_MR	g4063760	BLASTX	372	3e-32	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17211	GM_M23_A1_C02_MF	g343742	BLASTN	227	6e-09	64	Yeast (S.cerevisiae) mitochondrial ATPase complex subunit 9 proteolipid, 3' flank.
17212	GM_M23_A1_C04_MF	g3097320	BLASTN	872	2e-32	85	Glycine max gene for Bd 30K, complete cds
17213	GM_M23_A1_C04_MR	g2979597	BLASTN	405	3e-11	62	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17214	GM_M23_A1_C05_MR	g3426048	BLASTX	353	2e-31	84	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]
17215	GM_M23_A1_C10_MR	g100484	BLASTX	227	1e-31	59	hypothetical protein - garden snapdragon
17216	GM_M23_A1_D01_MR	g3776466	BLASTN	375	5e-10	64	Homo sapiens immunoglobulin-like transcript 10 protein gene, exons 7 and 8 and complete cds
17217	GM_M23_A1_D02_MR	g130582	BLASTX	223	3e-16	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17218	GM_M23_A1_D03_MR	g1142701	BLASTN	1225	5e-49	82	Glycine max satellite STR120-A.3.
17219	GM_M23_A1_D04_MR	g3097320	BLASTN	480	1e-14	68	Glycine max gene for Bd 30K, complete cds
17220	GM_M23_A1_D09_MF	g4038056	BLASTX	224	1e-16	50	(AC005897) putative transposon [Arabidopsis thaliana]
17221	GM_M23_A1_D10_MF	g2462058	BLASTX	333	2e-29	55	(Y13389) reverse transcriptase [Antirrhinum majus]
17222	GM_M23_A1_D11_MF	g1769897	BLASTX	160	4e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17223	GM_M23_A1_D12_MR	g3777527	BLASTX	711	3e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
17224	GM_M23_A1_E01_MF	g20999	BLASTN	303	5e-12	64	P.vulgaris gln-delta gene for plastid-located glutamine synthetase (promotor region)
17225	GM_M23_A1_F03_MF	g2586082	BLASTX	283	1e-22	43	(U72725) retrofit [Oryza longistaminata]
17226	GM_M23_A1_F03_MR	g3337361	BLASTX	240	1e-21	40	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
17227	GM_M23_A1_F04_MR	g4063760	BLASTX	134	1e-09	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17228	GM_M23_A1_F06_MF	g4063760	BLASTX	244	3e-38	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17229	GM_M23_A1_F10_MR	g3142328	BLASTN	1909	7e-80	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17230	GM_M23_A1_F11_MR	g905361	BLASTX	644	4e-66	98	(U22103) gag-protease polyprotein [Glycine max]
17231	GM_M23_A1_G02_MR	g505129	BLASTN	351	7e-09	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17232	GM_M23_A1_G03_MR	g100484	BLASTX	378	2e-33	52	hypothetical protein - garden snapdragon
17233	GM_M23_A1_G04_MF	g3687234	BLASTX	210	5e-15	39	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
17234	GM_M23_A1_G11_MR	g905361	BLASTX	232	1e-17	40	(U22103) gag-protease polyprotein [Glycine max]
17235	GM_M23_A1_G12_MR	g3341678	BLASTX	354	5e-31	52	(AC003672) putative zinc finger protein [Arabidopsis thaliana]
17236	GM_M23_A1_H05_MF	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17237	GM_M23_A1_H05_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17238	GM_M23_A1_H07_MR	g2384696	BLASTX	156	7e-10	48	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17239	GM_M23_A1_H08_MF	g4063760	BLASTX	253	1e-19	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17240	GM_M23_A2_A01_MR	g3097320	BLASTN	353	6e-09	68	Glycine max gene for Bd 30K, complete cds
17241	GM_M23_A2_A02_MF	g3810596	BLASTX	161	7e-10	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17242	GM_M23_A2_A08_MF	g18559	BLASTN	901	8e-34	76	G.max gene for catalase
17243	GM_M23_A2_A11_MR	g3319366	BLASTX	143	5e-09	56	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
17244	GM_M23_A2_B04_MR	g1167523	BLASTX	340	5e-32	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17245	GM_M23_A2_C01_MR	g1666236	BLASTX	218	4e-17	32	(U76261) unknown [Hordeum vulgare]
17246	GM_M23_A2_C06_MF	g4063756	BLASTN	443	6e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17247	GM_M23_A2_C08_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17248	GM_M23_A2_C08_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17249	GM_M23_A2_C10_MR	g18559	BLASTN	973	4e-37	77	G.max gene for catalase
17250	GM_M23_A2_C12_MR	g3510505	BLASTX	182	4e-21	41	(AF030881) pol polyprotein [Fugu rubripes]
17251	GM_M23_A2_D01_MF	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17252	GM_M23_A2_D01_MR	g4063756	BLASTN	429	2e-12	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17253	GM_M23_A2_D02_MR	g3046847	BLASTN	442	6e-13	67	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]
17254	GM_M23_A2_D03_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17255	GM_M23_A2_D11_MR	g476936	BLASTX	150	7e-09	90	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - mung bean
17256	GM_M23_A2_E02_MF	g2129618	BLASTX	192	4e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17257	GM_M23_A2_F03_MF	g3930515	BLASTX	121	4e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
17258	GM_M23_A2_F05_MF	g3901012	BLASTX	269	3e-27	82	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
17259	GM_M23_A2_F06_MF	g349606	BLASTN	361	4e-10	67	Buchnera aphidicola Arginyl tRNA synthetase (argS) gene, 5' end of cds and 16S ribosomal RNA promoter region.
17260	GM_M23_A2_F06_MR	g2129618	BLASTX	260	2e-20	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17261	GM_M23_A2_F07_MR	g3142328	BLASTN	1970	1e-82	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17262	GM_M23_A2_F11_MR	g905361	BLASTX	610	3e-61	97	(U22103) gag-protease polyprotein [Glycine max]
17263	GM_M23_A2_G01_MR	g3777526	BLASTN	418	7e-12	84	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17264	GM_M23_A2_G06_MR	g133421	BLASTX	616	2e-58	85	DNA-DIRECTED RNA POLYMERASE BETA CHAIN gi 81502 pir C29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast gi 295121 (M55297) RNA polymerase [Spinacia oleracea]
17265	GM_M23_A2_G08_MF	g4063760	BLASTX	221	4e-16	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17266	GM_M23_A2_H01_MF	g3758836	BLASTN	248	8e-09	69	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
17267	GM_M23_A2_H07_MR	g905361	BLASTX	192	3e-16	41	(U22103) gag-protease polyprotein [Glycine max]
17268	GM_M23_A2_H10_MF	g507910	BLASTN	366	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17269	GM_M23_A2_H10_MR	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
17270	GM_M23_A2_H12_MR	g3777527	BLASTX	693	3e-66	96	(AF053008) gag-pol polyprotein [Glycine max]
17271	GM_M23_B1_A03_MF	g342961	BLASTN	338	4e-09	63	paramecium species 4.172 mt dna dimer: replication init. region, clone 1.
17272	GM_M23_B1_A05_MF	g2129618	BLASTX	209	6e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17273	GM_M23_B1_A07_MR	g4038056	BLASTX	274	6e-22	47	(AC005897) putative transposon [Arabidopsis thaliana]
17274	GM_M23_B1_A11_MR	g4151068	BLASTX	241	2e-18	83	(Y10862) ribonucleotide reductase [Nicotiana tabacum]
17275	GM_M23_B1_B02_MF	g1944188	BLASTN	697	4e-25	73	Soybean DNA for nodulin 35, partial cds
17276	GM_M23_B1_B08_MR	g3859610	BLASTN	561	3e-18	65	Arabidopsis thaliana BAC T9E19
17277	GM_M23_B1_B11_MF	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17278	GM_M23_B1_C03_MF	g1666236	BLASTX	207	8e-16	30	(U76261) unknown [Hordeum vulgare]
17279	GM_M23_B1_C10_MF	g2098709	BLASTX	385	7e-35	68	(U82975) pectinesterase [Citrus sinensis]
17280	GM_M23_B1_C12_MR	g2462134	BLASTX	226	3e-17	35	(Y13368) reverse transcriptase [Beta vulgaris]
17281	GM_M23_B1_D07_MR	g2801680	BLASTN	468	9e-15	77	Glycine max telomere-associated sequence STAS9
17282	GM_M23_B1_D10_MR	g1708424	BLASTX	235	1e-27	65	ISOFLAVONE REDUCTASE HOMOLOG gi 1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]
17283	GM_M23_B1_D11_MR	g3695395	BLASTX	157	1e-09	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
17284	GM_M23_B1_D12_MF	g421955	BLASTX	103	2e-10	36	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17285	GM_M23_B1_D12_MR	g3810596	BLASTX	193	3e-13	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17286	GM_M23_B1_E02_MR	g2104945	BLASTN	482	8e-15	76	Glycine max copia-like retrotransposon Tgmr, complete sequence
17287	GM_M23_B1_E03_MR	g3287695	BLASTX	199	6e-29	82	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17288	GM_M23_B1_E04_MF	g3582333	BLASTX	148	7e-09	77	(AC005496) hypothetical protein [Arabidopsis thaliana]
17289	GM_M23_B1_E06_MR	g3250676	BLASTX	292	2e-24	44	(AL024486) putative protein [Arabidopsis thaliana]
17290	GM_M23_B1_F01_MF	g1144548	BLASTN	349	1e-09	62	Anopheles bwambae 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
17291	GM_M23_B1_F04_MF	g1167523	BLASTX	222	4e-16	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17292	GM_M23_B1_F04_MR	g3319362	BLASTX	280	1e-22	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17293	GM_M23_B1_F08_MF	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17294	GM_M23_B1_F08_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17295	GM_M23_B1_G01_MR	g3142328	BLASTN	800	3e-29	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17296	GM_M23_B1_G03_MF	g1146165	BLASTX	167	4e-11	74	(L47479) urophorphyrin III methylase [Arabidopsis thaliana]
17297	GM_M23_B1_G07_MF	g3047100	BLASTN	359	3e-09	65	Arabidopsis thaliana BAC F6N23
17298	GM_M23_B1_G08_MR	g3319366	BLASTX	155	2e-10	53	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
17299	GM_M23_B1_G12_MF	g100484	BLASTX	351	2e-30	59	hypothetical protein - garden snapdragon
17300	GM_M23_B1_H02_MR	g3777527	BLASTX	716	9e-69	94	(AF053008) gag-pol polyprotein [Glycine max]
17301	GM_M23_B1_H06_MF	g18695	BLASTN	449	2e-13	76	Soybean nodulin 22 gene
17302	GM_M23_B1_H07_MF	g1931647	BLASTX	162	3e-10	61	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]
17303	GM_M23_B1_H07_MR	g3135962	BLASTN	384	3e-10	65	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
17304	GM_M23_B1_H12_MR	g1946355	BLASTX	402	6e-36	52	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
17305	GM_M24_A1_A03_MF	g3097320	BLASTN	689	4e-24	74	Glycine max gene for Bd 30K, complete cds
17306	GM_M24_A1_A04_MF	g3645899	BLASTX	387	6e-34	59	(U68408) 5' end not determined experimentally [Zea mays]
17307	GM_M24_A1_A08_MF	g3097320	BLASTN	363	2e-09	67	Glycine max gene for Bd 30K, complete cds
17308	GM_M24_A1_A11_MR	g18559	BLASTN	966	9e-37	79	G.max gene for catalase
17309	GM_M24_A1_B07_MF	g507910	BLASTN	571	3e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
17310	GM_M24_A1_C07_MR	g2129618	BLASTX	178	1e-11	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17311	GM_M24_A1_C09_MF	g4063760	BLASTX	118	1e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17312	GM_M24_A1_C09_MR	g507910	BLASTN	695	8e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17313	GM_M24_A1_C10_MR	g2760830	BLASTX	470	7e-44	73	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
17314	GM_M24_A1_D04_MF	g626007	BLASTX	314	2e-26	57	phospholipase D (EC 3.1.4.4) - castor bean
17315	GM_M24_A1_D04_MR	g1711512	BLASTX	194	8e-14	86	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54) gi 1076577 pir S51598 signal recognition particle 54K protein - tomato (cv. UC82-B) gi 556902 (Z34527) 54-kD signal recognition particle (SRP) specific protein [Lycopersicon esculentum]
17316	GM_M24_A1_E02_MR	g587603	BLASTN	358	3e-09	62	P.falciparum gene for beta subunit RNA polymerase
17317	GM_M24_A1_E09_MR	g13767	BLASTN	337	4e-09	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
17318	GM_M24_A1_E10_MR	g1142699	BLASTN	494	5e-16	85	Glycine max satellite STR120-A.1.
17319	GM_M24_A1_F04_MR	g3550435	BLASTN	510	5e-16	62	Hordeum vulgare Hotr1 gene
17320	GM_M24_A1_F06_MR	g4063760	BLASTX	141	4e-10	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17321	GM_M24_A1_F11_MF	g1769898	BLASTX	116	2e-13	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17322	GM_M24_A1_F12_MR	g2262105	BLASTX	189	5e-13	57	(AC002343) unknown protein [Arabidopsis thaliana]
17323	GM_M24_A1_G04_MF	g4159702	BLASTN	497	2e-15	68	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence [Arabidopsis thaliana]
17324	GM_M24_A1_G05_MF	g3142328	BLASTN	872	2e-32	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17325	GM_M24_A1_H02_MF	g3097320	BLASTN	575	5e-19	86	Glycine max gene for Bd 30K, complete cds
17326	GM_M24_A1_H02_MR	g629693	BLASTX	301	5e-26	46	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
17327	GM_M24_A1_H04_MR	g3319345	BLASTX	106	5e-09	34	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
17328	GM_M24_A1_H07_MF	g4063760	BLASTX	407	6e-36	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17329	GM_M24_A1_H08_MF	g1168408	BLASTX	277	2e-23	93	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea gi 927507 (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]
17330	GM_M24_A2_A02_MF	g3097320	BLASTN	733	4e-26	77	Glycine max gene for Bd 30K, complete cds
17331	GM_M24_A2_A11_MR	g4160362	BLASTN	402	4e-11	64	Saccharomyces cerevisiae complete mitochondrial genome
17332	GM_M24_A2_B03_MF	g2586082	BLASTX	167	3e-10	58	(U72725) retrofit [Oryza longistaminata]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17333	GM_M24_A2_B07_MR	g2121303	BLASTN	360	3e-09	64	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
17334	GM_M24_A2_B08_MR	g130582	BLASTX	374	2e-32	52	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17335	GM_M24_A2_C02_MF	g2760837	BLASTX	382	1e-34	61	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]
17336	GM_M24_A2_C02_MR	g1946279	BLASTX	283	2e-29	50	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
17337	GM_M24_A2_C05_MR	g18695	BLASTN	371	7e-10	66	Soybean nodulin 22 gene
17338	GM_M24_A2_C07_MF	g4063760	BLASTX	197	1e-13	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17339	GM_M24_A2_C09_MR	g130582	BLASTX	226	1e-16	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17340	GM_M24_A2_C10_MF	g3176795	BLASTN	396	2e-11	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
17341	GM_M24_A2_C12_MF	g899342	BLASTX	251	1e-20	39	(X77110) chitinase, class V [Nicotiana tabacum]
17342	GM_M24_A2_D01_MR	g505129	BLASTN	349	8e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17343	GM_M24_A2_D02_MR	g4063760	BLASTX	336	5e-34	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17344	GM_M24_A2_D05_MR	g18559	BLASTN	361	3e-09	79	G.max gene for catalase
17345	GM_M24_A2_D07_MR	g1666236	BLASTX	144	9e-09	30	(U76261) unknown [Hordeum vulgare]
17346	GM_M24_A2_D09_MF	g3645899	BLASTX	389	4e-34	71	(U68408) 5' end not determined experimentally [Zea mays]
17347	GM_M24_A2_D10_MF	g2443320	BLASTX	226	2e-29	53	(D85597) polyprotein [Oryza australiensis]
17348	GM_M24_A2_E01_MF	g4038471	BLASTX	183	1e-18	76	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
17349	GM_M24_A2_E09_MR	g3097320	BLASTN	469	3e-14	68	Glycine max gene for Bd 30K, complete cds
17350	GM_M24_A2_E11_MF	g4063760	BLASTX	221	4e-16	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17351	GM_M24_A2_E12_MR	g3805964	BLASTX	560	2e-53	71	(Y13773) laccase [Populus balsamifera subsp. trichocarpa]
17352	GM_M24_A2_F04_MR	g18559	BLASTN	370	1e-09	70	G.max gene for catalase
17353	GM_M24_A2_F05_MF	g3142379	BLASTX	267	7e-29	68	(AF053008) envelope-like [Glycine max]
17354	GM_M24_A2_F07_MF	g2626753	BLASTX	195	2e-22	74	(AB008782) sulfate transporter [Arabidopsis thaliana]
17355	GM_M24_A2_F08_MF	g4033838	BLASTX	287	5e-24	63	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17356	GM_M24_A2_F08_MR	g3641780	BLASTN	354	6e-09	62	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
17357	GM_M24_A2_G03_MF	g3097320	BLASTN	451	2e-13	72	Glycine max gene for Bd 30K, complete cds
17358	GM_M24_A2_G06_MR	g3080423	BLASTX	320	9e-27	50	(AL022604) putative protein [Arabidopsis thaliana]
17359	GM_M24_A2_G08_MR	g3097320	BLASTN	418	7e-12	72	Glycine max gene for Bd 30K, complete cds
17360	GM_M24_A2_G10_MF	g2443320	BLASTX	216	2e-28	56	(D85597) polyprotein [Oryza australiensis]
17361	GM_M24_A2_H05_MF	g507910	BLASTN	524	5e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17362	GM_M24_A2_H05_MR	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17363	GM_M24_B1_A01_MF	g4063760	BLASTX	468	2e-42	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17364	GM_M24_B1_A08_MR	g4063756	BLASTN	485	7e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17365	GM_M24_B1_A12_MR	g3426334	BLASTN	424	4e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
17366	GM_M24_B1_B01_MR	g507910	BLASTN	591	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17367	GM_M24_B1_B02_MF	g1769897	BLASTX	305	7e-26	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17368	GM_M24_B1_B05_MR	g1480927	BLASTN	626	2e-21	83	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
17369	GM_M24_B1_B06_MF	g3482916	BLASTX	234	7e-18	39	(AC003970) Hypothetical protein [Arabidopsis thaliana]
17370	GM_M24_B1_B09_MR	g3810596	BLASTX	139	2e-13	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17371	GM_M24_B1_B11_MR	g3142328	BLASTN	472	2e-14	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17372	GM_M24_B1_C03_MR	g1769897	BLASTX	308	4e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17373	GM_M24_B1_C04_MF	g2827992	BLASTX	103	7e-12	64	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]
17374	GM_M24_B1_C05_MF	g3355473	BLASTX	183	2e-12	53	(AC004218) hypothetical protein [Arabidopsis thaliana]
17375	GM_M24_B1_C05_MR	g3513747	BLASTX	227	1e-16	33	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17376	GM_M24_B1_C06_MF	g3915873	BLASTX	658	6e-64	98	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) (NODULIN-100) >gi 2606081 (AF030231) sucrose synthase [Glycine max]
17377	GM_M24_B1_C06_MR	g2052508	BLASTX	153	9e-20	70	(U95759) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]
17378	GM_M24_B1_C11_MF	g4092470	BLASTN	829	2e-30	70	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
17379	GM_M24_B1_D03_MR	g4038056	BLASTX	116	1e-11	50	(AC005897) putative transposon [Arabidopsis thaliana]
17380	GM_M24_B1_D04_MF	g3377834	BLASTX	149	1e-08	27	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17381	GM_M24_B1_D05_MF	g4063760	BLASTX	448	2e-40	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17382	GM_M24_B1_D05_MR	g507910	BLASTN	434	5e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17383	GM_M24_B1_D07_MF	g3777527	BLASTX	238	8e-18	41	(AF053008) gag-pol polyprotein [Glycine max]
17384	GM_M24_B1_D07_MR	g3142328	BLASTN	652	1e-22	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17385	GM_M24_B1_D11_MF	g3810595	BLASTX	222	4e-16	45	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
17386	GM_M24_B1_E01_MR	g18559	BLASTN	710	4e-25	72	G.max gene for catalase
17387	GM_M24_B1_E03_MR	g2398523	BLASTX	159	1e-10	72	(Y13721) Transcription factor [Arabidopsis thaliana]
17388	GM_M24_B1_E07_MF	g66619	BLASTX	250	8e-25	74	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - tomato
17389	GM_M24_B1_E10_MR	g1931641	BLASTX	157	1e-09	43	(U95973) unknown protein [Arabidopsis thaliana]
17390	GM_M24_B1_E11_MR	g13556	BLASTN	244	4e-12	61	Yeast mitochondrial DNA with tRNA-Asp gene
17391	GM_M24_B1_E12_MR	g905361	BLASTX	205	8e-15	37	(U22103) gag-protease polyprotein [Glycine max]
17392	GM_M24_B1_F01_MR	g3779030	BLASTX	195	9e-15	28	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
17393	GM_M24_B1_F03_MR	g3777527	BLASTX	288	4e-23	43	(AF053008) gag-pol polyprotein [Glycine max]
17394	GM_M24_B1_F04_MR	g629693	BLASTX	173	9e-12	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
17395	GM_M24_B1_F06_MF	g1666236	BLASTX	97	6e-09	28	(U76261) unknown [Hordeum vulgare]
17396	GM_M24_B1_G07_MF	g18559	BLASTN	377	5e-10	75	G.max gene for catalase
17397	GM_M24_B1_G09_MR	g3845213	BLASTN	357	4e-09	62	Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence
17398	GM_M24_B1_G11_MF	g4063760	BLASTX	227	9e-17	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17399	GM_M24_B1_H06_MR	g2522228	BLASTX	249	3e-20	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
17400	GM_M24_B2_A03_MF	g130188	BLASTX	307	3e-31	71	PHYTOCHROME A gi 81937 pir S06856 phytochrome - garden pea gi 169132 (M37217) phytochrome [Pisum sativum] gi 295830 (X14077) phytochrome apoprotein [Pisum sativum] gi 226757 prf 1604466A phytochrome [Pisum sativum]
17401	GM_M24_B2_B02_MF	g3142328	BLASTN	1901	2e-79	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17402	GM_M24_B2_B04_MF	g4063756	BLASTN	450	3e-13	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17403	GM_M24_B2_B05_MR	g505129	BLASTN	422	4e-12	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17404	GM_M24_B2_C03_MR	g2462936	BLASTX	187	6e-14	49	(Y12321) open reading frame 2 [Brassica oleracea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17405	GM_M24_B2_C09_MF	g2245073	BLASTN	377	5e-10	69	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
17406	GM_M24_B2_C12_MF	g3142328	BLASTN	482	1e-29	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17407	GM_M24_B2_D04_MF	g3820976	BLASTN	374	7e-10	63	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
17408	GM_M24_B2_D05_MR	g2982431	BLASTX	239	5e-18	40	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
17409	GM_M24_B2_D06_MR	g2961349	BLASTX	189	3e-14	41	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
17410	GM_M24_B2_D08_MF	g3097320	BLASTN	496	2e-15	70	Glycine max gene for Bd 30K, complete cds
17411	GM_M24_B2_E04_MF	g18559	BLASTN	927	5e-35	77	G.max gene for catalase
17412	GM_M24_B2_E10_MF	g3645899	BLASTX	177	9e-16	41	(U68408) 5' end not determined experimentally [Zea mays]
17413	GM_M24_B2_E11_MF	g2522228	BLASTX	348	5e-31	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
17414	GM_M24_B2_E11_MR	g3319362	BLASTX	178	1e-11	31	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17415	GM_M24_B2_F02_MR	g99755	BLASTX	318	5e-29	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
17416	GM_M24_B2_F03_MF	g2586082	BLASTX	321	1e-26	55	(U72725) retrofit [Oryza longistaminata]
17417	GM_M24_B2_F05_MR	g2459417	BLASTX	154	6e-11	75	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]
17418	GM_M24_B2_F06_MF	g4063760	BLASTX	223	2e-16	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17419	GM_M24_B2_F09_MF	g2129618	BLASTX	196	1e-13	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17420	GM_M24_B2_G02_MF	g2764526	BLASTN	365	2e-09	60	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17421	GM_M24_B2_G04_MR	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17422	GM_M24_B2_G07_MR	g4063760	BLASTX	218	1e-19	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17423	GM_M24_B2_G09_MR	g1769899	BLASTX	315	2e-27	78	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17424	GM_M24_B2_G12_MF	g1769897	BLASTX	163	2e-10	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17425	GM_M24_B2_H01_MF	g4038056	BLASTX	251	2e-19	42	(AC005897) putative transposon [Arabidopsis thaliana]
17426	GM_M24_B2_H01_MR	g4150933	BLASTN	395	8e-11	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17427	GM_M24_B2_H03_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17428	GM_M24_B2_H03_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17429	GM_M24_B2_H04_MF	g2995405	BLASTX	172	4e-11	37	(Y12432) polyprotein [Ananas comosus]
17430	GM_M24_B2_H04_MR	g505129	BLASTN	423	4e-12	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17431	GM_M24_B2_H06_MF	g2522228	BLASTX	389	3e-35	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
17432	GM_M24_B2_H07_MR	g3777527	BLASTX	653	5e-62	93	(AF053008) gag-pol polyprotein [Glycine max]
17433	GM_M24_B2_H10_MR	g4063760	BLASTX	504	3e-46	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17434	GM_M24_B2_H11_MR	g3142328	BLASTN	862	4e-32	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17435	GM_M24_B2_H12_MF	g3036807	BLASTX	261	6e-26	67	(AL022373) putative protein [Arabidopsis thaliana]
17436	GM_M25_A1_A03_MF	g905361	BLASTX	618	1e-59	97	(U22103) gag-protease polyprotein [Glycine max]
17437	GM_M25_A1_A05_MR	g3142328	BLASTN	999	3e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17438	GM_M25_A1_B01_MR	g3777527	BLASTX	196	3e-25	80	(AF053008) gag-pol polyprotein [Glycine max]
17439	GM_M25_A1_B04_MR	g2656026	BLASTN	354	6e-09	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20
17440	GM_M25_A1_B10_MR	g507910	BLASTN	350	3e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence
17441	GM_M25_A1_C01_MF	g3142330	BLASTX	610	9e-59	93	(U96295) envelope-like [Glycine max]
17442	GM_M25_A1_C06_MF	g3645899	BLASTX	215	2e-22	48	(U68408) 5' end not determined experimentally [Zea mays]
17443	GM_M25_A1_D05_MR	g905361	BLASTX	714	9e-70	99	(U22103) gag-protease polyprotein [Glycine max]
17444	GM_M25_A1_D08_MR	g4160362	BLASTN	392	1e-10	63	Saccharomyces cerevisiae complete mitochondrial genome
17445	GM_M25_A1_D09_MF	g4160362	BLASTN	352	7e-09	64	Saccharomyces cerevisiae complete mitochondrial genome
17446	GM_M25_A1_E03_MR	g3845197	BLASTN	422	5e-12	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
17447	GM_M25_A1_E07_MF	g20612	BLASTN	376	2e-24	75	Phaseolus vulgaris tRNA-Pro(UGG1) gene cluster
17448	GM_M25_A1_E07_MR	g2244866	BLASTX	539	9e-50	73	(Z97337) hypothetical protein [Arabidopsis thaliana]
17449	GM_M25_A1_F02_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
17450	GM_M25_A1_F02_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17451	GM_M25_A1_F05_MR	g3645899	BLASTX	286	4e-23	48	(U68408) 5' end not determined experimentally [Zea mays]
17452	GM_M25_A1_F06_MR	g100484	BLASTX	193	2e-13	37	hypothetical protein - garden snapdragon
17453	GM_M25_A1_F08_MR	g2586082	BLASTX	224	3e-22	48	(U72725) retrofit [Oryza longistaminata]
17454	GM_M25_A1_F09_MF	g4038056	BLASTX	344	2e-29	54	(AC005897) putative transposon [Arabidopsis thaliana]
17455	GM_M25_A1_F11_MR	g3142328	BLASTN	733	3e-26	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17456	GM_M25_A1_G02_MF	g3097320	BLASTN	1208	1e-47	82	Glycine max gene for Bd 30K, complete cds
17457	GM_M25_A1_G03_MF	g1707020	BLASTX	407	3e-37	65	(U78721) hypothetical protein [Arabidopsis thaliana]
17458	GM_M25_A1_G05_MF	g505129	BLASTN	355	4e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17459	GM_M25_A1_G11_MR	g507910	BLASTN	552	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
17460	GM_M25_A1_G12_MR	g3845197	BLASTN	524	1e-16	70	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
17461	GM_M25_A1_H01_MF	g3142328	BLASTN	710	4e-25	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17462	GM_M25_A1_H05_MF	g1399271	BLASTX	326	6e-28	79	(U31833) calmodulin-domain protein kinase CDPK isoform 2 [Arabidopsis thaliana]
17463	GM_M25_A1_H12_MR	g2828327	BLASTN	510	7e-17	67	Lycopersicon esculentum cv Red River unknown sequence PCR random amplified RAPD band 10
17464	GM_M25_A2_A05_MF	g1916643	BLASTX	281	7e-24	60	(U71604) desacetoxyvindoline 4-hydroxylase [Catharanthus roseus]
17465	GM_M25_A2_A08_MR	g3033389	BLASTX	194	2e-13	37	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17466	GM_M25_A2_A10_MR	g3549672	BLASTX	154	1e-09	93	(AL031394) putative protein [Arabidopsis thaliana]
17467	GM_M25_A2_B02_MF	g170080	BLASTN	490	3e-15	78	Soybean seed lectin gene transposable element tgm1.
17468	GM_M25_A2_B08_MF	g3650039	BLASTX	269	1e-21	49	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17469	GM_M25_A2_B09_MF	g3142328	BLASTN	806	2e-29	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17470	GM_M25_A2_B11_MR	g2129618	BLASTX	201	4e-14	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17471	GM_M25_A2_C02_MR	g409571	BLASTN	333	6e-09	66	Helicoverpa armigera mitochondrion D-loop, partial 12S rRNA gene, and partial tRNA-Met gene.
17472	GM_M25_A2_C03_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17473	GM_M25_A2_C10_MF	g130582	BLASTX	171	3e-17	56	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17474	GM_M25_A2_D01_MR	g18588	BLASTN	370	1e-09	75	Soybean gene 3 for chalcone synthetase protein
17475	GM_M25_A2_D03_MF	g2997694	BLASTX	148	1e-09	37	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
17476	GM_M25_A2_D04_MF	g1171583	BLASTN	377	5e-10	61	P.falciparum complete gene map of plastid-like DNA (IR-A)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17477	GM_M25_A2_D04_MR	g2244752	BLASTX	146	1e-08	38	(Z97335) hypothetical protein [Arabidopsis thaliana]
17478	GM_M25_A2_D08_MF	g85105	BLASTX	183	4e-12	36	pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 gi 8702 (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]
17479	GM_M25_A2_D12_MR	g3367534	BLASTX	660	5e-63	90	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana]
17480	GM_M25_A2_E07_MF	g2129618	BLASTX	196	1e-13	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17481	GM_M25_A2_F03_MR	g116162	BLASTX	212	1e-16	56	G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) gi 2146780 pir S74672 mitotic-specific cyclin S13-7 - soybean (fragment) gi 829266 (X62303) mitotic cyclin [Glycine max]
17482	GM_M25_A2_F04_MF	g2323254	BLASTN	392	1e-10	64	Human Chromosome X, complete sequence [Homo sapiens]
17483	GM_M25_A2_F09_MR	g3097320	BLASTN	603	3e-20	69	Glycine max gene for Bd 30K, complete cds
17484	GM_M25_A2_F10_MR	g130582	BLASTX	281	2e-22	42	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17485	GM_M25_A2_F11_MR	g3097320	BLASTN	460	8e-14	69	Glycine max gene for Bd 30K, complete cds
17486	GM_M25_A2_F12_MF	g421955	BLASTX	206	2e-15	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17487	GM_M25_A2_G04_MF	g1171591	BLASTN	363	2e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
17488	GM_M25_A2_G05_MR	g2341025	BLASTX	143	5e-16	74	(AC000104) F19P19.2 [Arabidopsis thaliana]
17489	GM_M25_A2_G09_MF	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17490	GM_M25_A2_G09_MR	g3777527	BLASTX	698	8e-67	97	(AF053008) gag-pol polyprotein [Glycine max]
17491	GM_M25_A2_H01_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17492	GM_M25_A2_H02_MR	g1666236	BLASTX	198	8e-15	33	(U76261) unknown [Hordeum vulgare]
17493	GM_M25_A2_H05_MF	g4038056	BLASTX	251	2e-19	42	(AC005897) putative transposon [Arabidopsis thaliana]
17494	GM_M25_A2_H07_MR	g3845197	BLASTN	431	2e-12	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
17495	GM_M25_A2_H10_MR	g99922	BLASTX	455	2e-42	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17496	GM_M25_A2_H12_MF	g114610	BLASTX	248	5e-23	80	ATP SYNTHASE EPSILON CHAIN gi 67866 pir PWNTE H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain - common tobacco chloroplast gi 11839 (Z00044) ATPase epsilon subunit [Nicotiana tabacum] gi 552955 (K00507) ATPase epsilon subunit [Nicotiana tabacum] gi 225207 prf 1211235AM ATPase epsilon [Nicotiana tabacum]
17497	GM_M25_B1_A01_MR	g2842490	BLASTX	301	5e-26	51	(AL021749) heat-shock protein [Arabidopsis thaliana]
17498	GM_M25_B1_A05_MR	g2760331	BLASTX	232	2e-17	35	(AC002130) F1N21.16 [Arabidopsis thaliana]
17499	GM_M25_B1_A06_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17500	GM_M25_B1_A11_MR	g4126312	BLASTN	489	5e-15	64	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
17501	GM_M25_B1_B02_MF	g130582	BLASTX	415	9e-37	63	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17502	GM_M25_B1_B09_MF	g4063760	BLASTX	174	1e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17503	GM_M25_B1_B09_MR	g1769898	BLASTX	266	2e-21	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17504	GM_M25_B1_B11_MR	g285741	BLASTX	226	2e-17	49	(D14550) EDGP precursor [Daucus carota]
17505	GM_M25_B1_B12_MF	g729092	BLASTX	563	8e-54	81	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
17506	GM_M25_B1_B12_MR	g531389	BLASTX	255	1e-19	41	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
17507	GM_M25_B1_C05_MR	g505129	BLASTN	358	3e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17508	GM_M25_B1_C10_MR	g4063760	BLASTX	566	6e-53	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17509	GM_M25_B1_C12_MF	g2149808	BLASTX	167	2e-24	73	(U92853) maturase [Betula papyrifera]
17510	GM_M25_B1_D01_MR	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17511	GM_M25_B1_D05_MF	g4063760	BLASTX	123	6e-14	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17512	GM_M25_B1_D05_MR	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17513	GM_M25_B1_D06_MR	g13534	BLASTN	366	1e-09	61	Yeast (S. cerevisiae) mitochondrial gene for cytochrome B extending from map position 71.3 to 80.2. (Strain D273-10B.)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17514	GM_M25_B1_D09_MF	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17515	GM_M25_B1_D10_MF	g421955	BLASTX	196	2e-27	41	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17516	GM_M25_B1_E03_MR	g3184283	BLASTX	278	3e-22	69	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
17517	GM_M25_B1_E05_MF	g507910	BLASTN	386	8e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17518	GM_M25_B1_E07_MR	g2708743	BLASTX	116	2e-11	48	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
17519	GM_M25_B1_F03_MF	g4063760	BLASTX	494	3e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17520	GM_M25_B1_F06_MF	g905361	BLASTX	192	2e-13	36	(U22103) gag-protease polyprotein [Glycine max]
17521	GM_M25_B1_G04_MF	g4063756	BLASTN	480	1e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17522	GM_M25_B1_G04_MR	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17523	GM_M25_B1_G07_MR	g3650039	BLASTX	247	3e-19	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17524	GM_M25_B1_G10_MR	g905361	BLASTX	237	3e-18	42	(U22103) gag-protease polyprotein [Glycine max]
17525	GM_M25_B1_G12_MF	g2764526	BLASTN	428	3e-12	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17526	GM_M25_B2_A01_MF	g2522228	BLASTX	182	1e-12	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
17527	GM_M25_B2_A01_MR	g3777527	BLASTX	463	9e-47	94	(AF053008) gag-pol polyprotein [Glycine max]
17528	GM_M25_B2_A06_MF	g2522228	BLASTX	171	2e-11	38	(AB007466) reverse transcriptase-like protein [Vicia faba]
17529	GM_M25_B2_A07_MF	g1769897	BLASTX	183	1e-12	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17530	GM_M25_B2_A08_MF	g4063760	BLASTX	178	2e-11	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17531	GM_M25_B2_A10_MF	g3452140	BLASTX	180	3e-13	64	(AJ004901) resistance protein [Glycine max]
17532	GM_M25_B2_A11_MF	g3395435	BLASTX	256	1e-20	44	(AC004683) myosin heavy chain-like protein [Arabidopsis thaliana]
17533	GM_M25_B2_B02_MF	g3377855	BLASTX	161	1e-10	37	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
17534	GM_M25_B2_B03_MF	g1000971	BLASTN	293	5e-10	70	Hansenula wingei mitochondrial DNA, complete sequence
17535	GM_M25_B2_B04_MF	g3777527	BLASTX	177	3e-11	31	(AF053008) gag-pol polyprotein [Glycine max]
17536	GM_M25_B2_B05_MF	g3097320	BLASTN	489	4e-15	65	Glycine max gene for Bd 30K, complete cds
17537	GM_M25_B2_B08_MF	g3777527	BLASTX	572	2e-53	92	(AF053008) gag-pol polyprotein [Glycine max]
17538	GM_M25_B2_B09_MF	g292994	BLASTN	366	2e-10	64	Jalmenus evagoras evagoras mitochondrial D-loop DNA, transfer RNA-Met gene, and 12S ribosomal RNA gene, 5' end.
17539	GM_M25_B2_B09_MR	g2462058	BLASTX	153	3e-10	50	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17540	GM_M25_B2_C03_MR	g3758836	BLASTN	373	5e-11	64	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
17541	GM_M25_B2_C04_MR	g2501353	BLASTX	216	1e-22	89	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
17542	GM_M25_B2_C05_MF	g3033389	BLASTX	167	2e-10	37	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17543	GM_M25_B2_C11_MF	g3142328	BLASTN	894	2e-33	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17544	GM_M25_B2_D01_MR	g3873182	BLASTN	548	1e-17	68	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
17545	GM_M25_B2_D03_MR	g905361	BLASTX	680	4e-66	97	(U22103) gag-protease polyprotein [Glycine max]
17546	GM_M25_B2_D06_MR	g99922	BLASTX	692	2e-67	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17547	GM_M25_B2_D07_MF	g4150930	BLASTN	371	1e-09	71	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
17548	GM_M25_B2_D08_MF	g507910	BLASTN	740	8e-27	89	Glycine max BSR-101 satellite SB92 genomic sequence.
17549	GM_M25_B2_D08_MR	g4063756	BLASTN	464	6e-14	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17550	GM_M25_B2_D09_MR	g2764525	BLASTN	736	2e-26	68	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
17551	GM_M25_B2_D10_MF	g2462826	BLASTX	248	5e-19	54	(AF000657) unknown protein [Arabidopsis thaliana]
17552	GM_M25_B2_D10_MR	g2632254	BLASTX	167	5e-11	54	(Y12465) serine/threonine kinase [Sorghum bicolor]
17553	GM_M25_B2_D12_MF	g2522227	BLASTX	217	4e-17	55	(AB007466) retrotransposon-like gene, the first amino acid was determined to be glycine [Vicia faba]
17554	GM_M25_B2_E05_MF	g4063760	BLASTX	335	3e-28	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17555	GM_M25_B2_E06_MF	g3047116	BLASTX	184	4e-13	68	(AF058919) No definition line found [Arabidopsis thaliana]
17556	GM_M25_B2_E08_MF	g1684913	BLASTX	265	7e-21	46	(U77888) receptor-like protein kinase [Ipomoea nil]
17557	GM_M25_B2_F02_MF	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17558	GM_M25_B2_F02_MR	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17559	GM_M25_B2_F03_MF	g342964	BLASTN	349	1e-09	61	paramecium species 5.311 mt dna dimer: replication init. region.
17560	GM_M25_B2_F03_MR	g99730	BLASTX	164	5e-23	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17561	GM_M25_B2_F05_MF	g99922	BLASTX	309	7e-27	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17562	GM_M25_B2_F05_MR	g99922	BLASTX	176	3e-12	64	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17563	GM_M25_B2_G04_MF	g4063756	BLASTN	485	7e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17564	GM_M25_B2_G05_MF	g4038056	BLASTX	340	5e-29	50	(AC005897) putative transposon [Arabidopsis thaliana]
17565	GM_M25_B2_G05_MR	g3142328	BLASTN	1318	8e-53	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17566	GM_M25_B2_G06_MF	g1769897	BLASTX	167	6e-11	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17567	GM_M25_B2_G07_MR	g226407	BLASTX	286	6e-30	68	retrotransposon del1-46 [Lilium henryi]
17568	GM_M25_B2_G10_MF	g3176693	BLASTN	341	3e-15	78	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]
17569	GM_M25_B2_G11_MF	g3738302	BLASTX	91	6e-09	61	(AC005309) tubby-like protein [Arabidopsis thaliana]
17570	GM_M25_B2_G11_MR	g3337361	BLASTX	215	9e-16	62	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
17571	GM_M25_B2_G12_MR	g3319366	BLASTX	186	8e-14	40	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
17572	GM_M25_B2_H04_MR	g3319362	BLASTX	134	2e-25	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17573	GM_M25_B2_H05_MR	g1167523	BLASTX	156	3e-09	29	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17574	GM_M25_B2_H06_MR	g3426334	BLASTN	350	8e-09	61	Pisum sativum pectin methylesterase (repme1) gene, complete cds
17575	GM_M25_B2_H09_MF	g507910	BLASTN	393	4e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
17576	GM_M25_B2_H09_MR	g507910	BLASTN	387	7e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17577	GM_M25_B2_H10_MF	g4063756	BLASTN	450	3e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17578	GM_M25_B2_H12_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17579	GM_M25_B2_H12_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17580	GM_M26_A1_A04_MR	g3930515	BLASTX	107	1e-10	47	(AF059674) putative gag protein [Nicotiana tabacum]
17581	GM_M26_A1_A07_MF	g3287696	BLASTX	292	5e-24	55	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
17582	GM_M26_A1_A11_MF	g3859610	BLASTN	395	8e-11	65	Arabidopsis thaliana BAC T9E19
17583	GM_M26_A1_A12_MF	g3941522	BLASTX	175	1e-12	74	(AF062915) putative transcription factor [Arabidopsis thaliana]
17584	GM_M26_A1_B03_MF	g3142379	BLASTX	316	1e-27	56	(AF053008) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17585	GM_M26_A1_B05_MR	g3063690	BLASTN	353	7e-09	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)
17586	GM_M26_A1_B06_MR	g3695399	BLASTX	214	2e-15	40	(AF096372) contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]
17587	GM_M26_A1_B09_MF	g2522228	BLASTX	343	2e-30	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
17588	GM_M26_A1_C09_MF	g3142328	BLASTN	545	1e-17	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17589	GM_M26_A1_D02_MR	g4063760	BLASTX	300	1e-24	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17590	GM_M26_A1_D03_MF	g3176689	BLASTX	156	6e-09	29	(AC003671) Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]
17591	GM_M26_A1_D03_MR	g3461840	BLASTX	313	9e-26	44	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
17592	GM_M26_A1_D09_MF	g2342686	BLASTX	159	1e-10	46	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209) ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
17593	GM_M26_A1_E01_MR	g3645899	BLASTX	374	2e-32	59	(U68408) 5' end not determined experimentally [Zea mays]
17594	GM_M26_A1_E04_MF	g3650039	BLASTX	209	3e-15	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17595	GM_M26_A1_E11_MR	g3645899	BLASTX	241	3e-19	48	(U68408) 5' end not determined experimentally [Zea mays]
17596	GM_M26_A1_F09_MF	g218268	BLASTN	389	4e-11	76	Glycine max pol gene for reverse transcriptase, partial sequence
17597	GM_M26_A1_G01_MF	g3777527	BLASTX	594	9e-56	85	(AF053008) gag-pol polyprotein [Glycine max]
17598	GM_M26_A1_G03_MR	g3645899	BLASTX	366	1e-31	50	(U68408) 5' end not determined experimentally [Zea mays]
17599	GM_M26_A1_G05_MF	g3157933	BLASTX	224	1e-16	45	(AC002131) Contains similarity to box helicases gb U29097 from C. elegans and to the ENBP1 gene product gb X95995 from Vicia sativa. [Arabidopsis thaliana]
17600	GM_M26_A1_G08_MR	g461812	BLASTX	184	3e-26	47	CYTOCHROME P450 LXXII (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) gi 167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] gi 445604 prf 1909351A cytochrome P450 [Catharanthus roseus]
17601	GM_M26_A1_G09_MR	g2642431	BLASTX	338	2e-28	53	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
17602	GM_M26_A1_G10_MF	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17603	GM_M26_A1_G10_MR	g507910	BLASTN	371	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17604	GM_M26_A1_H06_MF	g2335089	BLASTN	847	3e-31	73	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17605	GM_M26_A2_A05_MR	g2129618	BLASTX	139	4e-09	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17606	GM_M26_A2_B03_MF	g322701	BLASTX	436	3e-40	88	Tubulin beta-2 chain - soybean
17607	GM_M26_A2_B04_MF	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
17608	GM_M26_A2_B04_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17609	GM_M26_A2_B11_MF	g3142379	BLASTX	289	1e-24	63	(AF053008) envelope-like [Glycine max]
17610	GM_M26_A2_C02_MF	g4006827	BLASTX	277	2e-22	48	(AC005970) subtilisin-like protease [Arabidopsis thaliana]
17611	GM_M26_A2_C02_MR	g1944188	BLASTN	529	3e-17	70	Soybean DNA for nodulin 35, partial cds
17612	GM_M26_A2_C06_MF	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17613	GM_M26_A2_C07_MR	g4063760	BLASTX	158	2e-09	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17614	GM_M26_A2_C12_MR	g505129	BLASTN	304	4e-10	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17615	GM_M26_A2_D02_MF	g3097320	BLASTN	444	5e-13	72	Glycine max gene for Bd 30K, complete cds
17616	GM_M26_A2_D02_MR	g2522230	BLASTX	301	5e-26	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17617	GM_M26_A2_D03_MR	g3097320	BLASTN	1182	2e-46	81	Glycine max gene for Bd 30K, complete cds
17618	GM_M26_A2_D06_MF	g3142328	BLASTN	976	3e-37	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17619	GM_M26_A2_D07_MR	g2522230	BLASTX	184	1e-13	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17620	GM_M26_A2_D10_MF	g99922	BLASTX	603	5e-58	88	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17621	GM_M26_A2_D12_MR	g18559	BLASTN	928	5e-35	77	G.max gene for catalase
17622	GM_M26_A2_E03_MR	g1666236	BLASTX	98	2e-09	38	(U76261) unknown [Hordeum vulgare]
17623	GM_M26_A2_F02_MF	g2462134	BLASTX	166	8e-11	33	(Y13368) reverse transcriptase [Beta vulgaris]
17624	GM_M26_A2_F03_MR	g1142699	BLASTN	1163	3e-46	83	Glycine max satellite STR120-A.1.
17625	GM_M26_A2_F04_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17626	GM_M26_A2_F05_MF	g1813704	BLASTX	227	9e-17	40	(U82559) aldehyde oxidase 1 homolog [Lycopersicon esculentum]
17627	GM_M26_A2_F08_MF	g4063760	BLASTX	368	9e-32	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17628	GM_M26_A2_F09_MR	g2598589	BLASTX	317	1e-27	46	(Y15367) MtN19 [Medicago truncatula]
17629	GM_M26_A2_G01_MR	g905361	BLASTX	385	2e-34	100	(U22103) gag-protease polyprotein [Glycine max]
17630	GM_M26_A2_G04_MF	g1230613	BLASTN	353	3e-09	75	Lupinus albus isoflavone reductase-like protein mRNA, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17631	GM_M26_A2_G06_MR	g130582	BLASTX	170	1e-10	44	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17632	GM_M26_A2_H02_MR	g3059060	BLASTN	416	9e-12	61	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
17633	GM_M26_A2_H05_MR	g2129581	BLASTX	496	9e-46	75	envelope Ca2+-ATPase precursor - Arabidopsis thaliana gi 471089 gnl PID d1003597 (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana]
17634	GM_M26_A2_H08_MF	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17635	GM_M26_A2_H08_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17636	GM_M26_B2_A07_MR	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17637	GM_M26_B2_C10_MR	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17638	GM_M26_B2_C11_MR	g1769898	BLASTX	148	4e-10	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17639	GM_M26_B2_D06_MR	g421955	BLASTX	134	2e-27	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17640	GM_M26_B2_D10_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17641	GM_M26_B2_E07_MR	g507910	BLASTN	389	6e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17642	GM_M26_B2_F03_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
17643	GM_M26_B2_F05_MR	g2351073	BLASTN	761	2e-27	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24
17644	GM_M26_B2_F08_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17645	GM_M26_B2_F10_MR	g3269288	BLASTX	142	4e-09	58	(AL030978) putative protein [Arabidopsis thaliana]
17646	GM_M26_B2_G02_MR	g905361	BLASTX	289	6e-24	96	(U22103) gag-protease polyprotein [Glycine max]
17647	GM_M26_B2_G03_MR	g13774	BLASTN	353	3e-09	60	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
17648	GM_M26_B2_G05_MR	g3097320	BLASTN	456	1e-13	70	Glycine max gene for Bd 30K, complete cds
17649	GM_M26_B2_G07_MR	g18559	BLASTN	997	3e-38	76	G.max gene for catalase
17650	GM_M26_B2_G08_MR	g1480927	BLASTN	1064	9e-42	94	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17651	GM_M26_B2_H01_MR	g3142328	BLASTN	1091	2e-42	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17652	GM_M26_B2_H03_MR	g1142702	BLASTN	343	5e-09	68	Glycine max satellite STR120-A.4.
17653	GM_M26_B2_H05_MR	g2808683	BLASTX	182	4e-12	35	(AJ002235) Cf-4 [Lycopersicon hirsutum]
17654	GM_M26_B2_H09_MR	g116054	BLASTX	158	6e-10	82	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) gi 280393 pir A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]
17655	GM_M26_B2_H10_MR	g3128201	BLASTX	126	3e-09	33	(AC004521) unknown protein [Arabidopsis thaliana]
17656	GM_M27_A1_B01_MR	g1769898	BLASTX	367	5e-41	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17657	GM_M27_A1_B03_MF	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17658	GM_M27_A1_B03_MR	g507910	BLASTN	638	3e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
17659	GM_M27_A1_B07_MF	g507910	BLASTN	488	2e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
17660	GM_M27_A1_B09_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17661	GM_M27_A1_B09_MR	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17662	GM_M27_A1_B11_MF	g2129709	BLASTX	160	1e-09	32	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17663	GM_M27_A1_C02_MF	g4038056	BLASTX	328	9e-28	52	(AC005897) putative transposon [Arabidopsis thaliana]
17664	GM_M27_A1_C03_MF	g3097320	BLASTN	543	2e-17	84	Glycine max gene for Bd 30K, complete cds
17665	GM_M27_A1_C04_MF	g4115916	BLASTX	188	1e-13	40	(AF118222) F3H7.9 gene product [Arabidopsis thaliana]
17666	GM_M27_A1_C08_MR	g1769897	BLASTX	233	6e-18	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17667	GM_M27_A1_C10_MR	g4063760	BLASTX	403	2e-35	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17668	GM_M27_A1_C12_MF	g18559	BLASTN	498	1e-15	67	G.max gene for catalase
17669	GM_M27_A1_C12_MR	g2995405	BLASTX	497	5e-46	67	(Y12432) polyprotein [Ananas comosus]
17670	GM_M27_A1_D01_MR	g2829915	BLASTX	286	2e-23	45	(AC002291) Hypothetical protein [Arabidopsis thaliana]
17671	GM_M27_A1_D02_MF	g3777527	BLASTX	132	3e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
17672	GM_M27_A1_D07_MF	g3930515	BLASTX	121	7e-09	47	(AF059674) putative gag protein [Nicotiana tabacum]
17673	GM_M27_A1_D07_MR	g1142699	BLASTN	1166	2e-46	83	Glycine max satellite STR120-A.1.
17674	GM_M27_A1_D10_MF	g2129618	BLASTX	202	3e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17675	GM_M27_A1_D11_MF	g2129618	BLASTX	203	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17676	GM_M27_A1_E04_MF	g3550435	BLASTN	469	4e-14	63	Hordeum vulgare Hotr1 gene
17677	GM_M27_A1_E10_MR	g3097320	BLASTN	433	1e-12	75	Glycine max gene for Bd 30K, complete cds
17678	GM_M27_A1_F03_MF	g3927831	BLASTX	193	7e-14	81	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17679	GM_M27_A1_F06_MF	g2129618	BLASTX	175	2e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17680	GM_M27_A1_F12_MR	g3097836	BLASTN	438	9e-13	64	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
17681	GM_M27_A1_G01_MF	g4063760	BLASTX	262	2e-20	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17682	GM_M27_A1_G09_MF	g3142328	BLASTN	963	1e-36	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17683	GM_M27_A1_G09_MR	g3645899	BLASTX	396	4e-37	61	(U68408) 5' end not determined experimentally [Zea mays]
17684	GM_M27_A1_H01_MR	g18559	BLASTN	975	3e-37	77	G.max gene for catalase
17685	GM_M27_A1_H05_MR	g18559	BLASTN	1026	2e-39	78	G.max gene for catalase
17686	GM_M27_A1_H06_MF	g99922	BLASTX	487	1e-47	80	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17687	GM_M27_A1_H08_MF	g2708743	BLASTX	170	1e-10	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
17688	GM_M27_A1_H10_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17689	GM_M27_A2_A02_MR	g3582328	BLASTX	145	3e-11	40	(AC005496) hypothetical protein [Arabidopsis thaliana]
17690	GM_M27_A2_A05_MR	g507910	BLASTN	620	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17691	GM_M27_A2_B05_MR	g2129709	BLASTX	311	1e-25	40	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17692	GM_M27_A2_B07_MR	g2213632	BLASTX	194	5e-14	52	(AC000103) F21J9.24 [Arabidopsis thaliana]
17693	GM_M27_A2_C04_MR	g3142328	BLASTN	688	4e-24	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17694	GM_M27_A2_D08_MR	g18559	BLASTN	666	4e-23	76	G.max gene for catalase
17695	GM_M27_A2_E04_MR	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17696	GM_M27_A2_E12_MR	g3142328	BLASTN	838	5e-31	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17697	GM_M27_A2_F02_MR	g2252634	BLASTX	428	4e-39	48	(U95973) hypothetical protein [Arabidopsis thaliana]
17698	GM_M27_A2_F06_MR	g3510262	BLASTX	153	1e-09	66	(AC005310) NAM like protein [Arabidopsis thaliana]
17699	GM_M27_A2_F10_MR	g1769898	BLASTX	135	9e-13	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17700	GM_M27_A2_G01_MR	g3059060	BLASTN	402	4e-11	65	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
17701	GM_M27_A2_G02_MR	g2864626	BLASTX	237	2e-18	43	(AL021811) cytochrome p450 - like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17702	GM_M27_A2_G06_MR	g1769897	BLASTX	287	7e-24	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17703	GM_M27_A2_G10_MR	g3645899	BLASTX	197	1e-13	49	(U68408) 5' end not determined experimentally [Zea mays]
17704	GM_M27_A2_H02_MR	g1769897	BLASTX	157	9e-10	29	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17705	GM_M27_A2_H08_MR	g3097320	BLASTN	559	3e-18	79	Glycine max gene for Bd 30K, complete cds
17706	GM_M27_A2_H11_MR	g4063760	BLASTX	414	1e-36	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17707	GM_M27_B2_A02_MF	g3097320	BLASTN	526	9e-17	73	Glycine max gene for Bd 30K, complete cds
17708	GM_M27_B2_B01_MF	g2465923	BLASTX	265	2e-25	64	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
17709	GM_M27_B2_B05_MF	g4033532	BLASTX	197	2e-23	61	(X78274) polygalacturonase-inhibiting protein [Glycine max]
17710	GM_M27_B2_B06_MF	g9908	BLASTN	358	3e-09	66	P. falciparum SD17 gene for knob-associated histidine-rich protein
17711	GM_M27_B2_B07_MF	g2495179	BLASTX	162	1e-10	85	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) gi 1084340 pir S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana gi 313150 (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] gi 313838 (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]
17712	GM_M27_B2_C01_MF	g2465923	BLASTX	268	1e-25	65	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
17713	GM_M27_B2_C03_MF	g3810835	BLASTX	146	8e-09	34	(AL032684) putative RNA-binding protein [Schizosaccharomyces pombe]
17714	GM_M27_B2_C06_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17715	GM_M27_B2_C08_MF	g4063756	BLASTN	480	1e-14	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17716	GM_M27_B2_D06_MF	g3097320	BLASTN	570	9e-19	76	Glycine max gene for Bd 30K, complete cds
17717	GM_M27_B2_D12_MF	g3777527	BLASTX	571	3e-53	97	(AF053008) gag-pol polyprotein [Glycine max]
17718	GM_M27_B2_E01_MF	g18559	BLASTN	518	2e-16	71	G.max gene for catalase
17719	GM_M27_B2_E03_MF	g3319362	BLASTX	171	6e-11	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17720	GM_M27_B2_F03_MF	g2129709	BLASTX	190	1e-12	34	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17721	GM_M27_B2_F08_MF	g3777526	BLASTN	526	9e-17	80	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
17722	GM_M27_B2_F11_MF	g170605	BLASTN	526	4e-17	67	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17723	GM_M27_B2_G03_MF	g3738114	BLASTN	439	9e-13	69	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
17724	GM_M27_B2_G05_MF	g3702731	BLASTN	475	2e-14	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]
17725	GM_M27_B2_G09_MF	g1418331	BLASTX	377	2e-33	54	(X95909) receptor like protein kinase [Arabidopsis thaliana]
17726	GM_M27_B2_G12_MF	g3033389	BLASTX	185	2e-12	41	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17727	GM_M27_B2_H03_MF	g1666236	BLASTX	152	2e-15	34	(U76261) unknown [Hordeum vulgare]
17728	GM_M27_B2_H08_MF	g3513301	BLASTN	352	7e-09	63	Homo sapiens chromosome 19, cosmid R26894, complete sequence [Homo sapiens]
17729	GM_M28_A1_A01_MF	g3097320	BLASTN	1207	1e-47	82	Glycine max gene for Bd 30K, complete cds
17730	GM_M28_A1_A02_MR	g3319362	BLASTX	378	5e-33	56	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17731	GM_M28_A1_A08_MF	g1438878	BLASTN	367	8e-10	80	Glycine max choline kinase GmCK1p mRNA, complete cds
17732	GM_M28_A1_B02_MF	g505129	BLASTN	376	5e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17733	GM_M28_A1_B08_MF	g2586082	BLASTX	256	9e-20	48	(U72725) retrofit [Oryza longistaminata]
17734	GM_M28_A1_C04_MR	g3142328	BLASTN	1148	4e-45	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17735	GM_M28_A1_C10_MF	g4063760	BLASTX	202	4e-14	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17736	GM_M28_A1_C10_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
17737	GM_M28_A1_C12_MR	g4063760	BLASTX	277	4e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17738	GM_M28_A1_D01_MF	g3142328	BLASTN	989	7e-38	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17739	GM_M28_A1_D01_MR	g3777527	BLASTX	663	4e-63	95	(AF053008) gag-pol polyprotein [Glycine max]
17740	GM_M28_A1_D02_MR	g1666236	BLASTX	213	1e-16	33	(U76261) unknown [Hordeum vulgare]
17741	GM_M28_A1_D09_MF	g2995405	BLASTX	186	2e-12	48	(Y12432) polyprotein [Ananas comosus]
17742	GM_M28_A1_E01_MF	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17743	GM_M28_A1_E12_MR	g507910	BLASTN	380	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17744	GM_M28_A1_F05_MR	g421955	BLASTX	421	1e-38	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17745	GM_M28_A1_F07_MR	g18559	BLASTN	667	3e-23	73	G.max gene for catalase
17746	GM_M28_A1_F10_MR	g1769898	BLASTX	344	6e-30	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17747	GM_M28_A1_G01_MR	g2522228	BLASTX	310	6e-27	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
17748	GM_M28_A1_G02_MF	g100484	BLASTX	223	2e-19	53	hypothetical protein - garden snapdragon
17749	GM_M28_A1_G02_MR	g226407	BLASTX	269	4e-21	42	retrotransposon del1-46 [Lilium henryi]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
17750	GM_M28_A1_G06_MR	g3810595	BLASTX	104	2e-10	55	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
17751	GM_M28_A1_H01_MF	g3860271	BLASTX	150	1e-08	36	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
17752	GM_M28_A1_H03_MF	g4038056	BLASTX	150	3e-14	41	(AC005897) putative transposon [Arabidopsis thaliana]
17753	GM_M28_A1_H06_MF	g536873	BLASTX	247	7e-19	42	(M34549) POL3 gene product [Saccharomyces cerevisiae]
17754	GM_M28_A1_H07_MF	g2462134	BLASTX	289	3e-24	50	(Y13368) reverse transcriptase [Beta vulgaris]
17755	GM_M28_A1_H09_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17756	GM_M28_A1_H10_MF	g1769899	BLASTX	235	3e-22	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17757	GM_M28_A1_H10_MR	g3097320	BLASTN	478	1e-14	70	Glycine max gene for Bd 30K, complete cds
17758	GM_M28_A2_A02_MR	g3426334	BLASTN	446	4e-13	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
17759	GM_M28_A2_A11_MR	g4140712	BLASTX	314	2e-27	47	(AF110183) putative integrase [Oryza sativa]
17760	GM_M28_A2_B05_MF	g2618603	BLASTN	436	1e-12	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]
17761	GM_M28_A2_B07_MF	g4138265	BLASTX	239	4e-19	81	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]
17762	GM_M28_A2_B12_MR	g18559	BLASTN	382	3e-10	64	G.max gene for catalase
17763	GM_M28_A2_C01_MR	g3337395	BLASTN	427	3e-12	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
17764	GM_M28_A2_C02_MR	g4160362	BLASTN	353	7e-09	62	Saccharomyces cerevisiae complete mitochondrial genome
17765	GM_M28_A2_C03_MF	g4063760	BLASTX	479	1e-43	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17766	GM_M28_A2_C03_MR	g3695395	BLASTX	235	5e-18	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
17767	GM_M28_A2_D03_MF	g2764526	BLASTN	701	1e-24	70	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17768	GM_M28_A2_D03_MR	g18559	BLASTN	857	8e-32	78	G.max gene for catalase
17769	GM_M28_A2_D05_MR	g3021268	BLASTX	177	2e-11	36	(AL022347) putative protein [Arabidopsis thaliana]
17770	GM_M28_A2_D09_MF	g3142328	BLASTN	1558	9e-64	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17771	GM_M28_A2_D10_MR	g2895633	BLASTN	360	1e-09	61	Zerene cesonia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
17772	GM_M28_A2_D12_MF	g3241935	BLASTN	513	4e-16	64	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
17773	GM_M28_A2_E05_MF	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17774	GM_M28_A2_E05_MR	g507910	BLASTN	380	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17775	GM_M28_A2_E09_MF	g2764526	BLASTN	414	1e-11	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17776	GM_M28_A2_F01_MF	g905361	BLASTX	399	6e-36	91	(U22103) gag-protease polyprotein [Glycine max]
17777	GM_M28_A2_F02_MF	g99729	BLASTX	129	5e-20	54	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
17778	GM_M28_A2_F03_MF	g3097320	BLASTN	580	3e-19	80	Glycine max gene for Bd 30K, complete cds
17779	GM_M28_A2_F10_MR	g2522230	BLASTX	293	4e-25	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17780	GM_M28_A2_F11_MF	g4092471	BLASTN	401	4e-11	64	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
17781	GM_M28_A2_G05_MR	g166949	BLASTX	430	1e-39	58	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]
17782	GM_M28_A2_G08_MR	g2264315	BLASTN	683	8e-24	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]
17783	GM_M28_A2_H05_MF	g4063760	BLASTX	360	2e-33	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17784	GM_M28_A2_H05_MR	g507910	BLASTN	587	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17785	GM_M28_A2_H06_MR	g3599418	BLASTN	400	4e-11	65	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
17786	GM_M28_A2_H07_MF	g2191149	BLASTX	229	4e-24	85	(AF007269) Similar to protein kinase [Arabidopsis thaliana]
17787	GM_M28_A2_H10_MF	g226407	BLASTX	366	2e-31	57	retrotransposon del1-46 [Lilium henryi]
17788	GM_M28_A2_H12_MF	g99922	BLASTX	596	3e-57	90	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17789	GM_M28_B1_A05_MR	g1785739	BLASTX	157	9e-22	38	(Y08502) orf240b [Arabidopsis thaliana]
17790	GM_M28_B1_A06_MR	g1142701	BLASTN	1215	1e-48	81	Glycine max satellite STR120-A.3.
17791	GM_M28_B1_A11_MR	g3033375	BLASTX	361	3e-32	58	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
17792	GM_M28_B1_A12_MR	g3046693	BLASTX	343	3e-35	87	(AL022140) receptor like protein (fragment) [Arabidopsis thaliana]
17793	GM_M28_B1_B03_MR	g1666236	BLASTX	121	9e-11	32	(U76261) unknown [Hordeum vulgare]
17794	GM_M28_B1_B04_MR	g2522228	BLASTX	416	3e-38	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
17795	GM_M28_B1_B06_MF	g3142328	BLASTN	531	9e-29	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17796	GM_M28_B1_B07_MR	g505129	BLASTN	360	3e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17797	GM_M28_B1_B09_MR	g2642431	BLASTX	283	1e-22	44	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
17798	GM_M28_B1_B10_MF	g2129618	BLASTX	168	1e-10	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17799	GM_M28_B1_B12_MR	g2781364	BLASTX	153	6e-10	29	(AC003113) F24O1.20 [Arabidopsis thaliana]
17800	GM_M28_B1_C06_MF	g1666236	BLASTX	148	3e-09	30	(U76261) unknown [Hordeum vulgare]
17801	GM_M28_B1_C06_MR	g18559	BLASTN	1076	9e-42	76	G.max gene for catalase
17802	GM_M28_B1_C10_MF	g2995405	BLASTX	389	2e-34	57	(Y12432) polyprotein [Ananas comosus]
17803	GM_M28_B1_D02_MR	g1633043	BLASTN	817	4e-30	82	Lupinus angustifolius conglutin gamma gene, complete cds
17804	GM_M28_B1_D04_MF	g2443320	BLASTX	291	2e-23	46	(D85597) polyprotein [Oryza australiensis]
17805	GM_M28_B1_D10_MF	g2462134	BLASTX	354	1e-31	50	(Y13368) reverse transcriptase [Beta vulgaris]
17806	GM_M28_B1_E01_MR	g4156188	BLASTN	426	3e-12	65	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
17807	GM_M28_B1_E03_MF	g3510505	BLASTX	244	1e-18	45	(AF030881) pol polyprotein [Fugu rubripes]
17808	GM_M28_B1_E06_MR	g3319362	BLASTX	276	4e-22	48	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17809	GM_M28_B1_E07_MF	g1769898	BLASTX	278	1e-22	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17810	GM_M28_B1_E08_MR	g3097320	BLASTN	705	7e-25	81	Glycine max gene for Bd 30K, complete cds
17811	GM_M28_B1_E11_MF	g2829910	BLASTX	249	4e-19	48	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]
17812	GM_M28_B1_F02_MR	g3021268	BLASTX	145	1e-13	71	(AL022347) putative protein [Arabidopsis thaliana]
17813	GM_M28_B1_F03_MF	g3176806	BLASTN	423	6e-13	65	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
17814	GM_M28_B1_F03_MR	g18695	BLASTN	475	1e-14	66	Soybean nodulin 22 gene
17815	GM_M28_B1_F05_MF	g421954	BLASTX	142	1e-16	42	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
17816	GM_M28_B1_F07_MR	g2995405	BLASTX	183	3e-12	67	(Y12432) polyprotein [Ananas comosus]
17817	GM_M28_B1_F08_MF	g2129618	BLASTX	158	2e-09	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17818	GM_M28_B1_F10_MR	g100484	BLASTX	282	5e-23	48	hypothetical protein - garden snapdragon
17819	GM_M28_B1_F11_MF	g3097320	BLASTN	406	2e-11	68	Glycine max gene for Bd 30K, complete cds
17820	GM_M28_B1_G01_MF	g1865677	BLASTX	153	5e-09	91	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
17821	GM_M28_B1_G07_MR	g4104931	BLASTX	164	8e-14	80	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
17822	GM_M28_B1_G08_MF	g1769899	BLASTX	267	2e-22	76	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
17823	GM_M28_B1_H02_MR	g3894211	BLASTN	441	7e-13	65	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
17824	GM_M28_B1_H03_MF	g2995405	BLASTX	153	4e-24	54	(Y12432) polyprotein [Ananas comosus]
17825	GM_M28_B1_H03_MR	g3650039	BLASTX	204	3e-16	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17826	GM_M28_B1_H08_MF	g2924772	BLASTX	197	5e-15	84	(AC002334) unknown protein [Arabidopsis thaliana]
17827	GM_M28_B1_H09_MR	g507910	BLASTN	403	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
17828	GM_M28_B1_H12_MR	g507910	BLASTN	374	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17829	GM_M28_B2_A05_MF	g4038056	BLASTX	161	6e-21	49	(AC005897) putative transposon [Arabidopsis thaliana]
17830	GM_M28_B2_A06_MR	g2462056	BLASTX	144	1e-11	50	(Y13388) reverse transcriptase [Antirrhinum majus]
17831	GM_M28_B2_A07_MF	g507910	BLASTN	356	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
17832	GM_M28_B2_A08_MR	g3033400	BLASTX	237	9e-18	41	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
17833	GM_M28_B2_A09_MF	g3047060	BLASTN	365	2e-09	63	Arabidopsis thaliana BAC F7N22
17834	GM_M28_B2_B05_MR	g1236920	BLASTN	358	3e-09	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
17835	GM_M28_B2_B10_MR	g1840106	BLASTN	353	2e-09	63	Human fragile site locus (FRA16B) minisatellite repeat
17836	GM_M28_B2_C04_MF	g130398	BLASTX	210	5e-15	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
17837	GM_M28_B2_C04_MR	g2462058	BLASTX	296	2e-25	49	(Y13389) reverse transcriptase [Antirrhinum majus]
17838	GM_M28_B2_C08_MR	g1431738	BLASTN	511	3e-16	81	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
17839	GM_M28_B2_C09_MF	g1171591	BLASTN	389	1e-10	65	P.falciparum complete gene map of plastid-like DNA (IR-B)
17840	GM_M28_B2_C12_MF	g507910	BLASTN	401	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17841	GM_M28_B2_C12_MR	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17842	GM_M28_B2_D02_MF	g2213608	BLASTX	174	4e-11	43	(AC000103) F21J9.2 [Arabidopsis thaliana]
17843	GM_M28_B2_D03_MR	g4063760	BLASTX	269	3e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17844	GM_M28_B2_D05_MF	g3402722	BLASTX	217	3e-16	93	(AC004261) CPDK-related protein [Arabidopsis thaliana]
17845	GM_M28_B2_D05_MR	g1174718	BLASTX	174	3e-11	48	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR gi 322579 pir JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana gi 166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17846	GM_M28_B2_D07_MR	g3402693	BLASTX	164	1e-18	88	(AC004697) unknown protein [Arabidopsis thaliana]
17847	GM_M28_B2_D08_MR	g3513747	BLASTX	288	5e-23	50	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17848	GM_M28_B2_D09_MR	g18768	BLASTN	432	4e-13	77	Soybean Tgm6 transposable element 3' end
17849	GM_M28_B2_D10_MR	g3184285	BLASTX	203	1e-17	62	(AC004136) hypothetical protein [Arabidopsis thaliana]
17850	GM_M28_B2_D12_MF	g1666236	BLASTX	160	2e-10	32	(U76261) unknown [Hordeum vulgare]
17851	GM_M28_B2_E02_MR	g3142328	BLASTN	1159	1e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17852	GM_M28_B2_E03_MF	g1169782	BLASTX	387	4e-35	72	FUSCA PROTEIN FUS6 gi 432446 (L26498) FUS6 [Arabidopsis thaliana]
17853	GM_M28_B2_E03_MR	g1769898	BLASTX	289	6e-24	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17854	GM_M28_B2_E04_MR	g1184075	BLASTX	178	9e-18	39	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
17855	GM_M28_B2_E12_MF	g18559	BLASTN	386	2e-10	71	G.max gene for catalase
17856	GM_M28_B2_F01_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17857	GM_M28_B2_F03_MR	g1143321	BLASTN	853	7e-32	90	Glycine max alfa-carboxyltransferase (accA-2) precursor mRNA, complete cds.
17858	GM_M28_B2_F04_MR	g2367675	BLASTX	176	2e-11	33	(AF017040) Pol [Dictyostelium discoideum]
17859	GM_M28_B2_F05_MR	g507910	BLASTN	574	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17860	GM_M28_B2_F06_MR	g4063760	BLASTX	299	2e-24	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17861	GM_M28_B2_F07_MR	g100484	BLASTX	251	1e-19	49	hypothetical protein - garden snapdragon
17862	GM_M28_B2_F12_MF	g1785744	BLASTX	197	5e-15	58	(Y08502) orf158 [Arabidopsis thaliana]
17863	GM_M28_B2_G01_MF	g4063760	BLASTX	443	8e-40	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17864	GM_M28_B2_G04_MF	g3319362	BLASTX	170	8e-11	38	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17865	GM_M28_B2_G05_MR	g4063760	BLASTX	380	4e-33	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17866	GM_M28_B2_G09_MR	g2995405	BLASTX	316	2e-26	56	(Y12432) polyprotein [Ananas comosus]
17867	GM_M28_B2_G10_MR	g4063760	BLASTX	555	9e-52	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17868	GM_M28_B2_H04_MR	g3033389	BLASTX	210	4e-15	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17869	GM_M28_B2_H05_MF	g2213582	BLASTX	175	4e-11	33	(AC000348) T7N9.2 [Arabidopsis thaliana]
17870	GM_M28_B2_H05_MR	g3319362	BLASTX	117	1e-13	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17871	GM_M28_B2_H09_MR	g2576361	BLASTX	170	3e-24	58	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]
17872	GM_M29_A1_A03_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
17873	GM_M29_A1_A05_MR	g3859610	BLASTN	585	2e-19	66	Arabidopsis thaliana BAC T9E19
17874	GM_M29_A1_A09_MR	g3482933	BLASTX	249	4e-27	74	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]
17875	GM_M29_A1_B04_MR	g2213594	BLASTX	311	3e-26	69	(AC000348) T7N9 14 [Arabidopsis thaliana]
17876	GM_M29_A1_C01_MR	g905361	BLASTX	624	3e-60	96	(U22103) gag-protease polyprotein [Glycine max]
17877	GM_M29_A1_C04_MR	g1769898	BLASTX	138	8e-11	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17878	GM_M29_A1_C06_MR	g1769898	BLASTX	427	3e-39	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17879	GM_M29_A1_D01_MR	g1769898	BLASTX	449	1e-41	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17880	GM_M29_A1_D02_MR	g4063770	BLASTX	218	5e-16	39	(AB004906) transposase [Ipomoea purpurea]
17881	GM_M29_A1_D06_MR	g4063760	BLASTX	477	2e-43	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17882	GM_M29_A1_D08_MR	g1169533	BLASTX	124	6e-11	78	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) gi 515827 (X80474) enolase [Neocallimastix frontalis]
17883	GM_M29_A1_D09_MR	g3097320	BLASTN	603	3e-20	69	Glycine max gene for Bd 30K, complete cds
17884	GM_M29_A1_E07_MR	g511658	BLASTN	245	2e-09	66	Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 4L, complete cds
17885	GM_M29_A1_F02_MR	g4092471	BLASTN	531	6e-17	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
17886	GM_M29_A1_F04_MR	g3777527	BLASTX	594	1e-55	98	(AF053008) gag-pol polyprotein [Glycine max]
17887	GM_M29_A1_F06_MR	g4063760	BLASTX	186	2e-12	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17888	GM_M29_A1_H04_MR	g4160362	BLASTN	385	2e-10	66	Saccharomyces cerevisiae complete mitochondrial genome
17889	GM_M29_A1_H11_MR	g4063756	BLASTN	456	1e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17890	GM_M29_A2_A01_MF	g100484	BLASTX	178	5e-19	53	hypothetical protein - garden snapdragon
17891	GM_M29_A2_A12_MR	g3297806	BLASTN	489	5e-15	68	Arabidopsis thaliana DNA chromosome 4, BAC clone F1715 (ESSAII project)
17892	GM_M29_A2_B01_MF	g1360090	BLASTX	289	1e-23	47	(X95576) C1C-Nt1 gene product [Nicotiana tabacum]
17893	GM_M29_A2_B02_MR	g3319345	BLASTX	213	2e-15	37	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
17894	GM_M29_A2_B04_MF	g4063760	BLASTX	280	2e-22	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17895	GM_M29_A2_B04_MR	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17896	GM_M29_A2_B07_MR	g3894389	BLASTX	210	3e-15	37	(AF053996) Hcr2-2A [Lycopersicon pimpinellifolium]
17897	GM_M29_A2_B08_MR	g18767	BLASTN	413	2e-12	70	Soybean Tgm6 transposable element 5' end
17898	GM_M29_A2_B11_MF	g3142328	BLASTN	944	8e-36	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17899	GM_M29_A2_C04_MR	g2642431	BLASTX	242	3e-18	56	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
17900	GM_M29_A2_C05_MR	g3176773	BLASTN	364	4e-10	62	Homo sapiens allele 3 fragile site locus (FRA10B) minisatellite, 5' sequence
17901	GM_M29_A2_C06_MF	g4063760	BLASTX	222	3e-16	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17902	GM_M29_A2_C06_MR	g1785739	BLASTX	240	2e-25	47	(Y08502) orf240b [Arabidopsis thaliana]
17903	GM_M29_A2_C07_MR	g2209031	BLASTX	300	2e-25	42	(AB001569) ORF of 1.56 kb [Daucus carota]
17904	GM_M29_A2_C11_MR	g1669680	BLASTN	363	2e-09	63	Human DNA sequence from PAC 293E14 contains ESTs, STS
17905	GM_M29_A2_D01_MF	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17906	GM_M29_A2_D01_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17907	GM_M29_A2_D02_MR	g2462134	BLASTX	266	1e-27	48	(Y13368) reverse transcriptase [Beta vulgaris]
17908	GM_M29_A2_D04_MR	g3128195	BLASTX	177	3e-12	79	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] gi 3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]
17909	GM_M29_A2_D05_MF	g3810596	BLASTX	262	1e-20	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17910	GM_M29_A2_D05_MR	g1167523	BLASTX	316	4e-26	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17911	GM_M29_A2_D08_MR	g1769898	BLASTX	162	3e-17	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17912	GM_M29_A2_E01_MF	g2995405	BLASTX	416	3e-37	55	(Y12432) polyprotein [Ananas comosus]
17913	GM_M29_A2_E04_MR	g3461840	BLASTX	333	6e-29	43	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
17914	GM_M29_A2_F03_MF	g2316016	BLASTX	201	7e-14	51	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
17915	GM_M29_A2_F07_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17916	GM_M29_A2_F08_MF	g2316016	BLASTX	202	6e-14	50	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
17917	GM_M29_A2_F09_MF	g905361	BLASTX	614	4e-59	91	(U22103) gag-protease polyprotein [Glycine max]
17918	GM_M29_A2_F09_MR	g4063760	BLASTX	323	6e-27	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17919	GM_M29_A2_G01_MF	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17920	GM_M29_A2_G01_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17921	GM_M29_A2_G08_MR	g4063760	BLASTX	594	6e-56	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17922	GM_M29_A2_G09_MR	g1705678	BLASTX	335	1e-28	87	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) gi 862480 (U20213) valosin-containing protein [Glycine max]
17923	GM_M29_A2_H01_MR	g3482913	BLASTX	216	4e-30	57	(AC003970) Similar to MtN21, gi 2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]
17924	GM_M29_A2_H02_MF	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17925	GM_M29_A2_H02_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17926	GM_M29_A2_H06_MF	g3142328	BLASTN	1903	1e-79	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17927	GM_M29_A2_H07_MF	g3142328	BLASTN	939	1e-35	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17928	GM_M29_A2_H08_MR	g3859610	BLASTN	435	1e-12	60	Arabidopsis thaliana BAC T9E19
17929	GM_M29_A2_H09_MF	g18559	BLASTN	932	3e-35	74	G.max gene for catalase
17930	GM_M29_A2_H10_MR	g1040875	BLASTX	164	1e-14	67	(U30382) expansin S1 precursor [Cucumis sativus]
17931	GM_M29_A2_H11_MF	g2995405	BLASTX	464	2e-42	65	(Y12432) polyprotein [Ananas comosus]
17932	GM_M29_B1_A02_MF	g18559	BLASTN	853	1e-31	75	G.max gene for catalase
17933	GM_M29_B1_A08_MF	g4115377	BLASTX	144	2e-15	72	(AC005967) unknown protein [Arabidopsis thaliana]
17934	GM_M29_B1_A08_MR	g3513747	BLASTX	228	1e-16	40	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17935	GM_M29_B1_A10_MF	g3777527	BLASTX	276	8e-22	41	(AF053008) gag-pol polyprotein [Glycine max]
17936	GM_M29_B1_B01_MF	g1666236	BLASTX	190	6e-14	31	(U76261) unknown [Hordeum vulgare]
17937	GM_M29_B1_B01_MR	g1769898	BLASTX	173	2e-22	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17938	GM_M29_B1_B02_MF	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
17939	GM_M29_B1_B02_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17940	GM_M29_B1_B04_MF	g3283026	BLASTX	153	2e-13	48	putative transposase [Arabidopsis thaliana]
17941	GM_M29_B1_B05_MR	g2864621	BLASTX	174	8e-15	42	hypothetical protein [Arabidopsis thaliana]
17942	GM_M29_B1_B07_MF	g99729	BLASTX	315	2e-27	47	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
17943	GM_M29_B1_B09_MF	g2522228	BLASTX	253	1e-20	45	(AB007466) reverse transcriptase-like protein [Vicia faba]
17944	GM_M29_B1_C01_MF	g2252846	BLASTX	264	6e-21	80	(AF013293) Similar to phospholipase D [Arabidopsis thaliana]
17945	GM_M29_B1_C03_MF	g3236253	BLASTX	334	1e-28	52	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]
17946	GM_M29_B1_C03_MR	g2443320	BLASTX	151	1e-11	40	(D85597) polyprotein [Oryza australiensis]
17947	GM_M29_B1_C06_MR	g4063756	BLASTN	413	1e-11	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17948	GM_M29_B1_D01_MF	g2801681	BLASTN	1044	7e-41	86	Glycine max telomere-associated sequence STAS10
17949	GM_M29_B1_D03_MF	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
17950	GM_M29_B1_D06_MF	g2522227	BLASTX	162	4e-16	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17951	GM_M29_B1_D10_MF	g4092471	BLASTN	358	4e-09	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
17952	GM_M29_B1_D10_MR	g3426334	BLASTN	441	6e-13	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17953	GM_M29_B1_D11_MF	g3142328	BLASTN	1489	1e-60	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17954	GM_M29_B1_D12_MF	g3068704	BLASTX	290	1e-23	90	(AF049236) unknown [Arabidopsis thaliana]
17955	GM_M29_B1_E07_MR	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17956	GM_M29_B1_E09_MR	g4063760	BLASTX	181	7e-12	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17957	GM_M29_B1_F02_MF	g2281100	BLASTX	165	2e-10	47	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]
17958	GM_M29_B1_F03_MR	g3097320	BLASTN	1092	2e-42	81	Glycine max gene for Bd 30K, complete cds
17959	GM_M29_B1_F05_MR	g3777527	BLASTX	677	1e-64	93	(AF053008) gag-pol polyprotein [Glycine max]
17960	GM_M29_B1_F10_MF	g3650039	BLASTX	221	2e-16	37	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17961	GM_M29_B1_F10_MR	g3868722	BLASTN	353	7e-09	76	Arabidopsis thaliana BAC T19G15, from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]
17962	GM_M29_B1_G02_MR	g4063760	BLASTX	473	5e-43	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17963	GM_M29_B1_G03_MR	g3142328	BLASTN	1229	9e-49	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17964	GM_M29_B1_G04_MF	g1184123	BLASTX	164	2e-11	52	(U20809) auxin-induced protein [Vigna radiata]
17965	GM_M29_B1_G04_MR	g3386605	BLASTX	179	3e-12	36	(AC004665) hypothetical protein [Arabidopsis thaliana]
17966	GM_M29_B1_G06_MF	g4063760	BLASTX	394	1e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17967	GM_M29_B1_G06_MR	g4063760	BLASTX	211	1e-30	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17968	GM_M29_B1_G07_MF	g2443320	BLASTX	252	2e-23	49	(D85597) polyprotein [Oryza australiensis]
17969	GM_M29_B1_G12_MF	g3142328	BLASTN	681	7e-24	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17970	GM_M29_B1_H01_MF	g3319345	BLASTX	163	2e-13	43	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
17971	GM_M29_B1_H01_MR	g2583133	BLASTX	143	2e-18	81	(AC002387) unknown protein [Arabidopsis thaliana]
17972	GM_M29_B1_H07_MR	g2129618	BLASTX	154	4e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17973	GM_M29_B1_H11_MF	g217930	BLASTN	367	2e-10	64	H.wingei mitochondrial tRNA gene
17974	GM_M29_B2_B01_MF	g3033389	BLASTX	179	9e-12	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17975	GM_M29_B2_B01_MR	g3033389	BLASTX	197	1e-13	33	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17976	GM_M29_B2_B05_MR	g2462936	BLASTX	140	1e-08	50	(Y12321) open reading frame 2 [Brassica oleracea]
17977	GM_M29_B2_B08_MF	g99755	BLASTX	342	8e-30	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
17978	GM_M29_B2_B09_MF	g2462134	BLASTX	159	5e-10	28	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
17979	GM_M29_B2_B10_MF	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17980	GM_M29_B2_B10_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17981	GM_M29_B2_C03_MR	g1480927	BLASTN	745	6e-27	88	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
17982	GM_M29_B2_C07_MF	g3097320	BLASTN	852	2e-31	73	Glycine max gene for Bd 30K, complete cds
17983	GM_M29_B2_C08_MF	g2462134	BLASTX	193	1e-13	43	(Y13368) reverse transcriptase [Beta vulgaris]
17984	GM_M29_B2_C10_MF	g2129473	BLASTX	268	1e-22	42	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
17985	GM_M29_B2_D03_MF	g1785740	BLASTX	240	1e-19	51	(Y08502) orf170 [Arabidopsis thaliana]
17986	GM_M29_B2_D05_MF	g3645899	BLASTX	312	7e-26	47	(U68408) 5' end not determined experimentally [Zea mays]
17987	GM_M29_B2_D08_MF	g3097320	BLASTN	390	1e-10	69	Glycine max gene for Bd 30K, complete cds
17988	GM_M29_B2_D09_MF	g905361	BLASTX	135	8e-10	29	(U22103) gag-protease polyprotein [Glycine max]
17989	GM_M29_B2_D09_MR	g905361	BLASTX	143	1e-09	27	(U22103) gag-protease polyprotein [Glycine max]
17990	GM_M29_B2_D11_MF	g1769898	BLASTX	346	7e-32	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17991	GM_M29_B2_E03_MR	g3777527	BLASTX	427	6e-38	73	(AF053008) gag-pol polyprotein [Glycine max]
17992	GM_M29_B2_E04_MR	g1666236	BLASTX	164	3e-13	31	(U76261) unknown [Hordeum vulgare]
17993	GM_M29_B2_E05_MR	g2522227	BLASTX	228	3e-18	42	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17994	GM_M29_B2_E12_MR	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17995	GM_M29_B2_F03_MR	g4063760	BLASTX	226	1e-16	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17996	GM_M29_B2_G01_MR	g3176800	BLASTN	373	1e-10	66	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 3' sequence
17997	GM_M29_B2_G04_MF	g4063760	BLASTX	382	2e-33	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17998	GM_M29_B2_G04_MR	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17999	GM_M29_B2_G05_MR	g4063760	BLASTX	263	1e-20	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18000	GM_M29_B2_G10_MF	g3142328	BLASTN	550	6e-18	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18001	GM_M29_B2_G12_MF	g3269281	BLASTX	157	2e-09	44	(AL030978) putative protein [Arabidopsis thaliana]
18002	GM_M29_B2_H01_MF	g2522227	BLASTX	171	8e-23	49	(AB007466) retrotransposon-like gene, the first amino acid was determined to be glycine [Vicia faba]
18003	GM_M29_B2_H01_MR	g4063760	BLASTX	168	2e-11	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18004	GM_M29_B2_H02_MF	g4063760	BLASTX	194	7e-25	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18005	GM_M29_B2_H04_MF	g507910	BLASTN	638	3e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
18006	GM_M29_B2_H04_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18007	GM_M29_B2_H08_MR	g3142328	BLASTN	812	8e-30	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18008	GM_M30_A1_A03_MR	g2181308	BLASTN	472	6e-15	80	H.sapiens telomeric DNA sequence, clone 12QTEL026, read 12QTELOO026.seq
18009	GM_M30_A1_A06_MF	g507910	BLASTN	359	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18010	GM_M30_A1_B02_MR	g399710	BLASTN	399	4e-11	77	G-protein coupled receptor type B {clone PPR1} [cattle, tongue, taste papillae, mRNA, 2059 nt]
18011	GM_M30_A1_B04_MR	g1809226	BLASTN	1489	3e-60	97	Human BAC clone RG104I04 from 7q21-7q22, complete sequence [Homo sapiens]
18012	GM_M30_A1_B07_MR	g3327414	BLASTN	679	1e-23	86	Homo sapiens chromosome 17, clone hRPK.879_D_6, complete sequence [Homo sapiens]
18013	GM_M30_A1_C01_MR	g1196433	BLASTX	128	5e-15	43	(M22334) unknown protein [Homo sapiens]
18014	GM_M30_A1_D10_MR	g3970967	BLASTN	388	2e-15	69	Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence [Homo sapiens]
18015	GM_M30_A1_D11_MR	g3924666	BLASTN	1212	1e-47	97	Homo sapiens BAC clone RG041D11 from 7q21, complete sequence [Homo sapiens]
18016	GM_M30_A1_E06_MF	g170002	BLASTN	403	2e-11	70	soybean leghemoglobin pseudogene, segment 2.
18017	GM_M30_A1_E10_MR	g3056604	BLASTN	658	3e-29	78	Homo sapiens chromosome 19, cosmid F9933, complete sequence [Homo sapiens]
18018	GM_M30_A1_F01_MR	g2342581	BLASTN	496	2e-15	70	Human DNA sequence from PAC 30P20 on chromosome Xq21.1-Xq21.3. Contains set pseudogene, ESTs and STS
18019	GM_M30_A1_F12_MR	g3115994	BLASTN	1327	7e-53	92	Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs...
18020	GM_M30_A1_H01_MR	g2695566	BLASTN	322	2e-14	68	Human Chromosome 15 pac pDJ138o23, complete sequence [Homo sapiens]
18021	GM_M30_A1_H08_MF	g3608154	BLASTX	187	8e-13	49	(AC005314) unknown protein [Arabidopsis thaliana]
18022	GM_M30_A1_H12_MR	g1841914	BLASTN	712	4e-25	81	Human DNA sequence from PAC 481A17 on chromosome X contains ESTs
18023	GM_M30_A2_A04_MF	g2129618	BLASTX	197	1e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18024	GM_M30_A2_A08_MF	g3097320	BLASTN	405	3e-11	71	Glycine max gene for Bd 30K, complete cds
18025	GM_M30_A2_A10_MF	g387902	BLASTX	119	3e-15	44	(L23524) ORF [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18026	GM_M30_A2_B09_MF	g3810596	BLASTX	340	5e-29	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18027	GM_M30_A2_B12_MF	g2995405	BLASTX	440	8e-40	57	(Y12432) polyprotein [Ananas comosus]
18028	GM_M30_A2_C02_MF	g3080374	BLASTX	188	7e-13	31	(AL022580) putative protein [Arabidopsis thaliana]
18029	GM_M30_A2_C05_MF	g2995405	BLASTX	238	4e-18	55	(Y12432) polyprotein [Ananas comosus]
18030	GM_M30_A2_C11_MF	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18031	GM_M30_A2_D05_MF	g3097320	BLASTN	411	1e-11	67	Glycine max gene for Bd 30K, complete cds
18032	GM_M30_A2_D10_MF	g2995405	BLASTX	504	9e-47	61	(Y12432) polyprotein [Ananas comosus]
18033	GM_M30_A2_D11_MF	g294042	BLASTN	373	8e-10	60	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
18034	GM_M30_A2_E03_MF	g2760322	BLASTX	153	6e-10	52	(AC002130) F1N21.7 [Arabidopsis thaliana]
18035	GM_M30_A2_E04_MF	g3513747	BLASTX	208	1e-28	45	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18036	GM_M30_A2_F01_MF	g507910	BLASTN	428	1e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18037	GM_M30_A2_F05_MF	g2655098	BLASTX	294	2e-24	69	(AF023472) peptide transporter [Hordeum vulgare]
18038	GM_M30_A2_F06_MF	g3777527	BLASTX	161	1e-11	45	(AF053008) gag-pol polyprotein [Glycine max]
18039	GM_M30_A2_F08_MF	g3777527	BLASTX	663	4e-63	95	(AF053008) gag-pol polyprotein [Glycine max]
18040	GM_M30_A2_G02_MF	g507910	BLASTN	424	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18041	GM_M30_A2_G06_MF	g342963	BLASTN	374	3e-10	66	paramecium species 5.87 mt dna dimer: replication init. region.
18042	GM_M30_A2_G09_MF	g2522227	BLASTX	203	1e-15	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18043	GM_M30_A2_H06_MF	g3097320	BLASTN	1079	8e-42	80	Glycine max gene for Bd 30K, complete cds
18044	GM_M30_A2_H09_MF	g2795809	BLASTX	199	3e-15	50	(AC003674) putative expansin [Arabidopsis thaliana]
18045	GM_M30_B1_A12_MF	g1236920	BLASTN	418	5e-12	65	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
18046	GM_M30_B1_B02_MF	g18559	BLASTN	404	3e-11	70	G.max gene for catalase
18047	GM_M30_B1_B05_MF	g905361	BLASTX	375	3e-33	83	(U22103) gag-protease polyprotein [Glycine max]
18048	GM_M30_B1_B07_MF	g99922	BLASTX	439	1e-40	70	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18049	GM_M30_B1_C02_MR	g3097320	BLASTN	1092	2e-42	81	Glycine max gene for Bd 30K, complete cds
18050	GM_M30_B1_C04_MR	g1076755	BLASTX	619	1e-59	81	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
18051	GM_M30_B1_D09_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18052	GM_M30_B1_D11_MF	g3645899	BLASTX	169	5e-14	41	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18053	GM_M30_B1_E12_MR	g507910	BLASTN	372	3e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18054	GM_M30_B1_F01_MF	g905361	BLASTX	407	7e-37	90	(U22103) gag-protease polyprotein [Glycine max]
18055	GM_M30_B1_F02_MR	g14293	BLASTN	338	4e-09	62	Yeast R0.54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
18056	GM_M30_B1_F04_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18057	GM_M30_B1_F04_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18058	GM_M30_B1_F05_MF	g3021268	BLASTX	146	1e-19	44	(AL022347) putative protein [Arabidopsis thaliana]
18059	GM_M30_B1_F07_MF	g2462134	BLASTX	255	2e-20	42	(Y13368) reverse transcriptase [Beta vulgaris]
18060	GM_M30_B1_F10_MF	g507910	BLASTN	494	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18061	GM_M30_B1_F11_MR	g2398527	BLASTX	170	4e-12	57	(Y13723) Transcription factor [Arabidopsis thaliana]
18062	GM_M30_B1_G01_MF	g2980777	BLASTX	176	6e-12	75	(AL022198) putative protein [Arabidopsis thaliana]
18063	GM_M30_B1_G04_MF	g1142702	BLASTN	1132	1e-44	97	Glycine max satellite STR120-A.4.
18064	GM_M30_B1_G04_MR	g3097320	BLASTN	1043	3e-40	78	Glycine max gene for Bd 30K, complete cds
18065	GM_M30_B1_G08_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18066	GM_M30_B1_G08_MR	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18067	GM_M30_B1_G12_MF	g2995405	BLASTX	154	6e-23	62	(Y12432) polyprotein [Ananas comosus]
18068	GM_M30_B1_H04_MF	g13767	BLASTN	339	3e-09	67	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
18069	GM_M30_B1_H05_MR	g4038056	BLASTX	207	9e-15	45	(AC005897) putative transposon [Arabidopsis thaliana]
18070	GM_M30_B1_H08_MR	g728905	BLASTX	206	2e-14	43	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
18071	GM_M30_B1_H10_MF	g3777527	BLASTX	307	4e-25	47	(AF053008) gag-pol polyprotein [Glycine max]
18072	GM_M30_B1_H12_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18073	GM_M30_B2_A03_MR	g3426334	BLASTN	384	2e-10	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18074	GM_M30_B2_A05_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18075	GM_M30_B2_A08_MF	g2462134	BLASTX	321	8e-28	40	(Y13368) reverse transcriptase [Beta vulgaris]
18076	GM_M30_B2_A09_MF	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18077	GM_M30_B2_B05_MF	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18078	GM_M30_B2_B11_MF	g18559	BLASTN	821	3e-30	75	G.max gene for catalase
18079	GM_M30_B2_B12_MF	g2995405	BLASTX	399	2e-35	59	(Y12432) polyprotein [Ananas comosus]
18080	GM_M30_B2_C04_MF	g2961349	BLASTX	197	1e-13	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
18081	GM_M30_B2_C04_MR	g1167523	BLASTX	172	1e-25	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18082	GM_M30_B2_C05_MR	g2832242	BLASTN	415	1e-11	61	Zea mays 22-kDa alpha zein gene cluster, complete sequence
18083	GM_M30_B2_C06_MR	g3819710	BLASTX	373	1e-33	71	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]
18084	GM_M30_B2_E06_MF	g4063760	BLASTX	309	2e-25	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18085	GM_M30_B2_E11_MF	g3047086	BLASTX	95	5e-09	35	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]
18086	GM_M30_B2_F07_MF	g2995405	BLASTX	349	5e-30	51	(Y12432) polyprotein [Ananas comosus]
18087	GM_M30_B2_F10_MR	g905361	BLASTX	194	1e-13	37	(U22103) gag-protease polyprotein [Glycine max]
18088	GM_M30_B2_G03_MF	g18559	BLASTN	376	5e-10	68	G.max gene for catalase
18089	GM_M30_B2_G04_MR	g3763969	BLASTN	404	3e-11	62	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
18090	GM_M30_B2_G05_MF	g2443320	BLASTX	166	3e-10	41	(D85597) polyprotein [Oryza australiensis]
18091	GM_M30_B2_G06_MF	g4063760	BLASTX	182	6e-12	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18092	GM_M30_B2_H12_MR	g320565	BLASTX	211	2e-16	48	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
18093	GM_M31_A1_A05_MR	g2995951	BLASTX	149	6e-10	54	(AF053564) auxin-induced protein [Mesembryanthemum crystallinum]
18094	GM_M31_A1_A09_MR	g18683	BLASTN	696	4e-30	81	G.max N-20t gene
18095	GM_M31_A1_A12_MR	g3550435	BLASTN	557	4e-18	63	Hordeum vulgare Hotr1 gene
18096	GM_M31_A1_B02_MR	g2827534	BLASTX	171	3e-11	88	(AL021633) predicted protein [Arabidopsis thaliana]
18097	GM_M31_A1_B08_MR	g629693	BLASTX	170	2e-11	29	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18098	GM_M31_A1_B09_MR	g116054	BLASTX	672	2e-65	98	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) gi 280393 pir A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]
18099	GM_M31_A1_B11_MR	g18559	BLASTN	1058	6e-41	78	G.max gene for catalase
18100	GM_M31_A1_C05_MR	g4063760	BLASTX	281	2e-22	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18101	GM_M31_A1_C11_MR	g1167523	BLASTX	358	1e-30	51	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18102	GM_M31_A1_C12_MR	g3776559	BLASTX	407	3e-37	77	(AC005388) Strong similarity to gene F14J9.26 gi 3482933 cdc2 protein kinase homolog from A. thaliana BAC gb AC003970. ESTs gb Z35332 and gb F19907 come from this gene. [Arabidopsis thaliana]
18103	GM_M31_A1_D05_MR	g2642431	BLASTX	267	6e-21	50	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
18104	GM_M31_A1_D10_MR	g4038056	BLASTX	387	4e-34	52	(AC005897) putative transposon [Arabidopsis thaliana]
18105	GM_M31_A1_D12_MR	g2995405	BLASTX	331	4e-28	49	(Y12432) polyprotein [Ananas comosus]
18106	GM_M31_A1_E11_MF	g507910	BLASTN	533	2e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18107	GM_M31_A1_E11_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18108	GM_M31_A1_F03_MF	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18109	GM_M31_A1_F03_MR	g4063760	BLASTX	279	3e-22	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18110	GM_M31_A1_F12_MF	g3212869	BLASTX	155	2e-09	72	(AC004005) unknown protein [Arabidopsis thaliana]
18111	GM_M31_A1_F12_MR	g2262116	BLASTX	163	3e-10	31	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
18112	GM_M31_A1_G10_MF	g3142328	BLASTN	690	6e-38	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18113	GM_M31_A1_G11_MF	g18559	BLASTN	870	2e-32	75	G.max gene for catalase
18114	GM_M31_A1_H03_MF	g1769898	BLASTX	404	1e-36	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18115	GM_M31_A1_H09_MR	g4063760	BLASTX	364	2e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18116	GM_M31_A2_A02_MR	g1335862	BLASTX	234	3e-18	83	(U42608) clathrin heavy chain [Glycine max]
18117	GM_M31_A2_A03_MF	g3097320	BLASTN	451	2e-13	71	Glycine max gene for Bd 30K, complete cds
18118	GM_M31_A2_A04_MF	g99922	BLASTX	545	7e-52	80	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18119	GM_M31_A2_A07_MF	g3869065	BLASTN	886	5e-33	72	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
18120	GM_M31_A2_A09_MR	g114734	BLASTX	147	1e-09	83	AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
18121	GM_M31_A2_A10_MF	g2911280	BLASTX	153	1e-22	68	(U73937) PK12 protein kinase [Nicotiana tabacum]
18122	GM_M31_A2_A12_MF	g3645899	BLASTX	218	4e-19	50	(U68408) 5' end not determined experimentally [Zea mays]
18123	GM_M31_A2_B04_MF	g4063760	BLASTX	266	6e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18124	GM_M31_A2_B05_MR	g3426334	BLASTN	439	7e-13	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18125	GM_M31_A2_B08_MR	g3777527	BLASTX	253	1e-40	90	(AF053008) gag-pol polyprotein [Glycine max]
18126	GM_M31_A2_B11_MR	g1769898	BLASTX	439	1e-40	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18127	GM_M31_A2_C01_MR	g18559	BLASTN	377	5e-10	71	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18128	GM_M31_A2_C05_MF	g4092470	BLASTN	502	1e-15	71	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
18129	GM_M31_A2_C05_MR	g126766	BLASTX	121	8e-10	67	MALATE SYNTHASE, GLYOXYSOMAL gi 68216 pir SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape gi 167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]
18130	GM_M31_A2_C09_MF	g18695	BLASTN	520	1e-16	82	Soybean nodulin 22 gene
18131	GM_M31_A2_C10_MF	g905361	BLASTX	99	5e-09	31	(U22103) gag-protease polyprotein [Glycine max]
18132	GM_M31_A2_C11_MF	g1769898	BLASTX	387	1e-34	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18133	GM_M31_A2_D01_MR	g1321941	BLASTX	119	1e-11	64	(Z48564) dihydrolipoamide dehydrogenase [Synechocystis PCC6803]
18134	GM_M31_A2_D02_MF	g1345132	BLASTX	152	7e-09	41	(U47029) ERECTA [Arabidopsis thaliana] gi 1389566 gnl PID d1012536 (D83257) receptor protein kinase [Arabidopsis thaliana] gi 3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
18135	GM_M31_A2_D03_MR	g2244976	BLASTX	230	2e-18	64	(Z97340) hypothetical protein [Arabidopsis thaliana]
18136	GM_M31_A2_D04_MF	g3097320	BLASTN	639	7e-22	81	Glycine max gene for Bd 30K, complete cds
18137	GM_M31_A2_D05_MF	g2570102	BLASTX	250	1e-20	42	(Y12603) CCLS 65 [Silene latifolia]
18138	GM_M31_A2_D06_MF	g3777527	BLASTX	655	3e-62	97	(AF053008) gag-pol polyprotein [Glycine max]
18139	GM_M31_A2_D06_MR	g3142328	BLASTN	910	3e-34	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18140	GM_M31_A2_E03_MF	g4038056	BLASTX	200	5e-14	41	(AC005897) putative transposon [Arabidopsis thaliana]
18141	GM_M31_A2_E04_MR	g507910	BLASTN	439	3e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18142	GM_M31_A2_E09_MF	g2673917	BLASTX	186	5e-12	65	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
18143	GM_M31_A2_E11_MF	g3845197	BLASTN	380	4e-10	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18144	GM_M31_A2_E12_MF	g3777527	BLASTX	547	1e-50	89	(AF053008) gag-pol polyprotein [Glycine max]
18145	GM_M31_A2_E12_MR	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18146	GM_M31_A2_F03_MF	g4063760	BLASTX	505	2e-46	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18147	GM_M31_A2_F03_MR	g343840	BLASTN	425	2e-12	63	Yeast (S.cerevisiae) strain B mitochondrial petite mutant b-1 ori1 region.
18148	GM_M31_A2_F05_MF	g3142328	BLASTN	1038	4e-40	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18149	GM_M31_A2_F10_MR	g4038056	BLASTX	356	9e-31	55	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18150	GM_M31_A2_G01_MF	g13373	BLASTN	384	3e-11	67	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
18151	GM_M31_A2_G04_MF	g507910	BLASTN	611	5e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18152	GM_M31_A2_G04_MR	g4063760	BLASTX	239	4e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18153	GM_M31_A2_G05_MF	g170029	BLASTN	370	1e-09	78	Glycine max cv. Dare nodulin 26 gene fragment.
18154	GM_M31_A2_G09_MR	g3319351	BLASTX	289	3e-23	40	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
18155	GM_M31_A2_G10_MF	g130405	BLASTX	115	3e-11	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
18156	GM_M31_A2_G10_MR	g3250695	BLASTX	166	8e-11	67	(AL024486) putative protein [Arabidopsis thaliana]
18157	GM_M31_A2_G11_MR	g2997694	BLASTX	226	5e-18	37	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
18158	GM_M31_A2_H03_MR	g905361	BLASTX	179	5e-12	32	(U22103) gag-protease polyprotein [Glycine max]
18159	GM_M31_A2_H06_MF	g3142379	BLASTX	265	8e-22	59	(AF053008) envelope-like [Glycine max]
18160	GM_M31_A2_H10_MR	g3777527	BLASTX	297	4e-24	46	(AF053008) gag-pol polyprotein [Glycine max]
18161	GM_M31_A2_H12_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18162	GM_M31_A2_H12_MR	g4092471	BLASTN	502	1e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18163	GM_M31_B1_A09_MF	g507910	BLASTN	410	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18164	GM_M31_B1_A09_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18165	GM_M31_B1_A11_MF	g4092471	BLASTN	378	5e-10	64	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18166	GM_M31_B1_A11_MR	g3873174	BLASTN	399	6e-11	61	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]
18167	GM_M31_B1_A12_MF	g100484	BLASTX	310	5e-26	55	hypothetical protein - garden snapdragon
18168	GM_M31_B1_B01_MF	g4063760	BLASTX	512	4e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18169	GM_M31_B1_B01_MR	g3142328	BLASTN	833	9e-31	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18170	GM_M31_B1_B02_MF	g100484	BLASTX	184	2e-12	45	hypothetical protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18171	GM_M31_B1_B05_MF	g4063760	BLASTX	349	9e-30	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18172	GM_M31_B1_B05_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18173	GM_M31_B1_B10_MF	g3645899	BLASTX	182	5e-12	55	(U68408) 5' end not determined experimentally [Zea mays]
18174	GM_M31_B1_C04_MR	g3777527	BLASTX	631	7e-63	95	(AF053008) gag-pol polyprotein [Glycine max]
18175	GM_M31_B1_C05_MR	g2924732	BLASTN	778	4e-28	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]
18176	GM_M31_B1_D03_MF	g1769898	BLASTX	254	4e-20	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18177	GM_M31_B1_D03_MR	g2522227	BLASTX	180	5e-13	60	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18178	GM_M31_B1_D06_MF	g3097320	BLASTN	950	5e-36	76	Glycine max gene for Bd 30K, complete cds
18179	GM_M31_B1_D11_MF	g4038056	BLASTX	340	3e-30	54	(AC005897) putative transposon [Arabidopsis thaliana]
18180	GM_M31_B1_D11_MR	g4063760	BLASTX	350	8e-30	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18181	GM_M31_B1_D12_MR	g4063756	BLASTN	484	8e-15	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18182	GM_M31_B1_E05_MR	g507910	BLASTN	396	3e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18183	GM_M31_B1_E06_MR	g3128228	BLASTX	463	4e-43	92	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] gi 3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
18184	GM_M31_B1_E07_MR	g3650039	BLASTX	279	9e-23	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
18185	GM_M31_B1_E08_MF	g1431738	BLASTN	863	2e-32	82	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
18186	GM_M31_B1_E12_MF	g2129618	BLASTX	148	3e-14	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18187	GM_M31_B1_F07_MF	g507910	BLASTN	460	4e-14	79	Glycine max BSR-101 satellite SB92 genomic sequence.
18188	GM_M31_B1_F10_MR	g18559	BLASTN	955	3e-36	76	G.max gene for catalase
18189	GM_M31_B1_G05_MR	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18190	GM_M31_B1_G08_MR	g226407	BLASTX	332	7e-28	51	retrotransposon del1-46 [Lilium henryi]
18191	GM_M31_B1_G09_MR	g3810596	BLASTX	174	3e-11	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18192	GM_M31_B1_G12_MR	g507910	BLASTN	394	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18193	GM_M31_B1_H01_MF	g1944192	BLASTN	1050	1e-41	90	Soybean mRNA for nodulin 35, complete cds
18194	GM_M31_B1_H02_MR	g3021270	BLASTX	261	5e-31	77	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]
18195	GM_M31_B1_H05_MR	g905361	BLASTX	154	3e-09	29	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18196	GM_M31_B2_A08_MF	g4049332	BLASTN	367	9e-18	66	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)
18197	GM_M31_B2_A09_MF	g2264320	BLASTN	489	5e-15	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
18198	GM_M31_B2_A10_MF	g2344894	BLASTX	158	1e-12	67	(AC002388) hypothetical protein [Arabidopsis thaliana]
18199	GM_M31_B2_B01_MF	g507910	BLASTN	456	5e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18200	GM_M31_B2_C10_MF	g18559	BLASTN	497	2e-15	75	G.max gene for catalase
18201	GM_M31_B2_C11_MF	g3097320	BLASTN	892	2e-33	77	Glycine max gene for Bd 30K, complete cds
18202	GM_M31_B2_D01_MF	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18203	GM_M31_B2_E02_MF	g4063760	BLASTX	462	7e-42	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18204	GM_M31_B2_E03_MF	g1326016	BLASTX	230	4e-17	41	TY3-2 orfB
18205	GM_M31_B2_E05_MF	g3643604	BLASTX	187	1e-12	37	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
18206	GM_M31_B2_E10_MF	g2827702	BLASTX	393	9e-36	71	(AL021684) predicted protein [Arabidopsis thaliana]
18207	GM_M31_B2_F03_MF	g498931	BLASTX	448	1e-41	68	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
18208	GM_M31_B2_G04_MF	g2270991	BLASTN	425	6e-13	84	Glycine max metallothionein-II protein mRNA, complete cds
18209	GM_M31_B2_G05_MF	g507910	BLASTN	383	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18210	GM_M31_B2_G08_MF	g4063760	BLASTX	531	3e-49	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18211	GM_M31_B2_H01_MF	g3142328	BLASTN	1437	3e-58	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18212	GM_M31_B2_H02_MF	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
18213	GM_M31_B2_H05_MF	g3645899	BLASTX	352	3e-30	55	(U68408) 5' end not determined experimentally [Zea mays]
18214	GM_M31_B2_H09_MF	g3096919	BLASTX	280	3e-23	49	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]
18215	GM_M31_B2_H11_MF	g3288442	BLASTN	467	5e-14	66	Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Ga...
18216	GM_M32_A1_A07_MF	g3142379	BLASTX	242	3e-19	72	(AF053008) envelope-like [Glycine max]
18217	GM_M32_A1_B04_MR	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
18218	GM_M32_A1_B05_MF	g3777527	BLASTX	180	1e-11	44	(AF053008) gag-pol polyprotein [Glycine max]
18219	GM_M32_A1_B05_MR	g2443899	BLASTN	397	7e-11	64	A. thaliana BAC T3F12 from chromsome IV, likely from the long arm, complete sequence [Arabidopsis thaliana]
18220	GM_M32_A1_B10_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18221	GM_M32_A1_C02_MF	g905361	BLASTX	171	4e-11	35	(U22103) gag-protease polyprotein [Glycine max]
18222	GM_M32_A1_C06_MR	g3273387	BLASTN	426	3e-12	68	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
18223	GM_M32_A1_C07_MR	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18224	GM_M32_A1_C09_MF	g3097320	BLASTN	432	2e-12	73	Glycine max gene for Bd 30K, complete cds
18225	GM_M32_A1_C09_MR	g4063760	BLASTX	222	3e-16	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18226	GM_M32_A1_D04_MF	g3777527	BLASTX	604	9e-57	98	(AF053008) gag-pol polyprotein [Glycine max]
18227	GM_M32_A1_D10_MR	g3645899	BLASTX	307	2e-25	50	(U68408) 5' end not determined experimentally [Zea mays]
18228	GM_M32_A1_E01_MR	g2462134	BLASTX	171	3e-11	33	(Y13368) reverse transcriptase [Beta vulgaris]
18229	GM_M32_A1_E02_MF	g3779026	BLASTX	315	5e-26	49	(AC005171) putative retrotransposon [Arabidopsis thaliana]
18230	GM_M32_A1_E05_MR	g2121303	BLASTN	410	2e-11	61	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
18231	GM_M32_A1_E07_MF	g3688172	BLASTX	152	2e-10	49	(AL031804) putative protein [Arabidopsis thaliana]
18232	GM_M32_A1_E08_MF	g507910	BLASTN	353	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18233	GM_M32_A1_E08_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18234	GM_M32_A1_E09_MR	g4063760	BLASTX	280	2e-22	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18235	GM_M32_A1_E12_MF	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18236	GM_M32_A1_E12_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18237	GM_M32_A1_F04_MF	g342963	BLASTN	378	2e-10	65	paramecium species 5.87 mt dna dimer: replication init. region.
18238	GM_M32_A1_F04_MR	g99755	BLASTX	289	6e-24	43	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
18239	GM_M32_A1_G08_MR	g4140712	BLASTX	252	8e-21	37	(AF110183) putative integrase [Oryza sativa]
18240	GM_M32_A1_G12_MR	g4063760	BLASTX	184	4e-12	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18241	GM_M32_A2_A10_MF	g18683	BLASTN	435	9e-13	77	G.max N-20t gene
18242	GM_M32_A2_A11_MF	g3859060	BLASTN	354	6e-09	62	Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, GSS, complete sequence [Homo sapiens]
18243	GM_M32_A2_B03_MR	g629693	BLASTX	146	4e-11	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18244	GM_M32_A2_B04_MF	g100484	BLASTX	97	4e-10	60	hypothetical protein - garden snapdragon
18245	GM_M32_A2_B05_MF	g18695	BLASTN	399	4e-11	72	Soybean nodulin 22 gene
18246	GM_M32_A2_B10_MF	g1142703	BLASTN	301	2e-17	77	Glycine max satellite STR120-B.1.
18247	GM_M32_A2_B12_MF	g3097320	BLASTN	1204	2e-47	83	Glycine max gene for Bd 30K, complete cds
18248	GM_M32_A2_C01_MF	g4038056	BLASTX	241	4e-24	57	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18249	GM_M32_A2_C02_MF	g4038056	BLASTX	223	9e-22	56	(AC005897) putative transposon [Arabidopsis thaliana]
18250	GM_M32_A2_C07_MR	g2462058	BLASTX	171	3e-12	55	(Y13389) reverse transcriptase [Antirrhinum majus]
18251	GM_M32_A2_C08_MR	g3142328	BLASTN	1093	1e-42	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18252	GM_M32_A2_D02_MF	g3097320	BLASTN	402	4e-11	71	Glycine max gene for Bd 30K, complete cds
18253	GM_M32_A2_D02_MR	g18559	BLASTN	402	3e-11	74	G.max gene for catalase
18254	GM_M32_A2_D06_MF	g3688172	BLASTX	168	1e-10	78	(AL031804) putative protein [Arabidopsis thaliana]
18255	GM_M32_A2_D10_MR	g2982538	BLASTN	309	7e-09	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-28, complete sequence [Plasmodium falciparum]
18256	GM_M32_A2_D11_MF	g2809207	BLASTX	154	2e-10	84	(AF042184) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Brassica napus]
18257	GM_M32_A2_E07_MR	g3319362	BLASTX	184	2e-19	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18258	GM_M32_A2_F03_MR	g3695395	BLASTX	191	2e-13	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
18259	GM_M32_A2_F04_MF	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18260	GM_M32_A2_F04_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18261	GM_M32_A2_F07_MR	g3777527	BLASTX	725	9e-70	96	(AF053008) gag-pol polyprotein [Glycine max]
18262	GM_M32_A2_F12_MR	g3513745	BLASTX	164	7e-10	31	(AF080118) contains similarity to reverse tranciptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
18263	GM_M32_A2_G01_MR	g4063760	BLASTX	536	9e-50	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18264	GM_M32_A2_G02_MR	g4063760	BLASTX	291	3e-33	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18265	GM_M32_A2_G03_MF	g343543	BLASTN	344	5e-09	62	T.brucei kinetoplast ATPase 6 edited mRNA, complete cds.
18266	GM_M32_A2_G05_MF	g2760837	BLASTX	139	1e-15	53	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]
18267	GM_M32_A2_G05_MR	g2129618	BLASTX	201	4e-14	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18268	GM_M32_A2_G06_MR	g3779026	BLASTX	361	6e-31	50	(AC005171) putative retrotransposon [Arabidopsis thaliana]
18269	GM_M32_A2_G10_MF	g4063760	BLASTX	271	2e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18270	GM_M32_A2_G11_MR	g3176811	BLASTN	397	7e-12	64	Homo sapiens allele 18 fragile site locus (FRA10B) minisatellite, 3' sequence
18271	GM_M32_A2_G12_MR	g3319362	BLASTX	282	9e-23	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18272	GM_M32_A2_H02_MR	g1778438	BLASTX	120	2e-09	53	(U82399) putative protein kinase PK1 [Arabidopsis thaliana]
18273	GM_M32_A2_H03_MR	g507910	BLASTN	511	2e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18274	GM_M32_A2_H06_MF	g629693	BLASTX	146	4e-12	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18275	GM_M32_A2_H12_MR	g3097320	BLASTN	451	2e-13	73	Glycine max gene for Bd 30K, complete cds
18276	GM_M32_B1_A02_MR	g3142328	BLASTN	614	8e-21	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18277	GM_M32_B1_A05_MF	g3550435	BLASTN	460	9e-14	63	Hordeum vulgare Hotr1 gene
18278	GM_M32_B1_A05_MR	g507910	BLASTN	668	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18279	GM_M32_B1_A11_MR	g2129618	BLASTX	235	1e-17	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18280	GM_M32_B1_B01_MF	g3777527	BLASTX	166	3e-11	40	(AF053008) gag-pol polyprotein [Glycine max]
18281	GM_M32_B1_B02_MR	g4063760	BLASTX	243	9e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18282	GM_M32_B1_B11_MR	g905361	BLASTX	239	2e-18	38	(U22103) gag-protease polyprotein [Glycine max]
18283	GM_M32_B1_B12_MR	g505129	BLASTN	385	1e-15	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18284	GM_M32_B1_C01_MR	g3493214	BLASTX	140	2e-15	43	(AF056940) pol polyprotein [Drosophila virilis]
18285	GM_M32_B1_C04_MF	g3097320	BLASTN	793	7e-29	74	Glycine max gene for Bd 30K, complete cds
18286	GM_M32_B1_C05_MF	g170080	BLASTN	1000	4e-57	97	Soybean seed lectin gene transposable element tgm1.
18287	GM_M32_B1_C09_MF	g3142379	BLASTX	197	2e-14	72	(AF053008) envelope-like [Glycine max]
18288	GM_M32_B1_C09_MR	g3777527	BLASTX	435	5e-58	98	(AF053008) gag-pol polyprotein [Glycine max]
18289	GM_M32_B1_D01_MR	g629693	BLASTX	166	5e-11	30	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18290	GM_M32_B1_D02_MR	g100484	BLASTX	376	4e-33	57	hypothetical protein - garden snapdragon
18291	GM_M32_B1_D05_MF	g3914056	BLASTX	118	5e-12	74	DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
18292	GM_M32_B1_D06_MR	g2995405	BLASTX	425	3e-38	71	(Y12432) polyprotein [Ananas comosus]
18293	GM_M32_B1_D07_MF	g3645899	BLASTX	221	4e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
18294	GM_M32_B1_D10_MF	g905361	BLASTX	421	2e-38	93	(U22103) gag-protease polyprotein [Glycine max]
18295	GM_M32_B1_D12_MR	g3845197	BLASTN	483	8e-15	64	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18296	GM_M32_B1_E01_MF	g1769897	BLASTX	164	2e-10	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18297	GM_M32_B1_E02_MR	g18559	BLASTN	693	2e-24	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18298	GM_M32_B1_E09_MR	g4006838	BLASTN	386	2e-10	68	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
18299	GM_M32_B1_F01_MF	g1345644	BLASTX	176	7e-12	51	CYTOCHROME P450 LXXXVI gi 940446 (X90458) cytochrome p450 [Arabidopsis thaliana]
18300	GM_M32_B1_F02_MR	g4063760	BLASTX	483	4e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18301	GM_M32_B1_F07_MR	g3522966	BLASTN	354	6e-09	65	Homo sapiens subtelomeric cosmid clone 5b-1, complete sequence [Homo sapiens]
18302	GM_M32_B1_F08_MR	g3935157	BLASTX	151	7e-09	63	(AC005106) T25N20.21 [Arabidopsis thaliana]
18303	GM_M32_B1_G02_MR	g3337395	BLASTN	426	3e-12	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
18304	GM_M32_B1_G04_MF	g3426038	BLASTX	271	5e-21	46	(AC005168) unknown protein [Arabidopsis thaliana]
18305	GM_M32_B1_G09_MF	g3930515	BLASTX	115	4e-10	46	(AF059674) putative gag protein [Nicotiana tabacum]
18306	GM_M32_B1_G11_MR	g18559	BLASTN	448	3e-13	76	G.max gene for catalase
18307	GM_M32_B1_H04_MF	g2264320	BLASTN	630	2e-21	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
18308	GM_M32_B1_H04_MR	g629693	BLASTX	151	2e-09	30	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18309	GM_M32_B1_H05_MF	g2569940	BLASTX	197	5e-14	50	(Y15194) GRS protein [Arabidopsis thaliana]
18310	GM_M32_B1_H08_MR	g2997694	BLASTX	183	1e-13	33	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
18311	GM_M32_B1_H09_MF	g3930515	BLASTX	121	5e-10	47	(AF059674) putative gag protein [Nicotiana tabacum]
18312	GM_M32_B2_A02_MR	g3777527	BLASTX	325	5e-27	49	(AF053008) gag-pol polyprotein [Glycine max]
18313	GM_M32_B2_A05_MR	g2213582	BLASTX	206	2e-14	28	(AC000348) T7N9.2 [Arabidopsis thaliana]
18314	GM_M32_B2_B04_MR	g3928543	BLASTX	215	4e-16	45	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]
18315	GM_M32_B2_B10_MR	g3777527	BLASTX	177	3e-11	44	(AF053008) gag-pol polyprotein [Glycine max]
18316	GM_M32_B2_C01_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18317	GM_M32_B2_C03_MR	g2462134	BLASTX	163	2e-10	34	(Y13368) reverse transcriptase [Beta vulgaris]
18318	GM_M32_B2_C07_MR	g531389	BLASTX	175	4e-11	42	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18319	GM_M32_B2_D04_MF	g3386533	BLASTN	490	3e-15	75	Glycine max mariner element Soymar1 transposase gene, complete cds
18320	GM_M32_B2_D04_MR	g3386533	BLASTN	1587	3e-65	97	Glycine max mariner element Soymar1 transposase gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18321	GM_M32_B2_D09_MF	g3142328	BLASTN	578	3e-19	67	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18322	GM_M32_B2_D10_MF	g3777527	BLASTX	297	4e-24	45	(AF053008) gag-pol polyprotein [Glycine max]
18323	GM_M32_B2_D12_MR	g4063760	BLASTX	452	9e-41	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18324	GM_M32_B2_F01_MR	g1236920	BLASTN	276	4e-10	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
18325	GM_M32_B2_F08_MR	g2995405	BLASTX	337	1e-28	46	(Y12432) polyprotein [Ananas comosus]
18326	GM_M32_B2_G06_MR	g587603	BLASTN	414	9e-12	61	P.falciparum gene for beta subunit RNA polymerase
18327	GM_M32_B2_H01_MR	g3097320	BLASTN	467	4e-14	76	Glycine max gene for Bd 30K, complete cds
18328	GM_M32_B2_H07_MR	g3142328	BLASTN	833	9e-31	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18329	GM_M32_B2_H11_MR	g4115365	BLASTX	169	1e-14	61	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18330	GM_M33_A1_A09_MR	g905361	BLASTX	181	3e-12	34	(U22103) gag-protease polyprotein [Glycine max]
18331	GM_M33_A1_A10_MF	g2781345	BLASTX	154	4e-09	93	(AC003113) F24O1.2 [Arabidopsis thaliana]
18332	GM_M33_A1_A12_MR	g4115536	BLASTX	170	6e-12	39	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
18333	GM_M33_A1_B02_MF	g3845197	BLASTN	373	8e-10	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18334	GM_M33_A1_B03_MR	g840618	BLASTN	468	2e-14	60	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
18335	GM_M33_A1_B04_MR	g4006828	BLASTX	194	2e-13	30	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
18336	GM_M33_A1_B05_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18337	GM_M33_A1_B05_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18338	GM_M33_A1_C02_MR	g349405	BLASTN	386	2e-10	64	Brassica napus (clone BnNa) DNA sequence.
18339	GM_M33_A1_C04_MR	g3513744	BLASTX	164	2e-11	37	(AF080118) contains similarity to Medicago truncatula MtN3 (GB:Y08726) [Arabidopsis thaliana]
18340	GM_M33_A1_C05_MF	g170296	BLASTN	401	4e-13	80	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) gene, exons 1-9.
18341	GM_M33_A1_C05_MR	g2281330	BLASTX	157	2e-10	51	(U85646) putative pectate lyase Nt59 [Nicotiana tabacum]
18342	GM_M33_A1_C10_MR	g4063760	BLASTX	554	1e-51	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18343	GM_M33_A1_C11_MF	g2522227	BLASTX	227	1e-20	45	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18344	GM_M33_A1_C12_MF	g3777527	BLASTX	628	2e-59	96	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18345	GM_M33_A1_D02_MR	g2245082	BLASTX	166	4e-11	31	(Z97343) SCARECROW homolog [Arabidopsis thaliana]
18346	GM_M33_A1_D03_MF	g2443320	BLASTX	294	8e-24	46	(D85597) polyprotein [Oryza australiensis]
18347	GM_M33_A1_D05_MR	g3777527	BLASTX	741	2e-71	96	(AF053008) gag-pol polyprotein [Glycine max]
18348	GM_M33_A1_D10_MF	g18559	BLASTN	863	4e-32	76	G.max gene for catalase
18349	GM_M33_A1_D11_MF	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18350	GM_M33_A1_D12_MF	g3820757	BLASTN	416	5e-12	63	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
18351	GM_M33_A1_E11_MR	g18559	BLASTN	677	1e-23	71	G.max gene for catalase
18352	GM_M33_A1_F10_MR	g2708743	BLASTX	254	1e-19	42	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
18353	GM_M33_A1_F11_MR	g905361	BLASTX	343	1e-29	93	(U22103) gag-protease polyprotein [Glycine max]
18354	GM_M33_A1_G03_MR	g4115536	BLASTX	172	3e-12	39	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
18355	GM_M33_A1_G04_MR	g3142328	BLASTN	1253	7e-50	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18356	GM_M33_A1_G09_MF	g4063760	BLASTX	334	4e-28	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18357	GM_M33_A1_H02_MF	g2129618	BLASTX	191	4e-13	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18358	GM_M33_A1_H07_MR	g1167523	BLASTX	300	2e-24	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18359	GM_M33_A1_H09_MR	g2583112	BLASTX	167	2e-11	40	(AC002387) putative PD1-like DNA-binding protein [Arabidopsis thaliana]
18360	GM_M33_A1_H10_MF	g507910	BLASTN	586	7e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18361	GM_M33_A2_A04_MF	g2414229	BLASTN	361	3e-09	64	Caenorhabditis elegans cosmid K03D10, complete sequence [Caenorhabditis elegans]
18362	GM_M33_A2_A07_MF	g2316016	BLASTX	397	1e-34	61	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
18363	GM_M33_A2_A08_MR	g4063760	BLASTX	326	3e-27	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18364	GM_M33_A2_A11_MF	g1769896	BLASTN	409	2e-11	64	A.thaliana lectin receptor kinase gene
18365	GM_M33_A2_B02_MR	g18559	BLASTN	552	5e-18	72	G.max gene for catalase
18366	GM_M33_A2_B09_MF	g1167523	BLASTX	115	2e-12	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18367	GM_M33_A2_B09_MR	g4160362	BLASTN	266	6e-12	69	Saccharomyces cerevisiae complete mitochondrial genome
18368	GM_M33_A2_B10_MF	g4038037	BLASTX	385	1e-33	60	(AC005936) hypothetical protein [Arabidopsis thaliana]
18369	GM_M33_A2_C01_MR	g18766	BLASTN	387	6e-11	80	Soybean Tgm5 transposable element
18370	GM_M33_A2_C03_MF	g3097320	BLASTN	817	6e-30	72	Glycine max gene for Bd 30K, complete cds
18371	GM_M33_A2_C03_MR	g3779021	BLASTX	165	4e-10	41	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18372	GM_M33_A2_C04_MF	g126406	BLASTX	278	7e-33	77	SEED LIPOXYGENASE-3 (L-3) gi 18677 (X06928) lipoxygenase [Glycine max]
18373	GM_M33_A2_C06_MF	g2961349	BLASTX	303	7e-25	49	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
18374	GM_M33_A2_C11_MR	g3451074	BLASTX	259	1e-20	50	(AL031326) putative protein [Arabidopsis thaliana]
18375	GM_M33_A2_D01_MF	g3337395	BLASTN	375	7e-10	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
18376	GM_M33_A2_D02_MR	g421955	BLASTX	164	8e-11	41	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
18377	GM_M33_A2_D04_MF	g2462134	BLASTX	347	8e-31	44	(Y13368) reverse transcriptase [Beta vulgaris]
18378	GM_M33_A2_D05_MF	g3513747	BLASTX	197	2e-13	47	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18379	GM_M33_A2_D07_MF	g3982831	BLASTX	615	6e-59	100	(AF083343) 101 kDa heat shock protein; HSP101 [Nicotiana tabacum]
18380	GM_M33_A2_D10_MF	g3021280	BLASTX	249	1e-19	38	(AL022347) serine /threonine kinase - like protein [Arabidopsis thaliana]
18381	GM_M33_A2_D10_MR	g1769899	BLASTX	128	3e-17	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18382	GM_M33_A2_E05_MR	g2586082	BLASTX	159	2e-09	37	(U72725) retrofit [Oryza longistaminata]
18383	GM_M33_A2_E07_MR	g4063756	BLASTN	362	3e-09	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18384	GM_M33_A2_E11_MF	g3779021	BLASTX	169	2e-10	34	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
18385	GM_M33_A2_E12_MF	g4038056	BLASTX	234	1e-17	50	(AC005897) putative transposon [Arabidopsis thaliana]
18386	GM_M33_A2_F03_MF	g320565	BLASTX	189	4e-14	54	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
18387	GM_M33_A2_F05_MF	g18559	BLASTN	953	3e-36	76	G.max gene for catalase
18388	GM_M33_A2_F07_MF	g4038056	BLASTX	279	2e-22	47	(AC005897) putative transposon [Arabidopsis thaliana]
18389	GM_M33_A2_F08_MF	g905361	BLASTX	149	9e-09	83	(U22103) gag-protease polyprotein [Glycine max]
18390	GM_M33_A2_F10_MF	g2104679	BLASTX	238	4e-30	86	(X97906) transcription factor [Vicia faba]
18391	GM_M33_A2_G03_MR	g3426334	BLASTN	563	2e-18	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18392	GM_M33_A2_G05_MF	g2443320	BLASTX	316	4e-26	52	(D85597) polyprotein [Oryza australiensis]
18393	GM_M33_A2_G07_MF	g2245029	BLASTX	159	1e-09	55	(Z97341) limonene cyclase homolog [Arabidopsis thaliana]
18394	GM_M33_A2_G08_MR	g4038056	BLASTX	358	6e-31	53	(AC005897) putative transposon [Arabidopsis thaliana]
18395	GM_M33_A2_G10_MR	g100484	BLASTX	343	1e-29	51	hypothetical protein - garden snapdragon
18396	GM_M33_A2_H02_MF	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18397	GM_M33_A2_H02_MR	g4063760	BLASTX	314	5e-26	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18398	GM_M33_A2_H04_MF	g507910	BLASTN	558	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18399	GM_M33_B1_B01_MF	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
18400	GM_M33_B1_C11_MF	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18401	GM_M33_B1_D09_MF	g3980359	BLASTN	360	3e-09	65	Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence [Homo sapiens]
18402	GM_M33_B1_F06_MF	g498167	BLASTN	536	4e-18	94	Soybean mRNA for leginsulin, complete cds
18403	GM_M33_B1_G09_MF	g507910	BLASTN	353	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18404	GM_M33_B1_H07_MF	g507910	BLASTN	650	9e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18405	GM_M33_B1_H11_MF	g2995405	BLASTX	332	3e-28	61	(Y12432) polyprotein [Ananas comosus]
18406	GM_M33_B2_E07_MR	g1817728	BLASTN	414	1e-11	72	Cloning vector pBeloBAC11
18407	GM_M34_A1_A04_MR	g18768	BLASTN	510	1e-16	69	Soybean Tgm6 transposable element 3' end
18408	GM_M34_A1_A05_MR	g3142328	BLASTN	1221	2e-48	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18409	GM_M34_A1_A12_MF	g218269	BLASTX	205	7e-16	52	(D12839) reverse transcriptase [Glycine max]
18410	GM_M34_A1_B01_MF	g3980412	BLASTX	185	2e-12	44	(AC004561) pumilio-like protein [Arabidopsis thaliana]
18411	GM_M34_A1_B01_MR	g22741	BLASTN	285	4e-11	86	G.max mitochondrial pseudo-atpA.
18412	GM_M34_A1_B02_MF	g3176795	BLASTN	391	3e-11	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
18413	GM_M34_A1_B02_MR	g3845298	BLASTN	391	1e-10	62	Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence
18414	GM_M34_A1_B03_MR	g2129618	BLASTX	251	2e-19	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18415	GM_M34_A1_B04_MF	g1688074	BLASTX	146	4e-09	35	(U46570) tetratricopeptide repeat protein [Homo sapiens]
18416	GM_M34_A1_B06_MF	g99922	BLASTX	396	8e-43	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18417	GM_M34_A1_B07_MR	g3746069	BLASTX	206	2e-14	43	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
18418	GM_M34_A1_B11_MF	g1666236	BLASTX	148	3e-09	30	(U76261) unknown [Hordeum vulgare]
18419	GM_M34_A1_B12_MF	g1334366	BLASTX	172	3e-12	80	(X02441) gtg start [Nicotiana tabacum]
18420	GM_M34_A1_C01_MF	g2190548	BLASTX	193	1e-14	71	(AC001229) EST gb ATTS1121 comes from this gene. [Arabidopsis thaliana]
18421	GM_M34_A1_C01_MR	g2995405	BLASTX	273	1e-23	43	(Y12432) polyprotein [Ananas comosus]
18422	GM_M34_A1_C02_MF	g3402758	BLASTX	256	4e-21	69	(AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]
18423	GM_M34_A1_C03_MF	g2995405	BLASTX	109	1e-12	41	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18424	GM_M34_A1_C06_MR	g1167523	BLASTX	249	5e-19	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18425	GM_M34_A1_C11_MR	g2351069	BLASTN	403	4e-11	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12
18426	GM_M34_A1_C12_MF	g507910	BLASTN	422	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18427	GM_M34_A1_C12_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18428	GM_M34_A1_D02_MR	g2995405	BLASTX	479	4e-44	61	(Y12432) polyprotein [Ananas comosus]
18429	GM_M34_A1_D04_MR	g2330651	BLASTX	301	2e-24	72	(Y14559) topoisomerase II [Pisum sativum]
18430	GM_M34_A1_D08_MF	g3142328	BLASTN	768	8e-28	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18431	GM_M34_A1_D09_MR	g2129618	BLASTX	179	9e-12	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18432	GM_M34_A1_E07_MF	g3426334	BLASTN	357	4e-09	59	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18433	GM_M34_A1_F06_MF	g4063760	BLASTX	211	2e-16	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18434	GM_M34_A1_F07_MF	g1785701	BLASTX	89	1e-10	48	(Y08501) orf154 [Arabidopsis thaliana]
18435	GM_M34_A1_F08_MF	g2995405	BLASTX	200	2e-22	48	(Y12432) polyprotein [Ananas comosus]
18436	GM_M34_A1_F10_MF	g3319362	BLASTX	191	1e-15	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18437	GM_M34_A1_F10_MR	g1167523	BLASTX	378	8e-33	51	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18438	GM_M34_A1_F12_MF	g3810596	BLASTX	218	1e-20	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18439	GM_M34_A1_G01_MF	g18559	BLASTN	360	3e-09	73	G.max gene for catalase
18440	GM_M34_A1_G04_MF	g3513747	BLASTX	244	2e-18	54	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18441	GM_M34_A1_G06_MF	g558922	BLASTN	627	5e-22	76	Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA, complete cds.
18442	GM_M34_A1_G07_MR	g3097320	BLASTN	356	4e-09	66	Glycine max gene for Bd 30K, complete cds
18443	GM_M34_A1_G11_MF	g4092471	BLASTN	469	4e-14	71	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18444	GM_M34_A1_H01_MF	g99730	BLASTX	328	1e-28	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
18445	GM_M34_A1_H01_MR	g3142328	BLASTN	1951	9e-82	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18446	GM_M34_A1_H02_MF	g1091678	BLASTX	143	8e-13	34	activator-like transposable element [Pennisetum glaucum]
18447	GM_M34_A1_H04_MF	g3779021	BLASTX	172	6e-12	40	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18448	GM_M34_A1_H05_MR	g1899158	BLASTN	382	2e-10	61	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds
18449	GM_M34_A1_H11_MR	g3426038	BLASTX	278	9e-22	91	(AC005168) unknown protein [Arabidopsis thaliana]
18450	GM_M34_A1_H12_MR	g2085783	BLASTN	386	2e-10	62	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
18451	GM_M34_A2_A08_MF	g3135269	BLASTX	219	6e-16	45	(AC003058) unknown protein [Arabidopsis thaliana]
18452	GM_M34_A2_A12_MF	g2995405	BLASTX	338	8e-29	55	(Y12432) polyprotein [Ananas comosus]
18453	GM_M34_A2_C12_MF	g507910	BLASTN	580	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18454	GM_M34_A2_D02_MF	g3142328	BLASTN	961	1e-36	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18455	GM_M34_A2_D06_MF	g3142328	BLASTN	1001	2e-38	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18456	GM_M34_A2_F04_MF	g1769897	BLASTX	311	1e-29	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18457	GM_M34_A2_F08_MF	g4050011	BLASTN	666	4e-23	66	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
18458	GM_M34_A2_G03_MF	g18683	BLASTN	489	3e-15	72	G.max N-20t gene
18459	GM_M34_A2_G11_MF	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18460	GM_M34_A2_H01_MF	g3415117	BLASTX	219	5e-16	70	(AF081203) villin 3 [Arabidopsis thaliana]
18461	GM_M34_A2_H02_MF	g2258317	BLASTX	137	7e-12	42	(AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]
18462	GM_M34_A2_H10_MF	g161840	BLASTN	360	2e-09	64	T.thermophila micronuclear region R DNA.
18463	GM_M34_B1_A04_MR	g4038056	BLASTX	378	4e-33	51	(AC005897) putative transposon [Arabidopsis thaliana]
18464	GM_M34_B1_A05_MR	g2129618	BLASTX	191	5e-13	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18465	GM_M34_B1_A08_MR	g4038056	BLASTX	285	5e-25	43	(AC005897) putative transposon [Arabidopsis thaliana]
18466	GM_M34_B1_B01_MR	g728483	BLASTX	238	4e-20	59	(L41046) endo-1,4-beta-glucanase [Pisum sativum]
18467	GM_M34_B1_B02_MF	g3293503	BLASTN	379	6e-11	64	Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds
18468	GM_M34_B1_B02_MR	g2791289	BLASTX	227	1e-16	37	(AJ000387) protease [Drosophila melanogaster]
18469	GM_M34_B1_B11_MR	g3097320	BLASTN	473	2e-14	72	Glycine max gene for Bd 30K, complete cds
18470	GM_M34_B1_C06_MR	g18559	BLASTN	988	9e-38	77	G.max gene for catalase
18471	GM_M34_B1_C10_MR	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18472	GM_M34_B1_D02_MR	g1769898	BLASTX	237	3e-18	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18473	GM_M34_B1_D04_MR	g3777527	BLASTX	255	1e-19	39	(AF053008) gag-pol polyprotein [Glycine max]
18474	GM_M34_B1_D06_MF	g2995405	BLASTX	247	5e-25	50	(Y12432) polyprotein [Ananas comosus]

Seq No	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18475	GM_M34_B1_D08_MF	g130582	BLASTX	323	6e-27	48	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18476	GM_M34_B1_D10_MF	g3176671	BLASTX	256	5e-20	67	(AC004393) Contains similarity to hypothetical gene B0495.7 gb 687822 from C. elegans cosmid gb U21317. [Arabidopsis thaliana]
18477	GM_M34_B1_D11_MR	g1431738	BLASTN	655	8e-23	93	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
18478	GM_M34_B1_E03_MF	g2264320	BLASTN	547	1e-17	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
18479	GM_M34_B1_E05_MF	g1769897	BLASTX	171	3e-11	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18480	GM_M34_B1_E08_MR	g130188	BLASTX	529	4e-49	86	PHYTOCHROME A gi 81937 pir S06856 phytochrome - garden pea gi 169132 (M37217) phytochrome [Pisum sativum] gi 295830 (X14077) phytochrome apoprotein [Pisum sativum] gi 226757 prf 1604466A phytochrome [Pisum sativum]
18481	GM_M34_B1_E09_MR	g3377848	BLASTX	169	2e-16	50	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
18482	GM_M34_B1_F05_MR	g1769897	BLASTX	292	7e-28	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18483	GM_M34_B1_F10_MF	g82231	BLASTX	165	1e-11	96	hypothetical protein 82 - common tobacco chloroplast gi 225200 prf 1211235AE ORF 82 [Nicotiana tabacum]
18484	GM_M34_B1_G07_MF	g3142328	BLASTN	1602	9e-66	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18485	GM_M34_B1_G09_MF	g18588	BLASTN	364	2e-09	74	Soybean gene 3 for chalcone synthetase protein
18486	GM_M34_B1_H04_MR	g18559	BLASTN	976	3e-37	77	G.max gene for catalase
18487	GM_M34_B1_H05_MF	g18559	BLASTN	666	4e-23	76	G.max gene for catalase
18488	GM_M34_B1_H06_MR	g2213582	BLASTX	161	1e-09	27	(AC000348) T7N9.2 [Arabidopsis thaliana]
18489	GM_M34_B1_H08_MR	g531389	BLASTX	246	1e-18	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18490	GM_M34_B1_H12_MR	g4063760	BLASTX	395	1e-34	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18491	GM_M34_B2_A12_MF	g1817728	BLASTN	612	1e-20	69	Cloning vector pBeloBAC11
18492	GM_M34_B2_B02_MF	g2579906	BLASTN	467	4e-15	70	Homo sapiens genomic DNA, 21q region, clone: Q6F8BG5
18493	GM_M34_B2_B03_MR	g2462058	BLASTX	214	9e-17	61	(Y13389) reverse transcriptase [Antirrhinum majus]
18494	GM_M34_B2_B09_MR	g3142328	BLASTN	938	2e-35	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18495	GM_M34_B2_B12_MR	g3097320	BLASTN	431	2e-12	70	Glycine max gene for Bd 30K, complete cds
18496	GM_M34_B2_C09_MR	g3924609	BLASTX	201	7e-14	56	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
18497	GM_M34_B2_D10_MR	g100484	BLASTX	195	1e-23	63	hypothetical protein - garden snapdragon
18498	GM_M34_B2_E11_MR	g3820757	BLASTN	382	2e-10	63	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
18499	GM_M34_B2_F08_MR	g1170031	BLASTX	671	3e-65	97	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) gi 541940 pir JQ2263 glutamate 1-semialdehyde aminotransferase (EC 2.6.1.-) precursor - soybean gi 310567 (L12453) glutamate 1-semialdehyde aminotransferase [Glycine max] gi 747968 (U20260) glutamate 1-semialdehyde aminotransferase [Glycine max]
18500	GM_M34_B2_F12_MR	g3142328	BLASTN	839	5e-31	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18501	GM_M34_B2_G05_MF	g3777526	BLASTN	487	5e-15	74	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
18502	GM_M34_B2_G07_MR	g4063756	BLASTN	454	2e-13	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18503	GM_M34_B2_G08_MR	g1732513	BLASTX	182	2e-13	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
18504	GM_M34_B2_G11_MR	g3513747	BLASTX	310	2e-25	51	(AF080118) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18505	GM_M35_A2_A05_MF	g507910	BLASTN	638	3e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18506	GM_M35_A2_A05_MR	g507910	BLASTN	551	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18507	GM_M35_A2_A07_MR	g342952	BLASTN	392	1e-11	63	paramecium species 1,168 mt dna dimer: replication init. region.
18508	GM_M35_A2_A11_MF	g4115365	BLASTX	129	2e-09	54	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18509	GM_M35_A2_A12_MF	g3600034	BLASTX	249	2e-20	52	(AF080119) No definition line found [Arabidopsis thaliana]
18510	GM_M35_A2_B03_MF	g1091678	BLASTX	135	1e-11	30	activator-like transposable element [Pennisetum glaucum]
18511	GM_M35_A2_B10_MF	g2129618	BLASTX	223	2e-16	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18512	GM_M35_A2_C01_MR	g4150930	BLASTN	375	7e-10	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18513	GM_M35_A2_C05_MF	g3687828	BLASTN	370	1e-09	64	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
18514	GM_M35_A2_C06_MR	g117519	BLASTX	138	2e-10	66	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) gi 99945 pir A39597 phytoene dehydrogenase (EC 1.3.-.-) - soybean gi 170044 (M64704) phytoene desaturase [Glycine max]
18515	GM_M35_A2_C09_MR	g3901012	BLASTX	238	2e-19	66	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
18516	GM_M35_A2_C10_MR	g3907448	BLASTN	401	5e-11	60	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
18517	GM_M35_A2_C12_MF	g4115365	BLASTX	293	1e-23	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18518	GM_M35_A2_D06_MR	g3645899	BLASTX	154	5e-11	34	(U68408) 5' end not determined experimentally [Zea mays]
18519	GM_M35_A2_D07_MF	g3599669	BLASTN	356	4e-09	64	Dictyostelium discoideum gene for TRFA, complete cds
18520	GM_M35_A2_D08_MF	g4038056	BLASTX	220	4e-26	51	(AC005897) putative transposon [Arabidopsis thaliana]
18521	GM_M35_A2_D09_MF	g1769898	BLASTX	366	2e-32	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18522	GM_M35_A2_D11_MF	g3097320	BLASTN	818	5e-30	78	Glycine max gene for Bd 30K, complete cds
18523	GM_M35_A2_E08_MR	g3142303	BLASTX	516	2e-47	77	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
18524	GM_M35_A2_F09_MF	g421955	BLASTX	155	1e-11	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
18525	GM_M35_A2_F09_MR	g2244749	BLASTX	248	8e-20	48	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
18526	GM_M35_A2_G01_MF	g4138581	BLASTX	168	1e-13	45	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]
18527	GM_M35_A2_G04_MF	g18559	BLASTN	651	2e-22	67	G.max gene for catalase
18528	GM_M35_A2_G09_MF	g507910	BLASTN	655	6e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18529	GM_M35_A2_G11_MF	g3777527	BLASTX	225	2e-16	64	(AF053008) gag-pol polyprotein [Glycine max]
18530	GM_M35_A2_G12_MF	g3645899	BLASTX	338	7e-33	58	(U68408) 5' end not determined experimentally [Zea mays]
18531	GM_M35_A2_H04_MR	g3193290	BLASTX	227	4e-17	49	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
18532	GM_M35_A2_H05_MF	g2642158	BLASTX	166	6e-11	41	(AC003000) hypothetical protein [Arabidopsis thaliana]
18533	GM_M35_A2_H06_MR	g4063760	BLASTX	277	5e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18534	GM_M35_A2_H07_MR	g2995405	BLASTX	474	2e-43	55	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18535	GM_M35_A2_H08_MF	g507910	BLASTN	382	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence
18536	GM_M35_B1_A05_MF	g441205	BLASTN	410	2e-11	73	Soybean lox1gm4 gene encoding lipxygenase L-4
18537	GM_M35_B1_A06_MF	g2462732	BLASTX	275	2e-22	67	(AC002292) Hypothetical Protein [Arabidopsis thaliana]
18538	GM_M35_B1_A07_MF	g2995405	BLASTX	220	3e-16	40	(Y12432) polyprotein [Ananas comosus]
18539	GM_M35_B1_B04_MR	g3142328	BLASTN	1040	4e-40	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18540	GM_M35_B1_B09_MF	g170605	BLASTN	488	2e-15	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
18541	GM_M35_B1_C02_MR	g3650039	BLASTX	271	7e-22	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
18542	GM_M35_B1_C10_MF	g3142328	BLASTN	804	2e-29	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18543	GM_M35_B1_C11_MR	g3273387	BLASTN	363	2e-09	67	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
18544	GM_M35_B1_D03_MF	g3097320	BLASTN	1092	2e-42	79	Glycine max gene for Bd 30K, complete cds
18545	GM_M35_B1_E02_MR	g114532	BLASTX	592	7e-59	91	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
18546	GM_M35_B1_F03_MR	g3645899	BLASTX	158	3e-21	40	(U68408) 5' end not determined experimentally [Zea mays]
18547	GM_M35_B1_F10_MR	g2443320	BLASTX	260	3e-20	48	(D85597) polyprotein [Oryza australiensis]
18548	GM_M35_B1_G03_MF	g209631	BLASTN	373	8e-10	66	Amsacta entomopoxvirus spheroidin gene, complete cds, and four vaccinia related orfs. >gi 1251578 gb I16670 I16670 Sequence 1 from patent US 5476781
18549	GM_M35_B1_G05_MR	g2264302	BLASTN	655	1e-22	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]
18550	GM_M35_B1_G08_MR	g3176777	BLASTN	425	3e-13	62	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence
18551	GM_M35_B2_A03_MF	g2764526	BLASTN	367	1e-09	59	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
18552	GM_M35_B2_A03_MR	g100484	BLASTX	202	2e-14	48	hypothetical protein - garden snapdragon
18553	GM_M35_B2_A04_MF	g3461846	BLASTX	266	8e-21	48	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
18554	GM_M35_B2_A07_MF	g531389	BLASTX	230	4e-22	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18555	GM_M35_B2_A10_MR	g4063760	BLASTX	209	7e-15	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18556	GM_M35_B2_B01_MF	g505129	BLASTN	371	8e-10	74	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18557	GM_M35_B2_B01_MR	g3510344	BLASTN	467	5e-14	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
18558	GM_M35_B2_B02_MR	g170606	BLASTN	726	3e-26	66	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
18559	GM_M35_B2_B03_MF	g1169198	BLASTX	144	5e-09	76	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR gi 479738 pir S35270 hypothetical protein - Arabidopsis thaliana gi 166926 (L11367) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]
18560	GM_M35_B2_C05_MR	g4056476	BLASTN	350	9e-09	66	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
18561	GM_M35_B2_D01_MF	g3142328	BLASTN	520	1e-16	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18562	GM_M35_B2_D02_MF	g4063760	BLASTX	418	4e-37	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18563	GM_M35_B2_D03_MR	g507910	BLASTN	341	8e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
18564	GM_M35_B2_D04_MR	g170080	BLASTN	455	1e-13	87	Soybean seed lectin gene transposable element tgm1.
18565	GM_M35_B2_D07_MF	g3645899	BLASTX	174	4e-11	56	(U68408) 5' end not determined experimentally [Zea mays]
18566	GM_M35_B2_D11_MF	g1769897	BLASTX	331	1e-28	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18567	GM_M35_B2_E01_MF	g4063760	BLASTX	590	2e-55	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18568	GM_M35_B2_E04_MF	g3176795	BLASTN	377	1e-10	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
18569	GM_M35_B2_F04_MF	g4115365	BLASTX	329	2e-27	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18570	GM_M35_B2_F07_MR	g2443320	BLASTX	136	2e-15	41	(D85597) polyprotein [Oryza australiensis]
18571	GM_M35_B2_F08_MR	g3142328	BLASTN	642	4e-22	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18572	GM_M35_B2_F09_MF	g2564750	BLASTN	384	3e-10	61	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
18573	GM_M35_B2_G06_MF	g100484	BLASTX	384	5e-34	54	hypothetical protein - garden snapdragon
18574	GM_M35_B2_G06_MR	g3603175	BLASTX	125	1e-09	50	(AF025374) TIRC7 [Homo sapiens]
18575	GM_M35_B2_G08_MF	g1707364	BLASTX	226	3e-17	83	(X94626) AATP2 [Arabidopsis thaliana]
18576	GM_M35_B2_H01_MR	g2522228	BLASTX	204	3e-15	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
18577	GM_M35_B2_H08_MF	g2462134	BLASTX	268	7e-22	36	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18578	GM_M35_B2_H09_MF	g507910	BLASTN	362	9e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18579	GM_M35_B2_H09_MR	g507910	BLASTN	379	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18580	GM_M36_A1_B01_MR	g4050011	BLASTN	460	9e-14	68	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
18581	GM_M36_A1_B03_MR	g2129618	BLASTX	180	7e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18582	GM_M36_A1_B07_MR	g3047068	BLASTX	190	5e-13	35	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
18583	GM_M36_A1_B10_MR	g4038056	BLASTX	279	2e-22	45	(AC005897) putative transposon [Arabidopsis thaliana]
18584	GM_M36_A1_C06_MR	g2213632	BLASTX	135	3e-13	40	(AC000103) F21J9.24 [Arabidopsis thaliana]
18585	GM_M36_A1_D01_MR	g18559	BLASTN	772	6e-28	72	G.max gene for catalase
18586	GM_M36_A1_D10_MR	g2765817	BLASTX	147	1e-08	54	(Z95352) AtMlo-h1 [Arabidopsis thaliana]
18587	GM_M36_A1_D11_MR	g2213632	BLASTX	170	1e-22	46	(AC000103) F21J9.24 [Arabidopsis thaliana]
18588	GM_M36_A1_F01_MR	g905361	BLASTX	109	3e-13	47	(U22103) gag-protease polyprotein [Glycine max]
18589	GM_M36_A1_F12_MR	g2522228	BLASTX	171	2e-21	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
18590	GM_M36_A1_G01_MR	g2586082	BLASTX	203	1e-28	67	(U72725) retrofit [Oryza longistaminata]
18591	GM_M36_A1_H07_MR	g507910	BLASTN	367	6e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18592	GM_M36_A1_H08_MR	g18559	BLASTN	848	2e-31	73	G.max gene for catalase
18593	GM_M36_A1_H12_MR	g905361	BLASTX	381	2e-42	79	(U22103) gag-protease polyprotein [Glycine max]
18594	GM_M36_B1_A01_MR	g3367520	BLASTX	219	1e-16	59	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb D12522 from A. thaliana. [Arabidopsis thaliana]
18595	GM_M36_B1_B03_MR	g507910	BLASTN	543	6e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18596	GM_M36_B1_B10_MR	g4063760	BLASTX	212	4e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18597	GM_M36_B1_C06_MR	g4063760	BLASTX	156	3e-09	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18598	GM_M36_B1_C07_MR	g1769898	BLASTX	182	3e-15	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18599	GM_M36_B1_C08_MR	g2462935	BLASTX	188	1e-12	40	(Y12321) open reading frame 1 [Brassica oleracea]
18600	GM_M36_B1_D06_MR	g3319362	BLASTX	174	3e-11	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18601	GM_M36_B1_D08_MR	g18559	BLASTN	857	8e-32	71	G.max gene for catalase
18602	GM_M36_B1_D09_MR	g3777527	BLASTX	218	1e-15	40	(AF053008) gag-pol polyprotein [Glycine max]
18603	GM_M36_B1_E07_MR	g3283026	BLASTX	220	2e-16	40	putative transposase [Arabidopsis thaliana]
18604	GM_M36_B1_E10_MR	g3695401	BLASTX	98	2e-10	39	(AF096373) No definition line found [Arabidopsis thaliana]
18605	GM_M36_B1_F01_MR	g3377834	BLASTX	153	4e-09	30	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18606	GM_M36_B1_F03_MR	g13774	BLASTN	428	1e-12	61	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
18607	GM_M36_B1_F04_MR	g2281647	BLASTX	214	8e-17	47	(AF003104) AP2 domain containing protein RAP2.11 [Arabidopsis thaliana]
18608	GM_M36_B1_F08_MR	g2281647	BLASTX	203	1e-15	50	(AF003104) AP2 domain containing protein RAP2.11 [Arabidopsis thaliana]
18609	GM_M36_B1_F09_MR	g3695395	BLASTX	197	8e-16	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
18610	GM_M36_B1_G11_MR	g629693	BLASTX	209	8e-16	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18611	GM_M36_B2_A01_MF	g905360	BLASTN	458	8e-14	65	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
18612	GM_M36_B2_A04_MR	g4063760	BLASTX	412	2e-36	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18613	GM_M36_B2_B06_MR	g507910	BLASTN	475	7e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18614	GM_M36_B2_C01_MR	g3097320	BLASTN	1073	1e-41	85	Glycine max gene for Bd 30K, complete cds
18615	GM_M36_B2_C03_MR	g2351065	BLASTN	410	2e-11	86	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15
18616	GM_M36_B2_D02_MR	g3142328	BLASTN	701	9e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18617	GM_M36_B2_D07_MR	g3142328	BLASTN	561	2e-18	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18618	GM_M36_B2_E01_MR	g3097320	BLASTN	440	7e-13	71	Glycine max gene for Bd 30K, complete cds
18619	GM_M37_A1_B03_MF	g4063756	BLASTN	443	6e-13	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18620	GM_M37_A1_B06_MF	g1769897	BLASTX	178	5e-12	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18621	GM_M37_A1_B12_MF	g100484	BLASTX	161	5e-10	37	hypothetical protein - garden snapdragon
18622	GM_M37_A1_C01_MR	g4038055	BLASTX	249	2e-35	61	(AC005897) putative cytochrome P450 [Arabidopsis thaliana]
18623	GM_M37_A1_C03_MF	g3201680	BLASTX	203	2e-15	60	(AF060941) extra-large G-protein [Arabidopsis thaliana]
18624	GM_M37_A1_C03_MR	g18559	BLASTN	991	6e-38	76	G.max gene for catalase
18625	GM_M37_A1_C04_MF	g3599418	BLASTN	1031	9e-40	75	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
18626	GM_M37_A1_C11_MR	g2429543	BLASTX	136	3e-10	35	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18627	GM_M37_A1_C12_MF	g4063760	BLASTX	445	5e-40	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18628	GM_M37_A1_D01_MF	g629693	BLASTX	131	5e-11	34	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18629	GM_M37_A1_D04_MF	g1621467	BLASTX	448	1e-41	80	(U73106) laccase [Liriodendron tulipifera]
18630	GM_M37_A1_D04_MR	g3193320	BLASTX	217	5e-16	52	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]
18631	GM_M37_A1_D07_MF	g3650035	BLASTX	267	5e-21	47	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
18632	GM_M37_A1_D11_MR	g2995405	BLASTX	276	3e-22	43	(Y12432) polyprotein [Ananas comosus]
18633	GM_M37_A1_D12_MR	g18559	BLASTN	867	3e-32	74	G.max gene for catalase
18634	GM_M37_A1_F01_MR	g629693	BLASTX	243	1e-19	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18635	GM_M37_A1_F06_MF	g4063735	BLASTN	399	6e-11	66	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]
18636	GM_M37_A1_F07_MF	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18637	GM_M37_A1_G01_MF	g2522228	BLASTX	321	1e-40	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
18638	GM_M37_A1_G01_MR	g3560029	BLASTN	474	1e-14	66	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
18639	GM_M37_A1_G10_MF	g122105	BLASTX	169	5e-12	53	HISTONE H4 gi 81288 pir S00939 histone H4 - Volvox carteri gi 21984 (X06963) put. histone H4 [Volvox carteri] gi 21987 (X06964) put. histone H4 [Volvox carteri]
18640	GM_M37_A1_G11_MR	g3777527	BLASTX	634	3e-62	95	(AF053008) gag-pol polyprotein [Glycine max]
18641	GM_M37_A1_G12_MR	g2129618	BLASTX	165	1e-11	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18642	GM_M37_A1_H01_MR	g3461813	BLASTX	220	2e-30	81	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]
18643	GM_M37_A1_H05_MF	g905361	BLASTX	176	1e-11	34	(U22103) gag-protease polyprotein [Glycine max]
18644	GM_M37_A1_H06_MF	g1666236	BLASTX	157	3e-10	29	(U76261) unknown [Hordeum vulgare]
18645	GM_M37_A1_H07_MF	g2924729	BLASTN	654	2e-22	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
18646	GM_M37_A1_H10_MF	g3777527	BLASTX	175	5e-11	35	(AF053008) gag-pol polyprotein [Glycine max]
18647	GM_M37_A1_H11_MR	g3834315	BLASTX	238	1e-18	46	(AC005679) F9K20.15 [Arabidopsis thaliana]
18648	GM_M37_A1_H12_MF	g4115365	BLASTX	218	2e-19	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18649	GM_M37_B1_A02_MR	g3142328	BLASTN	728	5e-26	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18650	GM_M37_B1_A03_MR	g3885341	BLASTX	427	2e-38	53	(AC005623) unknown protein [Arabidopsis thaliana]
18651	GM_M37_B1_A08_MF	g3142328	BLASTN	764	1e-27	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18652	GM_M37_B1_A08_MR	g18559	BLASTN	901	8e-34	73	G.max gene for catalase
18653	GM_M37_B1_A10_MR	g3097320	BLASTN	407	2e-11	77	Glycine max gene for Bd 30K, complete cds
18654	GM_M37_B1_A11_MR	g3142328	BLASTN	427	3e-12	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18655	GM_M37_B1_B03_MF	g3142328	BLASTN	630	1e-21	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18656	GM_M37_B1_B03_MR	g3645899	BLASTX	263	2e-32	50	(U68408) 5' end not determined experimentally [Zea mays]
18657	GM_M37_B1_B05_MF	g1769898	BLASTX	144	2e-11	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18658	GM_M37_B1_B07_MF	g1666236	BLASTX	144	9e-09	31	(U76261) unknown [Hordeum vulgare]
18659	GM_M37_B1_B10_MR	g3097320	BLASTN	460	8e-14	66	Glycine max gene for Bd 30K, complete cds
18660	GM_M37_B1_C01_MR	g4006838	BLASTN	432	2e-12	64	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
18661	GM_M37_B1_C04_MR	g3426334	BLASTN	520	2e-16	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18662	GM_M37_B1_C05_MF	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18663	GM_M37_B1_C05_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18664	GM_M37_B1_C06_MR	g3810596	BLASTX	296	3e-24	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18665	GM_M37_B1_C10_MF	g508826	BLASTN	350	8e-09	60	Drosophila melanogaster Oregon-R mitochondrial A+T region.
18666	GM_M37_B1_D03_MF	g3645899	BLASTX	344	3e-29	52	(U68408) 5' end not determined experimentally [Zea mays]
18667	GM_M37_B1_D05_MR	g3171875	BLASTN	438	9e-13	67	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
18668	GM_M37_B1_D07_MR	g2522227	BLASTX	112	4e-09	36	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18669	GM_M37_B1_D09_MR	g4063760	BLASTX	161	1e-18	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18670	GM_M37_B1_E01_MF	g3822223	BLASTX	175	1e-16	57	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
18671	GM_M37_B1_E02_MR	g3785992	BLASTN	380	4e-10	64	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18672	GM_M37_B1_E03_MR	g905361	BLASTX	238	2e-18	35	(U22103) gag-protease polyprotein [Glycine max]
18673	GM_M37_B1_E07_MF	g3845197	BLASTN	405	3e-11	64	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18674	GM_M37_B1_E07_MR	g2764525	BLASTN	467	3e-14	64	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
18675	GM_M37_B1_E08_MR	g3142328	BLASTN	858	7e-32	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18676	GM_M37_B1_E09_MR	g3406033	BLASTN	350	9e-09	58	Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
18677	GM_M37_B1_F01_MF	g3777527	BLASTX	612	1e-57	93	(AF053008) gag-pol polyprotein [Glycine max]
18678	GM_M37_B1_F02_MF	g3377856	BLASTX	305	4e-25	49	(AF076274) contains similarity to reverse tranciptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
18679	GM_M37_B1_F02_MR	g2522227	BLASTX	193	1e-14	48	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18680	GM_M37_B1_F03_MF	g2129618	BLASTX	230	3e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18681	GM_M37_B1_F07_MR	g4150930	BLASTN	400	5e-11	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
18682	GM_M37_B1_F08_MF	g100226	BLASTX	336	5e-29	47	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]
18683	GM_M37_B1_F09_MR	g3097836	BLASTN	471	3e-14	66	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
18684	GM_M37_B1_F10_MF	g3860246	BLASTX	147	4e-09	30	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
18685	GM_M37_B1_F12_MR	g1076581	BLASTX	164	9e-13	40	cf-9 protein precursor - tomato gi 563233 (U15936) Cf-9 precursor [Lycopersicon pimpinellifolium] gi 2792186 gnl PID e1240191 (AJ002236) Cf-9 [Lycopersicon pimpinellifolium]
18686	GM_M37_B1_G08_MR	g3810596	BLASTX	269	2e-21	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18687	GM_M37_B1_H01_MF	g3810595	BLASTX	272	2e-21	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
18688	GM_M37_B1_H05_MR	g2522230	BLASTX	290	7e-25	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18689	GM_M37_B1_H08_MR	g2194136	BLASTX	256	8e-20	45	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
18690	GM_M37_B2_A04_MR	g3319362	BLASTX	158	2e-16	39	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18691	GM_M37_B2_A07_MF	g3810596	BLASTX	200	5e-14	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18692	GM_M37_B2_A08_MR	g3777527	BLASTX	352	6e-30	76	(AF053008) gag-pol polyprotein [Glycine max]
18693	GM_M37_B2_A11_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18694	GM_M37_B2_A11_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18695	GM_M37_B2_B10_MF	g507910	BLASTN	412	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18696	GM_M37_B2_B10_MR	g507910	BLASTN	454	7e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18697	GM_M37_B2_C01_MF	g22102	BLASTN	572	7e-19	62	Zea mays A1 gene for 40.1kd A1 protein (NADPH-dependent reductase).
18698	GM_M37_B2_C01_MR	g3894211	BLASTN	411	2e-11	66	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
18699	GM_M37_B2_C03_MF	g320565	BLASTX	114	1e-09	59	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
18700	GM_M37_B2_C04_MF	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18701	GM_M37_B2_C10_MF	g2104945	BLASTN	386	2e-10	61	Glycine max copia-like retrotransposon Tgmr, complete sequence
18702	GM_M37_B2_C11_MF	g3985952	BLASTN	896	2e-33	73	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]
18703	GM_M37_B2_D05_MF	g3777527	BLASTX	309	3e-25	43	(AF053008) gag-pol polyprotein [Glycine max]
18704	GM_M37_B2_D05_MR	g1769898	BLASTX	289	6e-24	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18705	GM_M37_B2_D09_MF	g505129	BLASTN	360	3e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18706	GM_M37_B2_D09_MR	g3273387	BLASTN	417	8e-12	64	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
18707	GM_M37_B2_E04_MR	g1370171	BLASTN	572	1e-19	75	L.japonicus mRNA for small GTP-binding protein, RAB1X.
18708	GM_M37_B2_F01_MF	g3294467	BLASTX	159	3e-23	89	(U89341) phosphoglucomutase 1 [Zea mays]
18709	GM_M37_B2_F06_MF	g4063760	BLASTX	108	8e-09	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18710	GM_M37_B2_F10_MF	g13774	BLASTN	387	9e-11	68	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
18711	GM_M37_B2_F11_MR	g3142328	BLASTN	2117	2e-89	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18712	GM_M37_B2_G01_MF	g3142379	BLASTX	220	7e-17	57	(AF053008) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18713	GM_M37_B2_G03_MF	g1843447	BLASTN	420	6e-12	63	Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927
18714	GM_M37_B2_G04_MR	g2522228	BLASTX	233	2e-18	42	(AB007466) reverse transcriptase-like protein [Vicia faba]
18715	GM_M37_B2_G06_MF	g18559	BLASTN	782	2e-28	75	G.max gene for catalase
18716	GM_M37_B2_G09_MF	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
18717	GM_M37_B2_H01_MR	g3510505	BLASTX	251	3e-19	39	(AF030881) pol polyprotein [Fugu rubripes]
18718	GM_M37_B2_H02_MF	g531389	BLASTX	256	6e-24	48	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18719	GM_M37_B2_H05_MF	g2505874	BLASTX	284	8e-24	42	(Y12776) putative kinase [Arabidopsis thaliana]
18720	GM_M37_B2_H05_MR	g20749	BLASTN	512	5e-17	73	Pea PSU2 gene for U2 snRNA
18721	GM_M37_B2_H06_MR	g1769898	BLASTX	149	8e-09	31	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18722	GM_M37_B2_H09_MR	g170080	BLASTN	398	5e-11	68	Soybean seed lectin gene transposable element tgm1.
18723	GM_M37_B2_H11_MR	g2264308	BLASTN	321	5e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK22, complete sequence.
18724	GM_M38_A2_A02_MR	g18559	BLASTN	691	3e-24	70	G.max gene for catalase
18725	GM_M38_A2_A08_MR	g4063760	BLASTX	497	1e-45	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18726	GM_M38_A2_B03_MF	g3004545	BLASTX	308	3e-25	43	(AC003673) putative reverse transcriptase [Arabidopsis thaliana]
18727	GM_M38_A2_B05_MR	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18728	GM_M38_A2_B06_MR	g3097320	BLASTN	378	4e-10	65	Glycine max gene for Bd 30K, complete cds
18729	GM_M38_A2_B10_MF	g507910	BLASTN	573	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18730	GM_M38_A2_B10_MR	g4038056	BLASTX	398	3e-35	53	(AC005897) putative transposon [Arabidopsis thaliana]
18731	GM_M38_A2_B11_MR	g507910	BLASTN	453	7e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18732	GM_M38_A2_B12_MR	g18588	BLASTN	370	1e-09	73	Soybean gene 3 for chalcone synthetase protein
18733	GM_M38_A2_C01_MF	g3142328	BLASTN	1170	4e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18734	GM_M38_A2_C01_MR	g3510505	BLASTX	239	5e-18	41	(AF030881) pol polyprotein [Fugu rubripes]
18735	GM_M38_A2_C04_MF	g3135282	BLASTN	388	2e-10	60	Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence [Homo sapiens]
18736	GM_M38_A2_C04_MR	g3097320	BLASTN	450	2e-13	73	Glycine max gene for Bd 30K, complete cds
18737	GM_M38_A2_C05_MF	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18738	GM_M38_A2_C08_MF	g3810596	BLASTX	264	8e-21	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18739	GM_M38_A2_C10_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18740	GM_M38_A2_C10_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18741	GM_M38_A2_C11_MF	g4063760	BLASTX	216	1e-15	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18742	GM_M38_A2_D01_MF	g3021268	BLASTX	135	4e-13	69	(AL022347) putative protein [Arabidopsis thaliana]
18743	GM_M38_A2_D02_MR	g99729	BLASTX	162	1e-19	48	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
18744	GM_M38_A2_D04_MF	g1480927	BLASTN	1129	8e-45	93	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
18745	GM_M38_A2_D04_MR	g18559	BLASTN	729	5e-26	68	G.max gene for catalase
18746	GM_M38_A2_D06_MR	g3819164	BLASTX	237	2e-18	62	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]
18747	GM_M38_A2_D07_MF	g99922	BLASTX	565	6e-54	84	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18748	GM_M38_A2_D07_MR	g100484	BLASTX	340	3e-29	48	hypothetical protein - garden snapdragon
18749	GM_M38_A2_D08_MR	g3097320	BLASTN	748	8e-27	81	Glycine max gene for Bd 30K, complete cds
18750	GM_M38_A2_D11_MF	g3935167	BLASTX	171	3e-12	57	(AC004557) F17L21.10 [Arabidopsis thaliana]
18751	GM_M38_A2_D12_MF	g507910	BLASTN	592	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18752	GM_M38_A2_D12_MR	g18559	BLASTN	943	1e-35	74	G.max gene for catalase
18753	GM_M38_A2_E02_MR	g2194126	BLASTX	201	2e-17	52	(AC002062) EST gb T43335 comes from this gene. [Arabidopsis thaliana]
18754	GM_M38_A2_E04_MF	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18755	GM_M38_A2_E04_MR	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18756	GM_M38_A2_E06_MF	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18757	GM_M38_A2_G01_MR	g507910	BLASTN	488	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18758	GM_M38_A2_G04_MR	g2811096	BLASTN	360	3e-09	62	Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence [Homo sapiens]
18759	GM_M38_A2_G10_MF	g3097320	BLASTN	532	5e-17	67	Glycine max gene for Bd 30K, complete cds
18760	GM_M38_A2_G11_MF	g2244802	BLASTX	185	4e-15	33	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
18761	GM_M38_A2_G11_MR	g3779030	BLASTX	174	1e-12	29	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
18762	GM_M38_A2_G12_MR	g905361	BLASTX	621	6e-60	83	(U22103) gag-protease polyprotein [Glycine max]
18763	GM_M38_A2_H01_MR	g1350625	BLASTX	253	6e-21	80	CHLOROPLAST 50S RIBOSOMAL PROTEIN L1 PRECURSOR gi 577089 (X82776) chloroplast ribosomal protein L1 [Pisum sativum]
18764	GM_M38_A2_H04_MR	g4063760	BLASTX	283	9e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18765	GM_M38_A2_H06_MR	g4063756	BLASTN	449	3e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18766	GM_M38_A2_H10_MF	g4063760	BLASTX	482	5e-44	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18767	GM_M38_B1_A01_MF	g2586082	BLASTX	205	2e-14	40	(U72725) retrofit [Oryza longistaminata]
18768	GM_M38_B1_A04_MR	g2160179	BLASTX	154	1e-09	55	(AC000132) No definition line found [Arabidopsis thaliana]
18769	GM_M38_B1_A07_MF	g1769899	BLASTX	153	4e-20	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18770	GM_M38_B1_A08_MF	g3097320	BLASTN	410	2e-11	72	Glycine max gene for Bd 30K, complete cds
18771	GM_M38_B1_A09_MF	g3097320	BLASTN	1015	6e-39	81	Glycine max gene for Bd 30K, complete cds
18772	GM_M38_B1_A12_MR	g2245104	BLASTX	212	5e-15	37	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
18773	GM_M38_B1_B07_MR	g3097320	BLASTN	435	1e-12	72	Glycine max gene for Bd 30K, complete cds
18774	GM_M38_B1_B12_MF	g4063770	BLASTX	207	7e-15	40	(AB004906) transposase [Ipomoea purpurea]
18775	GM_M38_B1_C04_MR	g2833389	BLASTX	220	6e-16	86	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III) gi 1200154 gnl PID e223347 (X95759) glycogen (starch) synthase [Solanum tuberosum]
18776	GM_M38_B1_C05_MF	g2832657	BLASTX	330	1e-30	60	(AL021710) putative protein [Arabidopsis thaliana]
18777	GM_M38_B1_C05_MR	g342965	BLASTN	408	5e-12	63	paramecium species 7,227 mt dna dimer: replication init. region.
18778	GM_M38_B1_C06_MF	g3250687	BLASTX	188	7e-14	46	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
18779	GM_M38_B1_C06_MR	g13773	BLASTN	365	5e-10	65	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
18780	GM_M38_B1_C10_MR	g507910	BLASTN	593	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18781	GM_M38_B1_D02_MR	g1580757	BLASTN	416	9e-13	67	C.arietinum urate oxidase gene (partial).
18782	GM_M38_B1_D04_MR	g905361	BLASTX	255	3e-20	36	(U22103) gag-protease polyprotein [Glycine max]
18783	GM_M38_B1_D08_MR	g2660669	BLASTX	332	2e-27	67	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]
18784	GM_M38_B1_D12_MR	g905361	BLASTX	229	2e-17	35	(U22103) gag-protease polyprotein [Glycine max]
18785	GM_M38_B1_E09_MF	g2995405	BLASTX	154	6e-19	46	(Y12432) polyprotein [Ananas comosus]
18786	GM_M38_B1_E10_MR	g158813	BLASTN	375	2e-10	64	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
18787	GM_M38_B1_F01_MF	g905361	BLASTX	660	5e-64	96	(U22103) gag-protease polyprotein [Glycine max]
18788	GM_M38_B1_F02_MR	g507910	BLASTN	637	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
18789	GM_M38_B1_F05_MF	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18790	GM_M38_B1_F05_MR	g507910	BLASTN	580	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18791	GM_M38_B1_F07_MF	g2995405	BLASTX	202	1e-22	43	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
18792	GM_M38_B1_F09_MF	g2801423	BLASTN	398	6e-11	63	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
18793	GM_M38_B1_F12_MF	g905361	BLASTX	219	3e-16	40	(U22103) gag-protease polyprotein [Glycine max]
18794	GM_M38_B1_F12_MR	g507910	BLASTN	363	8e-10	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18795	GM_M38_B1_G01_MR	g2129559	BLASTX	190	1e-18	53	cellulase homolog OR16pep - Arabidopsis thaliana gi 1022807 (U37702) cellulase [Arabidopsis thaliana] gi 3493633 (AF074092) cellulase [Arabidopsis thaliana] gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
18796	GM_M38_B1_G04_MF	g12628	BLASTN	416	5e-12	62	Aedes albopictus mit-gene for large ribosomal subunit RNA (LSU)
18797	GM_M38_B1_G04_MR	g2342681	BLASTX	251	2e-19	56	(AC000106) F7G19.9 [Arabidopsis thaliana]
18798	GM_M38_B1_G06_MF	g3176689	BLASTX	170	2e-10	44	(AC003671) Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]
18799	GM_M38_B1_G07_MR	g4150933	BLASTN	395	8e-11	64	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
18800	GM_M38_B1_G08_MF	g1142702	BLASTN	351	2e-09	74	Glycine max satellite STR120-A.4.
18801	GM_M38_B1_H03_MF	g507910	BLASTN	553	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18802	GM_M38_B1_H10_MF	g99729	BLASTX	179	4e-13	41	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
18803	GM_M38_B1_H12_MR	g226407	BLASTX	217	1e-15	39	retrotransposon del1-46 [Lilium henryi]
18804	GM_M39_A2_A02_MR	g2655314	BLASTN	309	3e-11	65	Bactrocera xanthodes strain Vanuatu mitochondrial D-loop region, complete sequence
18805	GM_M39_A2_A03_MF	g3097320	BLASTN	515	3e-16	73	Glycine max gene for Bd 30K, complete cds
18806	GM_M39_A2_A12_MR	g2924257	BLASTN	423	4e-12	66	Tobacco chloroplast genome DNA
18807	GM_M39_A2_B04_MF	g507910	BLASTN	358	1e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18808	GM_M39_A2_B09_MR	g2997694	BLASTX	299	8e-26	41	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
18809	GM_M39_A2_B10_MF	g905361	BLASTX	208	4e-15	33	(U22103) gag-protease polyprotein [Glycine max]
18810	GM_M39_A2_B10_MR	g2522228	BLASTX	216	2e-16	35	(AB007466) reverse transcriptase-like protein [Vicia faba]
18811	GM_M39_A2_B11_MR	g3513301	BLASTN	365	2e-09	64	Homo sapiens chromosome 19, cosmid R26894, complete sequence [Homo sapiens]
18812	GM_M39_A2_C04_MR	g2911393	BLASTX	190	3e-14	85	(AF045927) cell division cycle protein 48 [Hordeum vulgare]
18813	GM_M39_A2_C06_MF	g2522228	BLASTX	172	2e-23	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
18814	GM_M39_A2_C06_MR	g3056582	BLASTX	108	5e-12	45	(AC004255) T1F9.3 [Arabidopsis thaliana]
18815	GM_M39_A2_C10_MR	g905361	BLASTX	222	1e-16	39	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18816	GM_M39_A2_D02_MR	g3269291	BLASTX	165	1e-21	82	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
18817	GM_M39_A2_D04_MF	g2462936	BLASTX	326	1e-28	48	(Y12321) open reading frame 2 [Brassica oleracea]
18818	GM_M39_A2_D05_MR	g531389	BLASTX	149	6e-18	34	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18819	GM_M39_A2_D10_MR	g4063770	BLASTX	155	3e-11	34	(AB004906) transposase [Ipomoea purpurea]
18820	GM_M39_A2_D12_MR	g3036785	BLASTN	363	2e-09	61	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/l,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island
18821	GM_M39_A2_E12_MR	g18559	BLASTN	376	5e-10	73	G.max gene for catalase
18822	GM_M39_A2_F01_MF	g3142328	BLASTN	1008	1e-38	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18823	GM_M39_A2_F01_MR	g3142330	BLASTX	733	9e-72	92	(U96295) envelope-like [Glycine max]
18824	GM_M39_A2_F02_MR	g3805853	BLASTX	561	2e-53	68	(AL031986) putative protein [Arabidopsis thaliana]
18825	GM_M39_A2_F10_MR	g3859610	BLASTN	726	9e-26	67	Arabidopsis thaliana BAC T9E19
18826	GM_M39_A2_F12_MF	g2462745	BLASTX	293	3e-24	44	(AC002292) Hypothetical protein [Arabidopsis thaliana]
18827	GM_M39_A2_G05_MR	g3777527	BLASTX	173	7e-11	32	(AF053008) gag-pol polyprotein [Glycine max]
18828	GM_M39_A2_G08_MR	g3777527	BLASTX	201	1e-29	67	(AF053008) gag-pol polyprotein [Glycine max]
18829	GM_M39_A2_G09_MR	g2760839	BLASTX	316	9e-27	52	(AC003105) putative receptor kinase [Arabidopsis thaliana]
18830	GM_M39_A2_G12_MR	g99922	BLASTX	375	2e-55	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18831	GM_M39_A2_H02_MR	g2764526	BLASTN	379	4e-10	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
18832	GM_M39_A2_H03_MF	g4063760	BLASTX	222	3e-16	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18833	GM_M39_A2_H04_MF	g4063760	BLASTX	229	6e-17	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18834	GM_M39_A2_H07_MR	g2160185	BLASTX	420	6e-38	51	(AC000132) Similar to S. pombe ISP4 (gb D83992). [Arabidopsis thaliana]
18835	GM_M39_A2_H08_MF	g3645899	BLASTX	274	4e-25	59	(U68408) 5' end not determined experimentally [Zea mays]
18836	GM_M39_A2_H10_MR	g2842490	BLASTX	225	7e-18	72	(AL021749) heat-shock protein [Arabidopsis thaliana]
18837	GM_M39_B2_A01_MF	g1769899	BLASTX	282	5e-24	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18838	GM_M39_B2_A03_MR	g505129	BLASTN	351	7e-09	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18839	GM_M39_B2_A05_MR	g3789709	BLASTN	359	3e-09	61	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
18840	GM_M39_B2_A11_MF	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18841	GM_M39_B2_A12_MF	g3056590	BLASTX	253	9e-20	69	(AC004255) T1F9.11 [Arabidopsis thaliana]
18842	GM_M39_B2_A12_MR	g4038056	BLASTX	214	5e-30	54	(AC005897) putative transposon [Arabidopsis thaliana]
18843	GM_M39_B2_B01_MF	g3859610	BLASTN	488	5e-15	63	Arabidopsis thaliana BAC T9E19
18844	GM_M39_B2_B02_MF	g2073447	BLASTN	358	4e-09	71	L.japonicus gln1, pge1 & krm genes
18845	GM_M39_B2_B04_MR	g3746069	BLASTX	277	5e-22	44	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
18846	GM_M39_B2_B05_MR	g130398	BLASTX	218	7e-16	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
18847	GM_M39_B2_B06_MF	g3097320	BLASTN	455	1e-13	69	Glycine max gene for Bd 30K, complete cds
18848	GM_M39_B2_B08_MR	g3047073	BLASTX	176	9e-12	37	(AF058825) contains similarity to retrotransposon-like proteins [Arabidopsis thaliana]
18849	GM_M39_B2_B10_MR	g3097320	BLASTN	760	2e-27	76	Glycine max gene for Bd 30K, complete cds
18850	GM_M39_B2_C05_MR	g1841475	BLASTX	153	3e-10	56	(Y11105) Myb26 [Pisum sativum]
18851	GM_M39_B2_C10_MF	g169934	BLASTN	1514	4e-62	99	G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds.
18852	GM_M39_B2_C12_MR	g1769897	BLASTX	335	2e-32	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18853	GM_M39_B2_D05_MR	g3319362	BLASTX	193	4e-21	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18854	GM_M39_B2_D07_MR	g2462058	BLASTX	102	9e-13	37	(Y13389) reverse transcriptase [Antirrhinum majus]
18855	GM_M39_B2_D11_MF	g4063760	BLASTX	251	2e-19	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18856	GM_M39_B2_E03_MF	g131289	BLASTX	573	4e-60	89	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum]
18857	GM_M39_B2_E05_MR	g18559	BLASTN	829	1e-30	81	G.max gene for catalase
18858	GM_M39_B2_E11_MF	g130582	BLASTX	303	9e-25	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18859	GM_M39_B2_F02_MR	g3283026	BLASTX	180	5e-14	30	putative transposase [Arabidopsis thaliana]
18860	GM_M39_B2_F05_MF	g507910	BLASTN	594	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18861	GM_M39_B2_F07_MR	g3777527	BLASTX	746	6e-72	97	(AF053008) gag-pol polyprotein [Glycine max]
18862	GM_M39_B2_F08_MR	g1167523	BLASTX	187	5e-24	52	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18863	GM_M39_B2_F12_MR	g3738114	BLASTN	360	3e-09	62	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]
18864	GM_M39_B2_G03_MF	g99755	BLASTX	209	5e-26	45	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
18865	GM_M39_B2_G06_MF	g2564750	BLASTN	498	2e-15	66	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
18866	GM_M39_B2_G07_MF	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18867	GM_M39_B2_G07_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18868	GM_M39_B2_G10_MF	g479805	BLASTX	120	6e-12	46	SNF2 protein homolog - human (fragment) gi 292498 (M89907) transcription activator [Homo sapiens]
18869	GM_M39_B2_H02_MR	g3377855	BLASTX	355	9e-32	49	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
18870	GM_M39_B2_H03_MR	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18871	GM_M39_B2_H08_MR	g3402690	BLASTX	235	9e-19	33	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]
18872	GM_M40_A1_A04_MF	g507910	BLASTN	507	3e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18873	GM_M40_A1_A05_MR	g13619	BLASTN	378	5e-11	64	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
18874	GM_M40_A1_B01_MF	g507910	BLASTN	363	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18875	GM_M40_A1_B04_MF	g4150930	BLASTN	407	2e-11	62	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
18876	GM_M40_A1_B07_MF	g99922	BLASTX	469	9e-54	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18877	GM_M40_A1_C12_MR	g3142328	BLASTN	995	4e-38	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18878	GM_M40_A1_D01_MF	g2462058	BLASTX	230	2e-18	57	(Y13389) reverse transcriptase [Antirrhinum majus]
18879	GM_M40_A1_D07_MR	g3097320	BLASTN	625	3e-21	74	Glycine max gene for Bd 30K, complete cds
18880	GM_M40_A1_D12_MR	g2213608	BLASTX	250	3e-19	42	(AC000103) F21J9.2 [Arabidopsis thaliana]
18881	GM_M40_A1_E04_MF	g18559	BLASTN	596	3e-22	69	G.max gene for catalase
18882	GM_M40_A1_E05_MR	g3777527	BLASTX	175	9e-31	92	(AF053008) gag-pol polyprotein [Glycine max]
18883	GM_M40_A1_F01_MR	g2443320	BLASTX	121	1e-09	58	(D85597) polyprotein [Oryza australiensis]
18884	GM_M40_A1_F12_MF	g3287269	BLASTN	390	1e-10	66	S.tuberosum mRNA for protein involved in starch metabolism

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18885	GM_M40_A1_G10_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18886	GM_M40_A1_H06_MF	g100484	BLASTX	381	1e-33	57	hypothetical protein - garden snapdragon
18887	GM_M40_A1_H07_MF	g4063760	BLASTX	286	3e-35	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18888	GM_M40_A1_H08_MR	g3142328	BLASTN	1422	1e-57	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18889	GM_M40_A1_H12_MR	g3097320	BLASTN	903	7e-34	77	Glycine max gene for Bd 30K, complete cds
18890	GM_M40_A2_A07_MF	g130582	BLASTX	202	5e-14	67	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18891	GM_M40_A2_A09_MF	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
18892	GM_M40_A2_A10_MF	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18893	GM_M40_A2_B01_MR	g3845213	BLASTN	355	5e-09	63	Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence
18894	GM_M40_A2_B02_MR	g3176771	BLASTN	405	3e-12	65	Homo sapiens allele 2 fragile site locus (FRA10B) minisatellite, 3' sequence
18895	GM_M40_A2_B03_MR	g3097320	BLASTN	394	8e-11	71	Glycine max gene for Bd 30K, complete cds
18896	GM_M40_A2_B10_MR	g3142328	BLASTN	1721	3e-71	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18897	GM_M40_A2_C01_MR	g3777527	BLASTX	693	3e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
18898	GM_M40_A2_D02_MF	g1431738	BLASTN	744	7e-27	88	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
18899	GM_M40_A2_D10_MF	g507910	BLASTN	624	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18900	GM_M40_A2_F07_MF	g295355	BLASTX	174	4e-12	48	(L13653) peroxidase [Lycopersicon esculentum]
18901	GM_M40_A2_G09_MR	g3142328	BLASTN	807	1e-29	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18902	GM_M40_A2_H01_MF	g4063760	BLASTX	254	1e-19	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18903	GM_M40_A2_H07_MF	g4063756	BLASTN	412	1e-11	74	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18904	GM_M40_B1_A07_MF	g3777527	BLASTX	209	1e-14	79	(AF053008) gag-pol polyprotein [Glycine max]
18905	GM_M40_B1_A08_MF	g4063760	BLASTX	315	4e-26	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18906	GM_M40_B1_A10_MR	g1167523	BLASTX	228	9e-17	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18907	GM_M40_B1_A12_MF	g3142379	BLASTX	382	1e-34	86	(AF053008) envelope-like [Glycine max]
18908	GM_M40_B1_B09_MF	g3097320	BLASTN	1083	5e-42	81	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18909	GM_M40_B1_B12_MR	g4140712	BLASTX	145	2e-09	40	(AF110183) putative integrase [Oryza sativa]
18910	GM_M40_B1_C02_MF	g2462935	BLASTX	126	3e-13	38	(Y12321) open reading frame 1 [Brassica oleracea]
18911	GM_M40_B1_C08_MF	g507910	BLASTN	445	2e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18912	GM_M40_B1_C09_MR	g2982452	BLASTX	353	3e-30	60	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
18913	GM_M40_B1_C12_MR	g3777527	BLASTX	230	6e-17	86	(AF053008) gag-pol polyprotein [Glycine max]
18914	GM_M40_B1_D06_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18915	GM_M40_B1_D11_MF	g2815075	BLASTN	391	1e-10	61	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
18916	GM_M40_B1_D12_MR	g3421038	BLASTN	405	3e-11	63	Human DNA sequence from clone 35C21 on chromosome 1q23-24. Contains STSs, complete sequence [Homo sapiens]
18917	GM_M40_B1_E04_MR	g507910	BLASTN	633	5e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18918	GM_M40_B1_E05_MR	g3033389	BLASTX	173	4e-11	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
18919	GM_M40_B1_E07_MR	g3097320	BLASTN	467	4e-14	70	Glycine max gene for Bd 30K, complete cds
18920	GM_M40_B1_E09_MR	g3142328	BLASTN	1100	7e-43	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18921	GM_M40_B1_E11_MF	g4006849	BLASTN	379	4e-10	73	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 1
18922	GM_M40_B1_F08_MR	g18559	BLASTN	653	1e-22	76	G.max gene for catalase
18923	GM_M40_B1_G01_MF	g3097320	BLASTN	360	3e-09	67	Glycine max gene for Bd 30K, complete cds
18924	GM_M40_B1_G03_MF	g3021268	BLASTX	158	1e-21	67	(AL022347) putative protein [Arabidopsis thaliana]
18925	GM_M40_B1_G06_MF	g13619	BLASTN	360	5e-10	62	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
18926	GM_M40_B1_H01_MF	g13774	BLASTN	356	2e-09	59	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
18927	GM_M40_B2_B06_MF	g226407	BLASTX	242	3e-18	43	retrotransposon del1-46 [Lilium henryi]
18928	GM_M40_B2_C03_MF	g3738293	BLASTX	255	3e-21	67	(AC005309) putative CCAAT-binding transcription factor subunit A (CBF-A) [Arabidopsis thaliana]
18929	GM_M40_B2_C05_MF	g1769898	BLASTX	312	2e-26	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18930	GM_M40_B2_D02_MR	g18768	BLASTN	518	5e-17	65	Soybean Tgm6 transposable element 3' end
18931	GM_M40_B2_D10_MF	g976284	BLASTX	133	2e-19	45	reverse transcriptase [Arabidopsis thaliana]
18932	GM_M40_B2_D11_MR	g2465923	BLASTX	171	7e-11	52	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
18933	GM_M40_B2_E02_MR	g3142330	BLASTX	185	6e-22	80	(U96295) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18934	GM_M40_B2_E06_MF	g18559	BLASTN	713	3e-25	85	G.max gene for catalase
18935	GM_M40_B2_E08_MF	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18936	GM_M40_B2_F01_MR	g4063760	BLASTX	437	4e-39	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18937	GM_M40_B2_F02_MR	g4092471	BLASTN	448	3e-13	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18938	GM_M40_B2_F03_MR	g13597	BLASTN	371	7e-10	59	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile
18939	GM_M40_B2_F05_MF	g6940	BLASTN	420	1e-12	67	C.elegans repetitive DNA
18940	GM_M40_B2_F09_MF	g2129618	BLASTX	213	2e-15	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18941	GM_M40_B2_G01_MR	g1769898	BLASTX	256	3e-20	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18942	GM_M40_B2_G02_MR	g4056462	BLASTX	179	2e-19	72	(AC005990) Strong similarity to gb Y09876 aldehyde dehydrogenase (NAD+) from Nicotiana tabacum and a member of the aldehyde dehydrogenase family PF 00171. ESTs gb F15117, gb R83958 and gb 586262 come from this gene. [Arabidopsis thaliana]
18943	GM_M40_B2_G12_MF	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
18944	GM_M40_B2_H03_MR	g905361	BLASTX	212	1e-15	34	(U22103) gag-protease polyprotein [Glycine max]
18945	GM_M40_B2_H04_MF	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18946	GM_M40_B2_H04_MR	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18947	GM_M40_B2_H12_MF	g2281115	BLASTX	206	5e-18	93	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]
18948	GM_M41_A1_A04_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18949	GM_M41_A1_A09_MR	g3341679	BLASTX	154	2e-09	65	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]
18950	GM_M41_A1_B09_MR	g3645899	BLASTX	218	2e-20	48	(U68408) 5' end not determined experimentally [Zea mays]
18951	GM_M41_A1_B10_MF	g3522943	BLASTX	474	4e-43	71	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
18952	GM_M41_A1_B12_MF	g2832304	BLASTX	353	2e-31	65	(AF044489) receptor-like protein kinase [Oryza sativa]
18953	GM_M41_A1_C07_MF	g4063760	BLASTX	498	1e-45	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18954	GM_M41_A1_C11_MF	g4063760	BLASTX	293	9e-24	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18955	GM_M41_A1_D01_MF	g1666236	BLASTX	187	1e-13	30	(U76261) unknown [Hordeum vulgare]
18956	GM_M41_A1_D03_MR	g905361	BLASTX	108	1e-11	45	(U22103) gag-protease polyprotein [Glycine max]
18957	GM_M41_A1_D04_MR	g3738114	BLASTN	378	5e-10	61	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18958	GM_M41_A1_D06_MR	g130582	BLASTX	392	3e-34	62	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18959	GM_M41_A1_D10_MR	g3142328	BLASTN	597	2e-43	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18960	GM_M41_A1_D12_MR	g507910	BLASTN	729	3e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
18961	GM_M41_A1_E08_MR	g507910	BLASTN	438	4e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18962	GM_M41_A1_F02_MR	g1076763	BLASTX	161	3e-10	38	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
18963	GM_M41_A1_F04_MR	g2129618	BLASTX	266	5e-21	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18964	GM_M41_A1_F05_MF	g421954	BLASTX	178	4e-13	38	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
18965	GM_M41_A1_F05_MR	g3582328	BLASTX	211	2e-24	43	(AC005496) hypothetical protein [Arabidopsis thaliana]
18966	GM_M41_A1_F10_MF	g3513745	BLASTX	156	5e-09	31	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
18967	GM_M41_A1_G04_MF	g507910	BLASTN	380	1e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18968	GM_M41_A1_G06_MR	g2864621	BLASTX	218	1e-16	38	hypothetical protein [Arabidopsis thaliana]
18969	GM_M41_A1_G09_MF	g3426039	BLASTX	414	5e-38	60	(AC005168) unknown protein [Arabidopsis thaliana]
18970	GM_M41_A1_H01_MF	g1438880	BLASTN	450	1e-13	80	Glycine max choline kinase GmCK2p mRNA, complete cds
18971	GM_M41_A1_H02_MF	g3779026	BLASTX	119	8e-16	34	(AC005171) putative retrotransposon [Arabidopsis thaliana]
18972	GM_M41_A1_H02_MR	g3777527	BLASTX	214	3e-15	32	(AF053008) gag-pol polyprotein [Glycine max]
18973	GM_M41_A1_H05_MF	g3142328	BLASTN	855	9e-32	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18974	GM_M41_A1_H05_MR	g3599418	BLASTN	369	1e-09	69	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
18975	GM_M41_A1_H12_MR	g507910	BLASTN	733	2e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
18976	GM_M41_A2_A01_MR	g401237	BLASTX	144	2e-12	62	UBIQUITIN-ACTIVATING ENZYME E1 2 gi 170684 (M90663) ubiquitin activating enyme [Triticum aestivum]
18977	GM_M41_A2_A02_MF	g2655314	BLASTN	373	4e-10	59	Bactrocera xanthodes strain Vanuatu mitochondrial D-loop region, complete sequence
18978	GM_M41_A2_A02_MR	g1040717	BLASTN	343	2e-09	65	D.polychroa microsatellite sequence (clone Dp ch1 F3)
18979	GM_M41_A2_A05_MR	g2996576	BLASTN	380	4e-10	59	Homo sapiens DNA sequence from PAC 29C18 on chromosome 22

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18980	GM_M41_A2_A07_MR	g3377848	BLASTX	172	7e-19	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
18981	GM_M41_A2_A11_MF	g3097320	BLASTN	918	1e-34	81	Glycine max gene for Bd 30K, complete cds
18982	GM_M41_A2_B01_MR	g3645899	BLASTX	162	4e-23	63	(U68408) 5' end not determined experimentally [Zea mays]
18983	GM_M41_A2_B03_MR	g1769899	BLASTX	192	2e-14	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18984	GM_M41_A2_B06_MR	g507910	BLASTN	581	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18985	GM_M41_A2_B07_MR	g2129618	BLASTX	237	6e-18	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18986	GM_M41_A2_B08_MF	g2443320	BLASTX	246	1e-18	38	(D85597) polyprotein [Oryza australiensis]
18987	GM_M41_A2_B09_MF	g905361	BLASTX	582	8e-56	91	(U22103) gag-protease polyprotein [Glycine max]
18988	GM_M41_A2_B10_MF	g4006828	BLASTX	193	3e-13	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
18989	GM_M41_A2_C04_MR	g3319351	BLASTX	262	2e-20	44	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
18990	GM_M41_A2_C05_MR	g114734	BLASTX	388	3e-35	97	AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
18991	GM_M41_A2_C11_MF	g3097320	BLASTN	623	4e-21	80	Glycine max gene for Bd 30K, complete cds
18992	GM_M41_A2_D02_MR	g3845255	BLASTN	403	4e-11	66	Plasmodium falciparum chromosome 2, section 50 of 73 of the complete sequence
18993	GM_M41_A2_D04_MF	g170080	BLASTN	391	4e-13	79	Soybean seed lectin gene transposable element tgm1.
18994	GM_M41_A2_D08_MF	g2995405	BLASTX	237	5e-18	44	(Y12432) polyprotein [Ananas comosus]
18995	GM_M41_A2_D10_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18996	GM_M41_A2_D12_MF	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18997	GM_M41_A2_E01_MR	g507910	BLASTN	725	4e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
18998	GM_M41_A2_E02_MF	g1617470	BLASTN	429	2e-12	61	Z.diploperennis DNA for Grande1-4 retrotransposon.
18999	GM_M41_A2_E07_MR	g3142328	BLASTN	551	6e-18	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19000	GM_M41_A2_E09_MF	g3845234	BLASTN	390	1e-10	63	Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence
19001	GM_M41_A2_E09_MR	g3777527	BLASTX	195	4e-13	46	(AF053008) gag-pol polyprotein [Glycine max]
19002	GM_M41_A2_E11_MF	g1871187	BLASTX	222	3e-16	51	(U90439) unknown protein [Arabidopsis thaliana]
19003	GM_M41_A2_F01_MF	g2522228	BLASTX	370	2e-33	69	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19004	GM_M41_A2_F01_MR	g548533	BLASTX	218	1e-38	78	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) gi 1076631 pir S49646 phosphoglycerate mutase (EC 5.4.2.1) - common tobacco gi 474168 (X70651) phosphoglycerate mutase [Nicotiana tabacum]
19005	GM_M41_A2_F02_MF	g3810596	BLASTX	168	1e-10	33	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19006	GM_M41_A2_F05_MR	g13581	BLASTN	380	6e-11	70	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
19007	GM_M41_A2_F06_MF	g4063756	BLASTN	405	3e-11	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19008	GM_M41_A2_F09_MF	g3845094	BLASTN	422	5e-12	60	Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence
19009	GM_M41_A2_F12_MR	g2765091	BLASTX	347	1e-30	64	(Y10982) putative cytochrome P450 [Glycine max]
19010	GM_M41_A2_G03_MR	g18559	BLASTN	788	1e-28	75	G.max gene for catalase
19011	GM_M41_A2_G04_MR	g507910	BLASTN	432	6e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19012	GM_M41_A2_G05_MF	g4063760	BLASTX	306	4e-25	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19013	GM_M41_A2_G07_MF	g4063760	BLASTX	165	8e-16	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19014	GM_M41_A2_G08_MR	g1709919	BLASTX	499	4e-47	82	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) gi 439105 (L23834) glutamine phosphoribosylpyrophosphate amidotransferase [Vigna aconitifolia]
19015	GM_M41_A2_H02_MR	g4063760	BLASTX	204	3e-14	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19016	GM_M41_A2_H04_MR	g3135969	BLASTN	423	4e-12	62	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
19017	GM_M41_A2_H06_MF	g3746069	BLASTX	158	2e-10	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19018	GM_M41_A2_H10_MF	g4063760	BLASTX	375	2e-32	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19019	GM_M41_B1_A02_MR	g3097320	BLASTN	569	1e-18	78	Glycine max gene for Bd 30K, complete cds
19020	GM_M41_B1_A03_MF	g507910	BLASTN	538	1e-17	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19021	GM_M41_B1_A04_MF	g905361	BLASTX	592	8e-57	88	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19022	GM_M41_B1_A04_MR	g1142699	BLASTN	1233	2e-49	87	Glycine max satellite STR120-A.1.
19023	GM_M41_B1_A05_MF	g550452	BLASTX	132	5e-12	76	(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]
19024	GM_M41_B1_A06_MR	g99922	BLASTX	527	6e-50	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19025	GM_M41_B1_A10_MF	g995751	BLASTN	365	1e-09	66	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
19026	GM_M41_B1_B07_MR	g100484	BLASTX	219	3e-16	44	hypothetical protein - garden snapdragon
19027	GM_M41_B1_B08_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19028	GM_M41_B1_B08_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19029	GM_M41_B1_C07_MF	g2827715	BLASTX	351	4e-30	69	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
19030	GM_M41_B1_C08_MR	g387902	BLASTX	170	3e-23	41	(L23524) ORF [Hordeum vulgare]
19031	GM_M41_B1_D02_MF	g2626751	BLASTN	349	8e-09	63	Triticum aestivum retrotransposon Tar1, partial sequence.
19032	GM_M41_B1_D06_MF	g3319362	BLASTX	256	6e-20	46	(AF077408) contains similarity to reverse transcriptase (Ptam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
19033	GM_M41_B1_D06_MR	g3599418	BLASTN	493	2e-15	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
19034	GM_M41_B1_D08_MF	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19035	GM_M41_B1_D08_MR	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19036	GM_M41_B1_D11_MF	g4063756	BLASTN	454	2e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19037	GM_M41_B1_D11_MR	g507910	BLASTN	570	4e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19038	GM_M41_B1_D12_MF	g130582	BLASTX	199	9e-14	32	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19039	GM_M41_B1_E03_MR	g462013	BLASTX	116	2e-10	80	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) gi 542022 pir S39558 HSP90 homolog - Madagascar periwinkle gi 348696 (L14594) heat shock protein 90 [Catharanthus roseus]
19040	GM_M41_B1_E10_MR	g4038056	BLASTX	353	2e-30	50	(AC005897) putative transposon [Arabidopsis thaliana]
19041	GM_M41_B1_F05_MR	g507910	BLASTN	506	3e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19042	GM_M41_B1_F06_MF	g538067	BLASTX	213	6e-16	45	(M77661) putative pol polyprotein [Magnaporthe grisea]

Seq No	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
19043	GM_M41_B1_F10_MR	g2522228	BLASTX	304	7e-38	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
19044	GM_M41_B1_F12_MR	g3860312	BLASTN	624	3e-22	73	Cicer arietinum mRNA for hypothetical protein, clone Can144
19045	GM_M41_B1_G01_MF	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19046	GM_M41_B1_G01_MR	g905361	BLASTX	424	9e-39	95	(U22103) gag-protease polyprotein [Glycine max]
19047	GM_M41_B1_G03_MR	g169110	BLASTN	415	3e-12	71	Pea lox2-like lipoxygenase gene, 5' flank.
19048	GM_M41_B1_H01_MF	g3687234	BLASTX	179	1e-11	35	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
19049	GM_M41_B1_H03_MR	g2995405	BLASTX	378	4e-33	45	(Y12432) polyprotein [Ananas comosus]
19050	GM_M41_B1_H09_MR	g2522227	BLASTX	199	3e-15	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19051	GM_M41_B1_H10_MR	g505129	BLASTN	325	3e-10	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19052	GM_M41_B1_H11_MF	g1142702	BLASTN	345	4e-09	74	Glycine max satellite STR120-A.4.
19053	GM_M41_B2_A07_MR	g342964	BLASTN	370	1e-10	62	paramecium species 5,311 mt dna dimer: replication init. region.
19054	GM_M41_B2_A10_MR	g226407	BLASTX	409	4e-36	54	retrotransposon del1-46 [Lilium henryi]
19055	GM_M41_B2_A12_MR	g3097320	BLASTN	558	3e-18	73	Glycine max gene for Bd 30K, complete cds
19056	GM_M41_B2_B02_MR	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19057	GM_M41_B2_B05_MR	g3097320	BLASTN	1280	6e-51	81	Glycine max gene for Bd 30K, complete cds
19058	GM_M41_B2_B07_MR	g2827718	BLASTX	197	1e-13	34	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
19059	GM_M41_B2_C02_MR	g728868	BLASTX	139	1e-13	37	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) gi 99824 pir S16748 proline-rich protein - rape (fragment) gi 22597 (X60376) proline-rich protein [Brassica napus]
19060	GM_M41_B2_C03_MR	g3599418	BLASTN	354	5e-09	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
19061	GM_M41_B2_C07_MR	g1666236	BLASTX	116	4e-12	30	(U76261) unknown [Hordeum vulgare]
19062	GM_M41_B2_C12_MR	g3097320	BLASTN	948	7e-36	88	Glycine max gene for Bd 30K, complete cds
19063	GM_M41_B2_D03_MR	g2129618	BLASTX	178	1e-11	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19064	GM_M41_B2_D04_MR	g3097320	BLASTN	587	1e-19	74	Glycine max gene for Bd 30K, complete cds
19065	GM_M41_B2_D05_MR	g2961380	BLASTX	167	7e-11	36	(AL022141) putative protein [Arabidopsis thaliana]
19066	GM_M41_B2_E10_MR	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19067	GM_M41_B2_E11_MR	g2801677	BLASTN	579	5e-20	64	Glycine max telomere-associated sequence STAS6
19068	GM_M41_B2_F03_MR	g4115365	BLASTX	309	2e-25	59	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19069	GM_M41_B2_F04_MR	g1345132	BLASTX	180	8e-12	36	(U47029) ERECTA [Arabidopsis thaliana] gi 1389566 gnl PID d1012536 (D83257) receptor protein kinase [Arabidopsis thaliana] gi 3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
19070	GM_M41_B2_F05_MR	g3810596	BLASTX	195	2e-13	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19071	GM_M41_B2_G03_MR	g3645899	BLASTX	379	4e-33	62	(U68408) 5' end not determined experimentally [Zea mays]
19072	GM_M41_B2_G05_MR	g3810595	BLASTX	179	5e-16	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19073	GM_M41_B2_G08_MR	g1769897	BLASTX	177	6e-12	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19074	GM_M41_B2_G10_MR	g3097320	BLASTN	1329	4e-53	82	Glycine max gene for Bd 30K, complete cds
19075	GM_M41_B2_H03_MR	g226407	BLASTX	495	3e-45	67	retrotransposon del1-46 [Lilium henryi]
19076	GM_M41_B2_H09_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19077	GM_M41_B2_H12_MR	g2982545	BLASTN	450	3e-13	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-52, complete sequence [Plasmodium falciparum]
19078	GM_M42_A1_A04_MF	g3097320	BLASTN	452	2e-13	69	Glycine max gene for Bd 30K, complete cds
19079	GM_M42_A1_A06_MR	g4063760	BLASTX	100	8e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19080	GM_M42_A1_A08_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19081	GM_M42_A1_A12_MF	g1706130	BLASTX	124	4e-10	68	CDPK-RELATED PROTEIN KINASE (PK421) gi 2129917 pir S60052 calcium-dependent protein kinase homolog - carrot gi 1103386 (X83869) CDPK-related protein kinase [Daucus carota]
19082	GM_M42_A1_B02_MF	g2558658	BLASTX	192	2e-14	41	(AC002354) No definition line found [Arabidopsis thaliana]
19083	GM_M42_A1_B10_MR	g218269	BLASTX	235	5e-19	66	(D12839) reverse transcriptase [Glycine max]
19084	GM_M42_A1_B11_MF	g2588629	BLASTN	392	1e-10	64	Human BAC clone GS303P24 from 7q21-22, complete sequence [Homo sapiens]
19085	GM_M42_A1_B12_MR	g100484	BLASTX	365	6e-32	53	hypothetical protein - garden snapdragon
19086	GM_M42_A1_C03_MR	g3695395	BLASTX	237	3e-18	50	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
19087	GM_M42_A1_C05_MF	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19088	GM_M42_A1_C05_MR	g507910	BLASTN	371	4e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
19089	GM_M42_A1_C10_MF	g507910	BLASTN	344	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19090	GM_M42_A1_C12_MR	g3645899	BLASTX	343	3e-29	54	(U68408) 5' end not determined experimentally [Zea mays]
19091	GM_M42_A1_D02_MR	g3779021	BLASTX	195	3e-13	35	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
19092	GM_M42_A1_D04_MF	g3283026	BLASTX	257	3e-20	40	putative transposase [Arabidopsis thaliana]
19093	GM_M42_A1_D07_MF	g2522227	BLASTX	187	8e-14	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19094	GM_M42_A1_D11_MF	g3142328	BLASTN	814	7e-30	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19095	GM_M42_A1_E04_MR	g2121303	BLASTN	420	6e-12	63	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
19096	GM_M42_A1_E08_MF	g170603	BLASTN	477	3e-15	67	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
19097	GM_M42_A1_F04_MF	g3097320	BLASTN	1056	9e-41	80	Glycine max gene for Bd 30K, complete cds
19098	GM_M42_A1_F11_MF	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19099	GM_M42_A1_G08_MF	g18559	BLASTN	817	5e-30	75	G.max gene for catalase
19100	GM_M42_A1_G09_MR	g99922	BLASTX	334	4e-34	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19101	GM_M42_A1_G11_MR	g2588611	BLASTN	360	3e-09	62	Human BAC clone RG335O22 from 7q21-q22, complete sequence [Homo sapiens]
19102	GM_M42_A1_G12_MR	g2191136	BLASTX	163	1e-10	36	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]
19103	GM_M42_A1_H01_MR	g3645899	BLASTX	201	2e-29	41	(U68408) 5' end not determined experimentally [Zea mays]
19104	GM_M42_A1_H03_MR	g3201680	BLASTX	176	1e-13	63	(AF060941) extra-large G-protein [Arabidopsis thaliana]
19105	GM_M42_A1_H04_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19106	GM_M42_A1_H07_MR	g2829902	BLASTX	246	3e-19	64	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]
19107	GM_M42_A1_H11_MR	g3097320	BLASTN	506	7e-16	69	Glycine max gene for Bd 30K, complete cds
19108	GM_M42_B1_A12_MF	g13096	BLASTN	459	8e-14	64	Leishmania tarentolae maxicircle DNA fragment
19109	GM_M42_B1_B01_MF	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19110	GM_M42_B1_B02_MF	g3097320	BLASTN	500	1e-15	72	Glycine max gene for Bd 30K, complete cds
19111	GM_M42_B1_B06_MF	g507910	BLASTN	523	5e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19112	GM_M42_B1_B11_MF	g3901012	BLASTX	255	4e-21	73	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
19113	GM_M42_B1_C02_MF	g1184075	BLASTX	228	2e-19	43	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
19114	GM_M42_B1_C07_MF	g3645899	BLASTX	377	7e-33	57	(U68408) 5' end not determined experimentally [Zea mays]
19115	GM_M42_B1_C09_MF	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19116	GM_M42_B1_C10_MF	g2281086	BLASTX	153	2e-09	37	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]
19117	GM_M42_B1_C11_MF	g3894383	BLASTX	230	8e-20	43	(AF053993) disease resistance protein [Lycopersicon esculentum]
19118	GM_M42_B1_D01_MF	g1769897	BLASTX	260	6e-21	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19119	GM_M42_B1_D08_MF	g507910	BLASTN	594	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19120	GM_M42_B1_D09_MF	g507910	BLASTN	461	3e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19121	GM_M42_B1_F01_MF	g3142328	BLASTN	966	8e-37	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19122	GM_M42_B1_F11_MF	g1666236	BLASTX	192	4e-14	38	(U76261) unknown [Hordeum vulgare]
19123	GM_M42_B1_G02_MF	g462627	BLASTX	131	2e-14	61	MSP1 PROTEIN (TAT-BINDING HOMOLOG 4) gi 1362427 pir A49506 MSP1 protein - yeast (Saccharomyces cerevisiae) gi 404217 (X68055) MSP1 protein [Saccharomyces cerevisiae] gi 531756 (X81069) probable regulatory subunit of 26S protease [Saccharomyces cerevisiae] gi 1323004 gnl PID e243375 (Z72813) ORF YGR028w [Saccharomyces cerevisiae]
19124	GM_M42_B1_G03_MF	g2522230	BLASTX	267	2e-22	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19125	GM_M42_B1_G06_MF	g3250687	BLASTX	284	3e-24	42	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
19126	GM_M42_B1_H08_MF	g3319351	BLASTX	216	2e-15	38	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
19127	GM_M42_B1_H09_MF	g3097320	BLASTN	860	6e-32	76	Glycine max gene for Bd 30K, complete cds
19128	GM_M42_B1_H10_MF	g4063760	BLASTX	484	3e-44	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19129	GM_M43_A1_A11_MF	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19130	GM_M43_A1_A12_MR	g1658457	BLASTX	175	9e-13	70	(U75248) reverse transcriptase [Gossypium barbadense]
19131	GM_M43_A1_B02_MR	g3461813	BLASTX	136	4e-11	89	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]
19132	GM_M43_A1_B03_MF	g18559	BLASTN	645	3e-22	69	G.max gene for catalase
19133	GM_M43_A1_B11_MF	g3142328	BLASTN	741	1e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19134	GM_M43_A1_C01_MR	g3142379	BLASTX	286	3e-24	66	(AF053008) envelope-like [Glycine max]
19135	GM_M43_A1_C04_MF	g4063760	BLASTX	210	7e-28	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19136	GM_M43_A1_C07_MR	g3142328	BLASTN	1209	7e-48	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19137	GM_M43_A1_D02_MF	g3777527	BLASTX	669	1e-63	97	(AF053008) gag-pol polyprotein [Glycine max]
19138	GM_M43_A1_D02_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19139	GM_M43_A1_D07_MF	g4063756	BLASTN	526	1e-16	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19140	GM_M43_A1_D08_MF	g2244915	BLASTX	165	4e-17	41	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
19141	GM_M43_A1_E08_MF	g2129618	BLASTX	170	9e-11	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19142	GM_M43_A1_E08_MR	g2764526	BLASTN	415	1e-11	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19143	GM_M43_A1_E09_MR	g100484	BLASTX	207	6e-15	33	hypothetical protein - garden snapdragon
19144	GM_M43_A1_E11_MF	g2522227	BLASTX	156	3e-10	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19145	GM_M43_A1_F07_MR	g2995405	BLASTX	218	2e-32	51	(Y12432) polyprotein [Ananas comosus]
19146	GM_M43_A1_F08_MF	g4038056	BLASTX	368	5e-32	54	(AC005897) putative transposon [Arabidopsis thaliana]
19147	GM_M43_A1_F08_MR	g3810595	BLASTX	144	9e-18	41	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19148	GM_M43_A1_F09_MF	g3006139	BLASTX	265	4e-22	43	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
19149	GM_M43_A1_G03_MF	g3777527	BLASTX	645	4e-61	93	(AF053008) gag-pol polyprotein [Glycine max]
19150	GM_M43_A1_G03_MR	g4038056	BLASTX	169	9e-11	43	(AC005897) putative transposon [Arabidopsis thaliana]
19151	GM_M43_A1_G05_MR	g3212102	BLASTN	608	2e-20	62	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]
19152	GM_M43_A1_G08_MF	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19153	GM_M43_A1_G09_MR	g3928116	BLASTN	395	8e-11	63	, complete sequence [Homo sapiens]
19154	GM_M43_A1_G12_MF	g2129618	BLASTX	228	5e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19155	GM_M43_A1_H03_MR	g2522228	BLASTX	207	2e-28	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
19156	GM_M43_A1_H05_MF	g3265161	BLASTN	369	6e-10	63	Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence
19157	GM_M43_A1_H07_MR	g18559	BLASTN	980	2e-37	79	G.max gene for catalase
19158	GM_M43_A2_A04_MF	g3142328	BLASTN	1030	1e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19159	GM_M43_A2_A12_MF	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19160	GM_M43_A2_A12_MR	g4063760	BLASTX	184	2e-19	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19161	GM_M43_A2_B01_MF	g8540	BLASTN	449	4e-14	66	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb M29744 DROSAT02 Drosophila satellite DNA fragment 1.672-614.
19162	GM_M43_A2_B04_MR	g4063760	BLASTX	228	6e-31	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19163	GM_M43_A2_B05_MF	g905361	BLASTX	423	1e-38	92	(U22103) gag-protease polyprotein [Glycine max]
19164	GM_M43_A2_B05_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19165	GM_M43_A2_B07_MF	g3702691	BLASTX	156	7e-29	80	(AB005902) AtPIP5K1 [Arabidopsis thaliana]
19166	GM_M43_A2_B07_MR	g1905774	BLASTN	411	1e-11	69	A.thaliana mRNA for protein kinase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19167	GM_M43_A2_B10_MF	g3777527	BLASTX	403	4e-44	89	(AF053008) gag-pol polyprotein [Glycine max]
19168	GM_M43_A2_B12_MF	g2499535	BLASTX	158	8e-10	70	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR gi 595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]
19169	GM_M43_A2_C01_MR	g2052034	BLASTN	414	1e-11	63	Human DNA sequence from PAC 450C20 on chromosome X
19170	GM_M43_A2_C04_MF	g2129618	BLASTX	138	4e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19171	GM_M43_A2_C05_MF	g507910	BLASTN	363	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19172	GM_M43_A2_C05_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19173	GM_M43_A2_C06_MR	g3319362	BLASTX	136	9e-22	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
19174	GM_M43_A2_D01_MF	g4150930	BLASTN	400	5e-11	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
19175	GM_M43_A2_D01_MR	g905361	BLASTX	114	1e-11	45	(U22103) gag-protease polyprotein [Glycine max]
19176	GM_M43_A2_D07_MF	g2576343	BLASTN	351	8e-09	63	Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence [Homo sapiens]
19177	GM_M43_A2_D10_MR	g3930515	BLASTX	132	8e-12	52	(AF059674) putative gag protein [Nicotiana tabacum]
19178	GM_M43_A2_E08_MF	g3142328	BLASTN	1455	4e-59	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19179	GM_M43_A2_E10_MR	g3097320	BLASTN	828	2e-30	72	Glycine max gene for Bd 30K, complete cds
19180	GM_M43_A2_E11_MF	g2129473	BLASTX	205	7e-16	42	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
19181	GM_M43_A2_F01_MR	g1244652	BLASTN	373	8e-10	60	Zea mays copia-type retroelement PREM-2 gag gene, complete cds.
19182	GM_M43_A2_F02_MR	g1244652	BLASTN	357	4e-09	59	Zea mays copia-type retroelement PREM-2 gag gene, complete cds.
19183	GM_M43_A2_F06_MF	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19184	GM_M43_A2_G07_MR	g3142328	BLASTN	1415	3e-57	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19185	GM_M43_A2_G08_MF	g559261	BLASTN	392	3e-11	67	Saccharomyces cerevisiae mitochondrion 21S R2 ribosomal RNA, 3' end.
19186	GM_M43_A2_G09_MR	g903472	BLASTN	341	3e-09	66	Stealth virus clone C16290 T3.
19187	GM_M43_A2_H01_MR	g3142328	BLASTN	645	3e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19188	GM_M43_A2_H05_MF	g507910	BLASTN	500	6e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19189	GM_M43_A2_H09_MR	g3142328	BLASTN	480	1e-14	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19190	GM_M43_A2_H12_MR	g2129473	BLASTX	331	3e-29	47	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
19191	GM_M43_B1_A03_MF	g2997591	BLASTX	353	2e-31	85	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]
19192	GM_M43_B1_A04_MR	g1144550	BLASTN	405	3e-12	60	Anopheles gambiae 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
19193	GM_M43_B1_A05_MR	g2864610	BLASTX	152	3e-18	55	(AL021811) putative protein [Arabidopsis thaliana]
19194	GM_M43_B1_A09_MR	g4063760	BLASTX	459	2e-42	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19195	GM_M43_B1_A10_MR	g1142701	BLASTN	1359	4e-55	85	Glycine max satellite STR120-A.3.
19196	GM_M43_B1_A11_MF	g3600059	BLASTX	348	5e-31	77	(AF080120) contains similarity to WB domains, G-beta repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03) [Arabidopsis thaliana]
19197	GM_M43_B1_A11_MR	g2829275	BLASTX	178	5e-26	77	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] gi 3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana]
19198	GM_M43_B1_B02_MR	g1769898	BLASTX	223	9e-17	31	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19199	GM_M43_B1_B06_MR	g1216393	BLASTN	422	5e-13	61	Trypanosoma cruzi ATPase subunit 6 mRNA, complete cds
19200	GM_M43_B1_B07_MR	g4063760	BLASTX	487	2e-44	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19201	GM_M43_B1_B11_MR	g3377834	BLASTX	154	3e-09	28	(AF075598) No definition line found [Arabidopsis thaliana]
19202	GM_M43_B1_C05_MR	g3777527	BLASTX	772	9e-75	93	(AF053008) gag-pol polyprotein [Glycine max]
19203	GM_M43_B1_C09_MF	g1769897	BLASTX	334	3e-32	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19204	GM_M43_B1_E02_MR	g3142328	BLASTN	905	5e-34	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19205	GM_M43_B1_E03_MR	g3097320	BLASTN	501	1e-15	69	Glycine max gene for Bd 30K, complete cds
19206	GM_M43_B1_E09_MR	g507910	BLASTN	468	1e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19207	GM_M43_B1_E10_MF	g2842524	BLASTX	126	6e-13	36	(AL021746) retrotransposable element [Schizosaccharomyces pombe]
19208	GM_M43_B1_E10_MR	g2760844	BLASTX	178	4e-12	78	(AC003105) hypothetical protein [Arabidopsis thaliana]
19209	GM_M43_B1_E11_MR	g3283026	BLASTX	168	9e-11	30	putative transposase [Arabidopsis thaliana]
19210	GM_M43_B1_F02_MF	g1666236	BLASTX	195	2e-14	30	(U76261) unknown [Hordeum vulgare]
19211	GM_M43_B1_F04_MR	g2832625	BLASTX	250	1e-19	78	(AL021711) putative protein [Arabidopsis thaliana]
19212	GM_M43_B1_F05_MR	g3097320	BLASTN	429	2e-12	72	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
19213	GM_M43_B1_F07_MR	g130582	BLASTX	346	2e-29	49	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19214	GM_M43_B1_F12_MR	g1785729	BLASTN	325	2e-14	67	A.thaliana mitochondrial genome, part B
19215	GM_M43_B1_G01_MR	g3142328	BLASTN	668	3e-23	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19216	GM_M43_B1_G03_MF	g1769897	BLASTX	376	6e-34	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19217	GM_M43_B1_G04_MF	g133913	BLASTX	525	9e-50	76	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70858 pir R3PM2 ribosomal protein S2 - garden pea chloroplast gi 12138 (X03912) ORF (aa 1-236) with homology to ribosomal protein S2; pid:g12138 [Pisum sativum]
19218	GM_M43_B1_G04_MR	g11748	BLASTN	1586	4e-66	89	Nicotiana debneyi chloroplast DNA for tRNA-Ile and ribosomal protein L2
19219	GM_M43_B1_G06_MR	g2792220	BLASTX	293	2e-24	38	(AF032688) NBS-LRR type resistance protein [Oryza sativa]
19220	GM_M43_B1_G07_MR	g3810595	BLASTX	461	1e-41	50	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19221	GM_M43_B1_G08_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19222	GM_M43_B1_G08_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19223	GM_M43_B1_G11_MF	g3777527	BLASTX	167	1e-17	40	(AF053008) gag-pol polyprotein [Glycine max]
19224	GM_M43_B1_G11_MR	g1769898	BLASTX	239	5e-20	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19225	GM_M43_B2_A03_MR	g2522226	BLASTN	440	6e-13	66	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
19226	GM_M43_B2_A07_MR	g18559	BLASTN	436	1e-12	74	G.max gene for catalase
19227	GM_M43_B2_A10_MF	g2052034	BLASTN	410	2e-11	64	Human DNA sequence from PAC 450C20 on chromosome X
19228	GM_M43_B2_A11_MF	g3142328	BLASTN	1022	2e-39	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19229	GM_M43_B2_A11_MR	g478084	BLASTX	147	1e-09	53	reverse transcriptase (copia-like retrotransposon) - Liriodendron tulipifera (fragment) gi 168310 (M94479) reverse transcriptase [Liriodendron tulipifera]
19230	GM_M43_B2_B04_MF	g507910	BLASTN	650	9e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19231	GM_M43_B2_B10_MR	g1673405	BLASTN	675	8e-24	76	C.annuum mRNA for xanthophyll epoxidase.
19232	GM_M43_B2_C01_MR	g2969943	BLASTN	411	2e-11	71	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
19233	GM_M43_B2_C10_MF	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
19234	GM_M43_B2_C10_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19235	GM_M43_B2_D04_MR	g3097320	BLASTN	691	3e-24	72	Glycine max gene for Bd 30K, complete cds
19236	GM_M43_B2_D10_MF	g421955	BLASTX	180	2e-12	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19237	GM_M43_B2_E08_MF	g2809247	BLASTX	159	7e-10	27	(AC002560) F21B7.16 [Arabidopsis thaliana]
19238	GM_M43_B2_E09_MF	g4063760	BLASTX	461	1e-41	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19239	GM_M43_B2_E12_MR	g133916	BLASTX	140	8e-09	57	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70857 pir R3SP2 ribosomal protein S2 - spinach chloroplast gi 12256 (X05916) rps2 protein (AA 1-236) [Spinacia oleracea]
19240	GM_M43_B2_F05_MR	g4092470	BLASTN	512	2e-16	74	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
19241	GM_M43_B2_F07_MF	g18559	BLASTN	479	1e-14	67	G.max gene for catalase
19242	GM_M43_B2_F07_MR	g3777527	BLASTX	139	3e-11	58	(AF053008) gag-pol polyprotein [Glycine max]
19243	GM_M43_B2_F09_MR	g1167523	BLASTX	222	4e-16	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19244	GM_M43_B2_F12_MR	g1142701	BLASTN	1086	9e-43	85	Glycine max satellite STR120-A.3.
19245	GM_M43_B2_G01_MF	g3142328	BLASTN	868	2e-32	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19246	GM_M43_B2_G03_MR	g3449334	BLASTN	364	2e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
19247	GM_M43_B2_G05_MF	g1946279	BLASTX	309	7e-27	42	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
19248	GM_M43_B2_G06_MR	g1769899	BLASTX	198	4e-15	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19249	GM_M43_B2_G10_MR	g2995405	BLASTX	176	3e-13	67	(Y12432) polyprotein [Ananas comosus]
19250	GM_M43_B2_G12_MF	g2995405	BLASTX	485	1e-44	61	(Y12432) polyprotein [Ananas comosus]
19251	GM_M43_B2_H06_MR	g629693	BLASTX	325	1e-28	58	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19252	GM_M43_B2_H09_MF	g421955	BLASTX	180	2e-12	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19253	GM_M44_A1_A02_MR	g3097320	BLASTN	758	2e-41	76	Glycine max gene for Bd 30K, complete cds
19254	GM_M44_A1_A11_MR	g3777527	BLASTX	360	1e-34	76	(AF053008) gag-pol polyprotein [Glycine max]
19255	GM_M44_A1_B02_MR	g905361	BLASTX	119	6e-12	47	(U22103) gag-protease polyprotein [Glycine max]
19256	GM_M44_A1_B04_MR	g3097320	BLASTN	1085	7e-50	79	Glycine max gene for Bd 30K, complete cds
19257	GM_M44_A1_B09_MR	g3426334	BLASTN	357	4e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19258	GM_M44_A1_C03_MF	g3738114	BLASTN	376	6e-10	60	Homo sapiens chromosome Y, clone 264.M.20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19259	GM_M44_A1_C07_MR	g3582335	BLASTX	379	1e-33	72	(AC005496) unknown protein [Arabidopsis thaliana]
19260	GM_M44_A1_C08_MR	g3097320	BLASTN	795	6e-45	77	Glycine max gene for Bd 30K, complete cds
19261	GM_M44_A1_D02_MR	g2764526	BLASTN	605	3e-20	67	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19262	GM_M44_A1_D04_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19263	GM_M44_A1_D04_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19264	GM_M44_A1_D07_MF	g130582	BLASTX	208	3e-29	55	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19265	GM_M44_A1_D09_MR	g3522938	BLASTX	158	4e-10	50	(AC004411) unknown protein [Arabidopsis thaliana]
19266	GM_M44_A1_D11_MR	g4063760	BLASTX	274	1e-21	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19267	GM_M44_A1_D12_MR	g3142379	BLASTX	197	3e-14	58	(AF053008) envelope-like [Glycine max]
19268	GM_M44_A1_E03_MF	g4115536	BLASTX	229	2e-18	50	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
19269	GM_M44_A1_E12_MF	g13773	BLASTN	391	3e-11	61	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
19270	GM_M44_A1_F02_MF	g1769898	BLASTX	232	9e-18	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19271	GM_M44_A1_F05_MF	g3212861	BLASTX	165	5e-11	43	(AC004005) unknown protein [Arabidopsis thaliana]
19272	GM_M44_A1_F07_MF	g507910	BLASTN	427	1e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19273	GM_M44_A1_G05_MF	g425194	BLASTX	134	1e-11	51	(L26243) heat shock protein [Spinacia oleracea] gi 2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]
19274	GM_M44_A1_G09_MF	g3142328	BLASTN	1535	1e-62	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19275	GM_M44_A1_G09_MR	g3097320	BLASTN	606	2e-20	74	Glycine max gene for Bd 30K, complete cds
19276	GM_M44_A1_H06_MR	g170080	BLASTN	416	7e-12	69	Soybean seed lectin gene transposable element tgm1.
19277	GM_M44_A1_H09_MR	g3777527	BLASTX	155	6e-11	50	(AF053008) gag-pol polyprotein [Glycine max]
19278	GM_M44_A2_C02_MR	g2462134	BLASTX	114	3e-10	29	(Y13368) reverse transcriptase [Beta vulgaris]
19279	GM_M44_A2_C07_MR	g4063760	BLASTX	167	1e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19280	GM_M44_A2_D11_MR	g629693	BLASTX	295	2e-25	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19281	GM_M44_A2_E11_MR	g3777527	BLASTX	358	2e-60	95	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19282	GM_M44_A2_F09_MR	g3142328	BLASTN	2085	5e-88	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19283	GM_M44_A2_G03_MR	g3845197	BLASTN	308	6e-10	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
19284	GM_M44_A2_G07_MR	g1588265	BLASTX	181	4e-12	80	100RNP protein [Spinacia oleracea]
19285	GM_M44_A2_G09_MR	g2264320	BLASTN	601	4e-20	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
19286	GM_M44_A2_G11_MR	g226407	BLASTX	268	7e-38	58	retrotransposon del1-46 [Lilium henryi]
19287	GM_M44_A2_H12_MR	g2335097	BLASTX	179	8e-12	62	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
19288	GM_M44_B1_A10_MF	g2529683	BLASTX	467	1e-43	70	(AC002535) unknown protein [Arabidopsis thaliana]
19289	GM_M44_B1_A12_MF	g3676469	BLASTX	161	4e-10	34	(AF053884) (R)-(+)-mandelonitrile lyase isoform MDL4 precursor [Prunus serotina] gi 3676471 (AF053885) (R)-(+)-mandelonitrile lyase isoform MDL4 precursor [Prunus serotina]
19290	GM_M44_B1_C04_MF	g477280	BLASTX	157	9e-10	83	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato gi 410633 bbs 136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]
19291	GM_M44_B1_D01_MF	g18559	BLASTN	880	7e-33	74	G.max gene for catalase
19292	GM_M44_B1_E03_MF	g2708743	BLASTX	218	1e-15	34	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
19293	GM_M44_B1_E07_MF	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19294	GM_M44_B1_E10_MF	g170606	BLASTN	759	8e-28	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
19295	GM_M44_B1_F08_MF	g2832625	BLASTX	158	8e-10	47	(AL021711) putative protein [Arabidopsis thaliana]
19296	GM_M44_B1_G04_MF	g3510336	BLASTN	435	1e-12	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
19297	GM_M44_B1_G08_MF	g3860271	BLASTX	210	4e-15	31	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
19298	GM_M44_B1_G09_MF	g2522230	BLASTX	210	2e-16	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19299	GM_M44_B1_H02_MF	g18695	BLASTN	508	4e-16	75	Soybean nodulin 22 gene
19300	GM_M44_B1_H03_MF	g2073447	BLASTN	362	3e-09	65	L.japonicus gln1, pge1 & krm genes
19301	GM_M44_B1_H04_MF	g99755	BLASTX	342	8e-30	47	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19302	GM_M44_B2_A10_MF	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19303	GM_M44_B2_B07_MF	g3645899	BLASTX	183	2e-15	54	(U68408) 5' end not determined experimentally [Zea mays]
19304	GM_M44_B2_C01_MF	g3142379	BLASTX	238	5e-22	85	(AF053008) envelope-like [Glycine max]
19305	GM_M44_B2_C03_MR	g100484	BLASTX	313	2e-26	58	hypothetical protein - garden snapdragon
19306	GM_M44_B2_D02_MF	g3645899	BLASTX	156	3e-09	43	(U68408) 5' end not determined experimentally [Zea mays]
19307	GM_M44_B2_D05_MR	g3142328	BLASTN	772	5e-28	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19308	GM_M44_B2_E02_MF	g2104945	BLASTN	1187	8e-47	83	Glycine max copia-like retrotransposon Tgmr, complete sequence
19309	GM_M44_B2_E12_MF	g3097320	BLASTN	584	2e-19	80	Glycine max gene for Bd 30K, complete cds
19310	GM_M44_B2_F07_MF	g422418	BLASTX	159	1e-09	36	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
19311	GM_M44_B2_F12_MF	g2264317	BLASTN	445	5e-13	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]
19312	GM_M44_B2_G01_MF	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19313	GM_M44_B2_G06_MF	g4063760	BLASTX	168	2e-10	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19314	GM_M44_B2_G07_MF	g2129618	BLASTX	174	3e-11	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19315	GM_M44_B2_G10_MR	g3599418	BLASTN	1194	4e-47	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
19316	GM_M44_B2_G12_MF	g4050011	BLASTN	477	1e-14	68	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
19317	GM_M44_B2_H04_MF	g3763850	BLASTN	457	1e-13	82	Glycine max GmENOD93 gene for early nodulin, complete cds
19318	GM_M44_B2_H06_MF	g3063445	BLASTX	186	2e-12	46	(AC003981) F22O13.7 [Arabidopsis thaliana]
19319	GM_M44_B2_H08_MF	g3142328	BLASTN	562	2e-18	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19320	GM_M45_A1_A05_MF	g4063770	BLASTX	189	6e-13	41	(AB004906) transposase [Ipomoea purpurea]
19321	GM_M45_A1_A07_MR	g3777527	BLASTX	382	4e-33	87	(AF053008) gag-pol polyprotein [Glycine max]
19322	GM_M45_A1_A10_MF	g3810596	BLASTX	278	2e-22	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19323	GM_M45_A1_D04_MF	g133917	BLASTX	160	4e-11	93	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
19324	GM_M45_A1_D11_MR	g3097320	BLASTN	697	2e-24	76	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19325	GM_M45_A1_E02_MF	g3142328	BLASTN	736	2e-26	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19326	GM_M45_A1_E07_MF	g3319351	BLASTX	86	8e-10	47	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
19327	GM_M45_A1_E09_MF	g18559	BLASTN	756	3e-27	75	G.max gene for catalase
19328	GM_M45_A1_F02_MF	g3142328	BLASTN	736	2e-26	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19329	GM_M45_A1_G02_MF	g3142328	BLASTN	1485	2e-60	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19330	GM_M45_A2_A08_MR	g3746069	BLASTX	161	1e-10	58	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19331	GM_M45_A2_B07_MF	g4063760	BLASTX	401	3e-35	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19332	GM_M45_A2_B09_MF	g322662	BLASTX	147	8e-14	82	S-receptor kinase-related protein - Chinese kale gi 17915 (Z18883) S-receptor kinase related protein [Brassica oleracea]
19333	GM_M45_A2_C06_MR	g507910	BLASTN	472	1e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19334	GM_M45_A2_C08_MF	g1769898	BLASTX	334	9e-29	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19335	GM_M45_A2_C08_MR	g1769898	BLASTX	327	5e-28	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19336	GM_M45_A2_C10_MF	g2464905	BLASTX	171	2e-20	64	(Z99708) minor allergen [Arabidopsis thaliana]
19337	GM_M45_A2_D02_MR	g3510505	BLASTX	212	4e-15	35	(AF030881) pol polyprotein [Fugu rubripes]
19338	GM_M45_A2_D04_MF	g3645899	BLASTX	270	6e-28	66	(U68408) 5' end not determined experimentally [Zea mays]
19339	GM_M45_A2_D05_MF	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19340	GM_M45_A2_D06_MF	g507910	BLASTN	424	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19341	GM_M45_A2_D10_MF	g18559	BLASTN	519	2e-16	72	G.max gene for catalase
19342	GM_M45_A2_F10_MF	g3250687	BLASTX	198	4e-15	37	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
19343	GM_M45_A2_G03_MF	g3845197	BLASTN	375	6e-10	66	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
19344	GM_M45_A2_G05_MF	g507910	BLASTN	500	6e-16	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19345	GM_M45_A2_G08_MF	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19346	GM_M45_A2_G09_MR	g3645899	BLASTX	140	2e-09	38	(U68408) 5' end not determined experimentally [Zea mays]
19347	GM_M45_B1_B02_MF	g3097320	BLASTN	492	3e-15	73	Glycine max gene for Bd 30K, complete cds
19348	GM_M45_B1_B03_MR	g2522230	BLASTX	108	2e-14	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19349	GM_M45_B1_B04_MR	g3810596	BLASTX	245	8e-19	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19350	GM_M45_B1_B05_MF	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19351	GM_M45_B1_C02_MR	g2924771	BLASTX	192	9e-14	47	(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]
19352	GM_M45_B1_C06_MF	g3176707	BLASTX	175	4e-12	58	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]
19353	GM_M45_B1_C08_MF	g507910	BLASTN	481	4e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19354	GM_M45_B1_C12_MR	g18559	BLASTN	690	3e-24	74	G.max gene for catalase
19355	GM_M45_B1_D01_MF	g2264302	BLASTN	430	2e-12	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]
19356	GM_M45_B1_D02_MR	g4063760	BLASTX	157	3e-09	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19357	GM_M45_B1_D09_MF	g226407	BLASTX	238	5e-23	41	retrotransposon del1-46 [Lilium henryi]
19358	GM_M45_B1_E01_MR	g3860246	BLASTX	143	1e-08	37	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
19359	GM_M45_B1_E03_MF	g4006831	BLASTX	266	7e-21	44	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
19360	GM_M45_B1_E08_MF	g905361	BLASTX	558	3e-53	91	(U22103) gag-protease polyprotein [Glycine max]
19361	GM_M45_B1_F01_MR	g1769899	BLASTX	305	2e-26	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19362	GM_M45_B1_F02_MR	g1076545	BLASTX	233	8e-19	85	guanine nucleotide regulatory protein - fava bean gi 547478 (Z37503) guanine nucleotide regulatory protein [Vicia faba] gi 1098297 prf 2115367E small GTP-binding protein [Vicia faba]
19363	GM_M45_B1_F03_MF	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19364	GM_M45_B1_F03_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19365	GM_M45_B1_F05_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19366	GM_M45_B1_F10_MF	g1256945	BLASTN	369	1e-09	65	Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.
19367	GM_M45_B1_F11_MF	g82207	BLASTX	234	3e-17	74	hypothetical protein 1708 - common tobacco chloroplast
19368	GM_M45_B1_F11_MR	g18559	BLASTN	769	8e-28	72	G.max gene for catalase
19369	GM_M45_B1_G02_MF	g3142328	BLASTN	653	1e-22	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19370	GM_M45_B1_G04_MR	g18768	BLASTN	353	1e-09	65	Soybean Tgm6 transposable element 3' end
19371	GM_M45_B1_G11_MF	g4038056	BLASTX	265	5e-21	38	(AC005897) putative transposon [Arabidopsis thaliana]
19372	GM_M45_B1_H02_MF	g3912919	BLASTX	150	8e-09	85	(AF001308) hypothetical protein [Arabidopsis thaliana]
19373	GM_M45_B1_H03_MF	g2781345	BLASTX	231	2e-17	69	(AC003113) F24O1.2 [Arabidopsis thaliana]
19374	GM_M45_B1_H09_MF	g2462134	BLASTX	260	5e-21	46	(Y13368) reverse transcriptase [Beta vulgaris]
19375	GM_M45_B1_H09_MR	g2351060	BLASTX	311	4e-27	78	(AB006660) sucrose-phosphate synthase [Citrus unshiu]
19376	GM_M45_B1_H10_MF	g3142328	BLASTN	1150	4e-45	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19377	GM_M45_B1_H12_MR	g2827663	BLASTX	188	6e-13	39	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
19378	GM_M45_B2_A01_MF	g3600044	BLASTX	175	1e-12	49	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
19379	GM_M45_B2_A05_MR	g975703	BLASTN	722	1e-25	80	P.sativum GR gene
19380	GM_M45_B2_A09_MF	g507910	BLASTN	430	8e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19381	GM_M45_B2_A09_MR	g507910	BLASTN	412	5e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19382	GM_M45_B2_B05_MF	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19383	GM_M45_B2_B07_MF	g3377848	BLASTX	258	3e-21	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
19384	GM_M45_B2_B08_MR	g4006831	BLASTX	192	5e-13	27	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
19385	GM_M45_B2_B10_MR	g13581	BLASTN	338	4e-09	62	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
19386	GM_M45_B2_C01_MF	g507910	BLASTN	368	5e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
19387	GM_M45_B2_C01_MR	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19388	GM_M45_B2_C04_MR	g421955	BLASTX	146	8e-09	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19389	GM_M45_B2_C05_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19390	GM_M45_B2_C05_MR	g507910	BLASTN	410	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19391	GM_M45_B2_C07_MR	g4063760	BLASTX	488	1e-44	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19392	GM_M45_B2_D03_MF	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19393	GM_M45_B2_D06_MF	g3777527	BLASTX	206	2e-14	33	(AF053008) gag-pol polyprotein [Glycine max]
19394	GM_M45_B2_D10_MF	g3283026	BLASTX	169	8e-11	40	putative transposase [Arabidopsis thaliana]
19395	GM_M45_B2_D11_MR	g2129618	BLASTX	160	9e-10	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19396	GM_M45_B2_E05_MR	g2997694	BLASTX	172	2e-12	42	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
19397	GM_M45_B2_F04_MF	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19398	GM_M45_B2_F04_MR	g507910	BLASTN	357	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19399	GM_M45_B2_F08_MF	g1769896	BLASTN	370	1e-09	72	A.thaliana lectin receptor kinase gene
19400	GM_M45_B2_F12_MR	g3777527	BLASTX	167	3e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
19401	GM_M45_B2_G03_MF	g629693	BLASTX	205	2e-15	53	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19402	GM_M45_B2_G03_MR	g3142379	BLASTX	117	8e-13	67	(AF053008) envelope-like [Glycine max]
19403	GM_M45_B2_G07_MR	g3859610	BLASTN	528	8e-17	65	Arabidopsis thaliana BAC T9E19

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19404	GM_M45_B2_H06_MF	g2129618	BLASTX	200	5e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19405	GM_M45_B2_H07_MF	g2245104	BLASTX	166	4e-10	41	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
19406	GM_M45_B2_H08_MR	g507910	BLASTN	555	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19407	GM_M45_B2_H10_MF	g18559	BLASTN	736	2e-26	73	G.max gene for catalase
19408	GM_M45_B2_H10_MR	g1040717	BLASTN	410	2e-12	63	D.polychroa microsatellite sequence (clone Dp ch1 F3)
19409	GM_M45_B2_H11_MR	g2979554	BLASTX	163	1e-09	38	(AC003680) CDC4 like protein [Arabidopsis thaliana]
19410	GM_M45_B2_H12_MF	g905361	BLASTX	158	2e-14	32	(U22103) gag-protease polyprotein [Glycine max]
19411	GM_M46_A1_B04_MF	g3176798	BLASTN	398	8e-12	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
19412	GM_M46_A1_C04_MF	g4063760	BLASTX	223	9e-26	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19413	GM_M46_A1_D11_MF	g1769898	BLASTX	266	4e-24	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19414	GM_M46_A1_F03_MF	g18559	BLASTN	760	2e-27	74	G.max gene for catalase
19415	GM_M46_A1_G06_MF	g4063760	BLASTX	177	1e-25	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19416	GM_M46_A1_H05_MF	g1076313	BLASTX	194	9e-22	56	cyclin delta-3 - Arabidopsis thaliana
19417	GM_M46_A1_H08_MF	g2443320	BLASTX	198	2e-23	45	(D85597) polyprotein [Oryza australiensis]
19418	GM_M46_A2_B01_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19419	GM_M46_A2_B05_MR	g3142328	BLASTN	1325	4e-53	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19420	GM_M46_A2_B06_MR	g536873	BLASTX	313	7e-26	43	(M34549) POL3 gene product [Saccharomyces cerevisiae]
19421	GM_M46_A2_B11_MR	g1171577	BLASTX	199	6e-26	51	(X95343) hypersensitivity-related gene [Nicotiana tabacum]
19422	GM_M46_A2_C12_MF	g2104945	BLASTN	516	2e-16	79	Glycine max copia-like retrotransposon Tgmr, complete sequence
19423	GM_M46_A2_D04_MR	g1769898	BLASTX	525	9e-50	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19424	GM_M46_A2_D08_MF	g507910	BLASTN	400	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19425	GM_M46_A2_D09_MR	g3097320	BLASTN	709	5e-25	69	Glycine max gene for Bd 30K, complete cds
19426	GM_M46_A2_D10_MR	g1666236	BLASTX	211	3e-16	31	(U76261) unknown [Hordeum vulgare]
19427	GM_M46_A2_D12_MF	g3894387	BLASTX	275	5e-22	47	(AF053995) Hcr2-0B [Lycopersicon esculentum]
19428	GM_M46_A2_F02_MR	g3777527	BLASTX	704	2e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
19429	GM_M46_A2_F04_MR	g2522228	BLASTX	460	7e-43	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
19430	GM_M46_A2_F10_MF	g170605	BLASTN	471	1e-14	62	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
19431	GM_M46_A2_G01_MR	g3377848	BLASTX	108	1e-11	42	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
19432	GM_M46_A2_G02_MR	g507910	BLASTN	628	9e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19433	GM_M46_A2_G04_MR	g1840106	BLASTN	433	2e-13	63	Human fragile site locus (FRA16B) minisatellite repeat
19434	GM_M46_A2_G06_MR	g20749	BLASTN	592	1e-20	74	Pea PSU2 gene for U2 snRNA

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19435	GM_M46_A2_G07_MF	g3650039	BLASTX	260	1e-20	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
19436	GM_M46_A2_G09_MF	g2696018	BLASTN	447	4e-13	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9
19437	GM_M46_A2_G09_MR	g18559	BLASTN	808	1e-29	70	G.max gene for catalase
19438	GM_M46_A2_G12_MR	g170029	BLASTN	382	3e-10	60	Glycine max cv. Dare nodulin 26 gene fragment.
19439	GM_M46_A2_H03_MF	g4063760	BLASTX	165	3e-11	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19440	GM_M46_A2_H08_MF	g4063760	BLASTX	262	1e-20	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19441	GM_M46_A2_H08_MR	g3273825	BLASTN	352	6e-09	63	Glycine max nodule-enhanced malate dehydrogenase (Mdh) gene, promoter region
19442	GM_M46_A2_H11_MR	g3123908	BLASTX	405	5e-37	54	(AF038392) pre-mRNA splicing factor [Homo sapiens]
19443	GM_M46_B1_A02_MR	g3810596	BLASTX	208	4e-23	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19444	GM_M46_B1_A05_MR	g3097320	BLASTN	984	2e-37	81	Glycine max gene for Bd 30K, complete cds
19445	GM_M46_B1_A06_MR	g3142328	BLASTN	954	3e-36	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19446	GM_M46_B1_A09_MR	g3985958	BLASTN	447	4e-13	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]
19447	GM_M46_B1_B01_MR	g3142328	BLASTN	964	1e-36	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19448	GM_M46_B1_B05_MR	g4103987	BLASTX	265	4e-29	85	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]
19449	GM_M46_B1_B10_MR	g3779021	BLASTX	236	1e-18	39	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
19450	GM_M46_B1_C05_MR	g18559	BLASTN	1082	5e-42	77	G.max gene for catalase
19451	GM_M46_B1_D09_MR	g4063760	BLASTX	364	2e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19452	GM_M46_B1_E02_MR	g3097320	BLASTN	482	9e-15	68	Glycine max gene for Bd 30K, complete cds
19453	GM_M46_B1_E03_MR	g18559	BLASTN	999	3e-38	74	G.max gene for catalase
19454	GM_M46_B1_E04_MR	g130592	BLASTX	203	4e-28	48	ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE ; ENDONUCLEASE; REVERSE TRANSCRIPTASE] >gi 75491 pir QQCV5 hypothetical protein 5 - cauliflower mosaic virus (strains Strasbourg, CM1841 and D/H) >gi 58826 (V00141) reading frame (V) [Cauliflower mosaic virus]
19455	GM_M46_B1_E07_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19456	GM_M46_B1_E10_MR	g1706082	BLASTX	172	6e-25	68	serine carboxypeptidase II-3 precursor (CP-MII.3) gi 629787 pir S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley gi 619350 bbs 153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] gi 474392 (X78877) serine carboxylase II-3 [Hordeum vulgare]
19457	GM_M46_B1_F02_MR	g18559	BLASTN	328	2e-10	76	G.max gene for catalase
19458	GM_M46_B1_F07_MR	g4092470	BLASTN	439	9e-13	63	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
19459	GM_M46_B1_G06_MR	g3758836	BLASTN	298	4e-11	65	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
19460	GM_M46_B1_G10_MR	g2708743	BLASTX	191	8e-13	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
19461	GM_M46_B1_G12_MR	g4063760	BLASTX	298	2e-50	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19462	GM_M46_B1_H01_MR	g3097320	BLASTN	414	1e-11	76	Glycine max gene for Bd 30K, complete cds
19463	GM_M46_B1_H03_MR	g4038056	BLASTX	310	8e-26	41	(AC005897) putative transposon [Arabidopsis thaliana]
19464	GM_M46_B1_H04_MR	g507910	BLASTN	610	6e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19465	GM_M46_B1_H12_MR	g2995405	BLASTX	463	1e-43	58	(Y12432) polyprotein [Ananas comosus]
19466	GM_M46_B2_A02_MF	g170082	BLASTN	360	6e-10	83	Soybean Met-i-tRNA gene.
19467	GM_M46_B2_B01_MF	g3319366	BLASTX	137	1e-14	53	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
19468	GM_M46_B2_B02_MR	g3777527	BLASTX	693	5e-69	95	(AF053008) gag-pol polyprotein [Glycine max]
19469	GM_M46_B2_B04_MR	g3097320	BLASTN	531	5e-17	79	Glycine max gene for Bd 30K, complete cds
19470	GM_M46_B2_B05_MR	g4115365	BLASTX	120	1e-10	35	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
19471	GM_M46_B2_B08_MF	g1710663	BLASTX	152	9e-09	60	Putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) gi 1204209 gnl PID e223661 (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe]
19472	GM_M46_B2_B08_MR	g1899025	BLASTX	171	2e-11	73	(U28215) hexokinase 2 [Arabidopsis thaliana] gi 3687232 (AC005169) hexokinase [Arabidopsis thaliana]
19473	GM_M46_B2_B09_MR	g4006828	BLASTX	164	3e-10	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
19474	GM_M46_B2_B10_MR	g3355474	BLASTX	195	4e-16	68	(AC004218) unknown protein [Arabidopsis thaliana]
19475	GM_M46_B2_C02_MR	g4063770	BLASTX	87	1e-10	29	(AB004906) transposase [Ipomoea purpurea]
19476	GM_M46_B2_C03_MR	g1174162	BLASTX	287	2e-32	96	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana]
19477	GM_M46_B2_C05_MF	g905361	BLASTX	205	8e-15	35	(U22103) gag-protease polyprotein [Glycine max]
19478	GM_M46_B2_C08_MR	g3097320	BLASTN	386	2e-10	71	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19479	GM_M46_B2_C09_MR	g507910	BLASTN	394	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19480	GM_M46_B2_D01_MR	g2213582	BLASTX	172	1e-11	43	(AC000348) T7N9.2 [Arabidopsis thaliana]
19481	GM_M46_B2_D04_MF	g507910	BLASTN	566	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19482	GM_M46_B2_D04_MR	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19483	GM_M46_B2_D05_MR	g3269282	BLASTX	261	2e-20	38	(AL030978) putative protein [Arabidopsis thaliana]
19484	GM_M46_B2_D08_MF	g2961349	BLASTX	199	9e-14	45	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
19485	GM_M46_B2_D12_MR	g507910	BLASTN	340	9e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19486	GM_M46_B2_E07_MF	g3319359	BLASTN	367	1e-09	64	Arabidopsis thaliana BAC T7M24
19487	GM_M46_B2_E07_MR	g3746069	BLASTX	186	5e-15	47	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19488	GM_M46_B2_E11_MR	g508826	BLASTN	471	3e-14	63	Drosophila melanogaster Oregon-R mitochondrial A+T region.
19489	GM_M46_B2_F02_MF	g3810596	BLASTX	141	2e-13	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19490	GM_M46_B2_F02_MR	g1480927	BLASTN	1896	4e-80	94	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
19491	GM_M46_B2_F03_MR	g507910	BLASTN	404	1e-11	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19492	GM_M46_B2_F08_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19493	GM_M46_B2_G02_MF	g3935164	BLASTX	296	6e-24	44	(AC004557) F17L21.7 [Arabidopsis thaliana]
19494	GM_M46_B2_G04_MF	g310932	BLASTN	351	9e-10	75	Nicotiana tabacum ribosomal protein L17 mRNA, complete cds.
19495	GM_M46_B2_G07_MF	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19496	GM_M46_B2_G07_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19497	GM_M46_B2_G12_MR	g4092470	BLASTN	369	1e-09	64	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
19498	GM_M46_B2_H07_MF	g3777527	BLASTX	151	2e-17	44	(AF053008) gag-pol polyprotein [Glycine max]
19499	GM_M46_B2_H09_MR	g3645899	BLASTX	245	1e-26	43	(U68408) 5' end not determined experimentally [Zea mays]
19500	GM_M46_B2_H11_MF	g4063760	BLASTX	157	3e-09	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19501	GM_M46_B2_H12_MR	g3645899	BLASTX	232	2e-17	56	(U68408) 5' end not determined experimentally [Zea mays]
19502	GM_M47_A1_B08_MF	g2522230	BLASTX	189	4e-14	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19503	GM_M47_A1_B10_MF	g1946371	BLASTX	230	2e-17	48	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]
19504	GM_M47_A1_C03_MF	g2642165	BLASTX	195	4e-14	69	(AC003000) hypothetical protein [Arabidopsis thaliana]
19505	GM_M47_A1_C05_MF	g505129	BLASTN	411	1e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19506	GM_M47_A1_C08_MF	g507910	BLASTN	580	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19507	GM_M47_A1_D07_MF	g18495	BLASTN	390	1e-10	62	Cotton set 5A Lea gene for seed protein D-29
19508	GM_M47_A1_D11_MF	g2708743	BLASTX	214	3e-15	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
19509	GM_M47_A1_G04_MF	g1769898	BLASTX	449	1e-41	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19510	GM_M47_A1_G09_MF	g3097320	BLASTN	416	8e-12	71	Glycine max gene for Bd 30K, complete cds
19511	GM_M47_A1_G11_MF	g18559	BLASTN	759	2e-27	73	G.max gene for catalase
19512	GM_M47_A1_G12_MF	g4063756	BLASTN	375	7e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19513	GM_M47_A1_H07_MF	g4063760	BLASTX	238	6e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19514	GM_M47_A2_B02_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19515	GM_M47_A2_B04_MF	g77236	BLASTX	200	1e-14	39	pol polyprotein - mink cell focus-forming virus (fragment) >gi 50857 (X52622) integrase (409 AA) [Mus musculus]
19516	GM_M47_A2_B05_MF	g905361	BLASTX	354	5e-31	79	(U22103) gag-protease polyprotein [Glycine max]
19517	GM_M47_A2_B07_MR	g1931641	BLASTX	180	5e-12	72	(U95973) unknown protein [Arabidopsis thaliana]
19518	GM_M47_A2_B08_MF	g3377855	BLASTX	346	2e-34	63	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
19519	GM_M47_A2_B12_MR	g3645899	BLASTX	320	7e-28	55	(U68408) 5' end not determined experimentally [Zea mays]
19520	GM_M47_A2_C03_MF	g905361	BLASTX	628	1e-60	97	(U22103) gag-protease polyprotein [Glycine max]
19521	GM_M47_A2_C08_MR	g3426334	BLASTN	480	1e-14	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19522	GM_M47_A2_C10_MR	g2564750	BLASTN	364	2e-09	63	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
19523	GM_M47_A2_C12_MF	g114734	BLASTX	198	4e-15	92	Auxin-induced protein AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
19524	GM_M47_A2_D01_MF	g100484	BLASTX	252	1e-19	46	hypothetical protein - garden snapdragon
19525	GM_M47_A2_D02_MR	g2443320	BLASTX	208	1e-14	36	(D85597) polyprotein [Oryza australiensis]
19526	GM_M47_A2_D04_MF	g1888357	BLASTX	99	2e-12	68	(X98130) alpha-mannosidase [Arabidopsis thaliana] gi 1890154 gnl PID e307744 (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
19527	GM_M47_A2_D08_MF	g3777527	BLASTX	575	1e-53	89	(AF053008) gag-pol polyprotein [Glycine max]
19528	GM_M47_A2_D08_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19529	GM_M47_A2_D10_MR	g1167523	BLASTX	402	2e-35	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19530	GM_M47_A2_D11_MF	g421954	BLASTX	294	2e-24	45	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19531	GM_M47_A2_D11_MR	g3810596	BLASTX	301	8e-25	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19532	GM_M47_A2_F04_MF	g3810596	BLASTX	157	2e-09	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19533	GM_M47_A2_F06_MF	g905361	BLASTX	188	6e-13	34	(U22103) gag-protease polyprotein [Glycine max]
19534	GM_M47_A2_F08_MF	g3777527	BLASTX	322	1e-26	65	(AF053008) gag-pol polyprotein [Glycine max]
19535	GM_M47_A2_F10_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19536	GM_M47_A2_G02_MF	g3319362	BLASTX	161	7e-10	33	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
19537	GM_M47_A2_G03_MF	g507910	BLASTN	541	8e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19538	GM_M47_A2_G03_MR	g507910	BLASTN	536	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19539	GM_M47_A2_G06_MF	g3142328	BLASTN	990	7e-38	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19540	GM_M47_A2_G06_MR	g3645899	BLASTX	234	1e-17	43	(U68408) 5' end not determined experimentally [Zea mays]
19541	GM_M47_A2_G07_MR	g3184283	BLASTX	322	9e-29	77	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
19542	GM_M47_A2_G10_MR	g3492803	BLASTX	239	8e-18	47	(AJ002479) ENBP1 [Medicago truncatula]
19543	GM_M47_A2_G12_MF	g421954	BLASTX	193	2e-13	38	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
19544	GM_M47_A2_H05_MR	g1272349	BLASTX	262	2e-21	51	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
19545	GM_M47_A2_H10_MR	g4063760	BLASTX	409	3e-36	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19546	GM_M47_B2_A01_MF	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19547	GM_M47_B2_A02_MF	g507910	BLASTN	607	8e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19548	GM_M47_B2_A10_MR	g2065531	BLASTX	418	3e-38	69	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
19549	GM_M47_B2_B02_MF	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19550	GM_M47_B2_B02_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19551	GM_M47_B2_B06_MR	g1769898	BLASTX	308	6e-26	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19552	GM_M47_B2_B11_MF	g2462134	BLASTX	203	8e-15	39	(Y13368) reverse transcriptase [Beta vulgaris]
19553	GM_M47_B2_C01_MF	g4063760	BLASTX	183	4e-12	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19554	GM_M47_B2_C01_MR	g629693	BLASTX	418	2e-38	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19555	GM_M47_B2_C04_MR	g421955	BLASTX	323	3e-28	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19556	GM_M47_B2_C05_MR	g3097320	BLASTN	1173	4e-46	81	Glycine max gene for Bd 30K, complete cds
19557	GM_M47_B2_C12_MF	g507910	BLASTN	617	3e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19558	GM_M47_B2_C12_MR	g507910	BLASTN	616	3e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19559	GM_M47_B2_D03_MR	g2129618	BLASTX	103	8e-12	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19560	GM_M47_B2_D06_MF	g3044184	BLASTN	348	1e-08	65	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen gene, complete cds
19561	GM_M47_B2_D08_MR	g4063756	BLASTN	535	4e-17	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19562	GM_M47_B2_D10_MR	g3777527	BLASTX	591	2e-55	88	(AF053008) gag-pol polyprotein [Glycine max]
19563	GM_M47_B2_E01_MF	g18768	BLASTN	346	3e-09	74	Soybean Tgm6 transposable element 3' end
19564	GM_M47_B2_E04_MR	g439616	BLASTN	1576	2e-65	92	Soybean G protein alpha subunit mRNA, complete cds.
19565	GM_M47_B2_E05_MR	g3810595	BLASTX	159	2e-09	35	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19566	GM_M47_B2_E07_MR	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19567	GM_M47_B2_E08_MR	g3142328	BLASTN	1089	2e-42	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19568	GM_M47_B2_E09_MR	g3746069	BLASTX	208	1e-14	38	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19569	GM_M47_B2_E12_MF	g4063760	BLASTX	333	4e-28	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19570	GM_M47_B2_F02_MR	g1144549	BLASTN	254	1e-08	69	Anopheles gambiae 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
19571	GM_M47_B2_F04_MR	g13536	BLASTN	370	6e-10	63	Yeast (S. cerevisiae) mitochondrial genes for several tRNAs (Thr(2), Cys(2) and His). >gi 343930 gb K00537 YSCMTTGO1 Yeast (S.cerevisiae) mitochondrial cap-oxi1 region: Thr-2, Cys-2 and His-tRNA genes.
19572	GM_M47_B2_F08_MF	g3142328	BLASTN	689	3e-24	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19573	GM_M47_B2_F10_MF	g3777527	BLASTX	645	4e-61	96	(AF053008) gag-pol polyprotein [Glycine max]
19574	GM_M47_B2_F10_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19575	GM_M47_B2_G04_MF	g3046850	BLASTN	362	3e-09	80	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]
19576	GM_M47_B2_G05_MF	g3688173	BLASTX	211	5e-15	33	(AL031804) putative protein [Arabidopsis thaliana]
19577	GM_M47_B2_G06_MR	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19578	GM_M47_B2_G08_MR	g2564750	BLASTN	355	5e-09	59	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
19579	GM_M47_B2_H03_MR	g18559	BLASTN	360	2e-11	72	G.max gene for catalase
19580	GM_M47_B2_H08_MF	g3777527	BLASTX	631	1e-59	96	(AF053008) gag-pol polyprotein [Glycine max]
19581	GM_M47_B2_H08_MR	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19582	GM_M47_B2_H09_MF	g2522228	BLASTX	292	5e-25	75	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19583	GM_M47_B2_H10_MR	g3355474	BLASTX	160	2e-10	65	(AC004218) unknown protein [Arabidopsis thaliana]
19584	GM_M47_B2_H11_MR	g3142328	BLASTN	990	7e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19585	GM_M48_B1_C08_MF	g3777527	BLASTX	271	3e-21	68	(AF053008) gag-pol polyprotein [Glycine max]
19586	GM_M48_B1_C09_MF	g629693	BLASTX	301	5e-26	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19587	GM_M48_B1_C09_MR	g4050011	BLASTN	535	4e-17	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
19588	GM_M48_B1_C10_MR	g3171875	BLASTN	447	4e-13	63	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
19589	GM_M48_B1_D03_MR	g4063760	BLASTX	170	1e-10	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19590	GM_M48_B1_D10_MR	g1931641	BLASTX	181	4e-14	70	(U95973) unknown protein [Arabidopsis thaliana]
19591	GM_M48_B1_D12_MF	g3097320	BLASTN	963	1e-36	78	Glycine max gene for Bd 30K, complete cds
19592	GM_M48_B1_D12_MR	g2129618	BLASTX	186	2e-12	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19593	GM_M48_B1_E11_MR	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19594	GM_M48_B1_F06_MR	g4063760	BLASTX	596	3e-56	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19595	GM_M48_B1_G01_MR	g1196896	BLASTN	386	1e-10	81	Glycine max acidic ribosomal protein P0 mRNA, complete cds
19596	GM_M48_B1_G07_MF	g130582	BLASTX	284	9e-23	51	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19597	GM_M48_B1_G09_MF	g3097320	BLASTN	849	2e-31	74	Glycine max gene for Bd 30K, complete cds
19598	GM_M48_B1_G12_MF	g2588616	BLASTN	376	6e-10	64	Human BAC clone RG119P24 from 7q31, complete sequence [Homo sapiens]
19599	GM_M48_B1_G12_MR	g2244916	BLASTX	176	1e-14	31	(Z97339) hypothetical protein [Arabidopsis thaliana]
19600	GM_M48_B1_H02_MF	g322662	BLASTX	171	1e-19	73	S-receptor kinase-related protein - Chinese kale gi 17915 (Z18883) S-receptor kinase related protein [Brassica oleracea]
19601	GM_M48_B1_H04_MR	g4063760	BLASTX	565	7e-53	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19602	GM_M48_B1_H06_MR	g3097320	BLASTN	718	2e-25	75	Glycine max gene for Bd 30K, complete cds
19603	GM_M48_B1_H08_MR	g3810596	BLASTX	232	2e-17	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19604	GM_M48_B1_H09_MR	g4063760	BLASTX	482	6e-44	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19605	GM_M48_B1_H10_MF	g18559	BLASTN	924	7e-35	80	G.max gene for catalase
19606	GM_M48_B2_A01_MR	g3941524	BLASTX	213	1e-16	88	(AF062916) putative transcription factor [Arabidopsis thaliana]
19607	GM_M48_B2_A04_MR	g3860271	BLASTX	214	1e-15	31	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
19608	GM_M48_B2_A08_MF	g130582	BLASTX	152	1e-08	58	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19609	GM_M48_B2_B03_MF	g3097320	BLASTN	706	6e-25	79	Glycine max gene for Bd 30K, complete cds
19610	GM_M48_B2_B05_MF	g4063760	BLASTX	142	2e-09	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19611	GM_M48_B2_B05_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19612	GM_M48_B2_B06_MR	g507910	BLASTN	516	1e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19613	GM_M48_B2_B07_MF	g3097320	BLASTN	1067	3e-41	81	Glycine max gene for Bd 30K, complete cds
19614	GM_M48_B2_B08_MR	g1762671	BLASTN	365	1e-09	62	Elenchus japonica 18S ribosomal RNA gene, partial sequence
19615	GM_M48_B2_B09_MF	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19616	GM_M48_B2_B09_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19617	GM_M48_B2_C01_MF	g400246	BLASTX	247	3e-20	84	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) gi 169665 (M62758) S-adenosylmethionine synthetase [Petroselinum crispum]
19618	GM_M48_B2_C03_MR	g18559	BLASTN	368	1e-09	72	G.max gene for catalase
19619	GM_M48_B2_C07_MF	g3617837	BLASTX	256	6e-32	70	(AF035820) gibberellin action negative regulator SPY [Hordeum vulgare]
19620	GM_M48_B2_C10_MF	g4063760	BLASTX	557	5e-52	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19621	GM_M48_B2_D02_MR	g2522230	BLASTX	249	2e-20	34	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19622	GM_M48_B2_D05_MF	g2764526	BLASTN	489	4e-15	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19623	GM_M48_B2_D06_MR	g3695395	BLASTX	240	1e-18	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
19624	GM_M48_B2_D08_MR	g3337395	BLASTN	362	9e-10	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19625	GM_M48_B2_D12_MF	g3142328	BLASTN	1885	9e-79	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19626	GM_M48_B2_D12_MR	g2522230	BLASTX	185	8e-24	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19627	GM_M48_B2_E10_MR	g2129618	BLASTX	210	5e-15	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19628	GM_M48_B2_E12_MR	g99730	BLASTX	246	7e-29	48	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
19629	GM_M48_B2_F01_MF	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19630	GM_M48_B2_F01_MR	g507910	BLASTN	368	5e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
19631	GM_M48_B2_F08_MR	g3176795	BLASTN	400	1e-11	62	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
19632	GM_M48_B2_F10_MF	g4063760	BLASTX	427	4e-38	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19633	GM_M48_B2_F10_MR	g2995405	BLASTX	422	7e-38	54	(Y12432) polyprotein [Ananas comosus]
19634	GM_M48_B2_F11_MF	g4063760	BLASTX	160	1e-09	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19635	GM_M48_B2_G05_MR	g3176711	BLASTX	262	1e-20	48	(AC002392) bZIP-like protein [Arabidopsis thaliana]
19636	GM_M48_B2_G06_MR	g3885334	BLASTX	258	4e-22	66	(AC005623) putative argonaute protein [Arabidopsis thaliana]
19637	GM_M48_B2_G09_MF	g2586082	BLASTX	280	3e-22	50	(U72725) retrofit [Oryza longistaminata]
19638	GM_M48_B2_G10_MR	g4138290	BLASTX	200	3e-15	77	(AJ005841) thioredoxin M [Oryza sativa]
19639	GM_M48_B2_H02_MR	g3426334	BLASTN	436	1e-12	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19640	GM_M48_B2_H04_MR	g4160362	BLASTN	391	6e-12	63	Saccharomyces cerevisiae complete mitochondrial genome
19641	GM_M48_B2_H09_MF	g3645899	BLASTX	169	1e-10	36	(U68408) 5' end not determined experimentally [Zea mays]
19642	GM_M48_B2_H10_MF	g2801676	BLASTN	751	8e-28	74	Glycine max telomere-associated sequence STAS5
19643	GM_M48_B2_H10_MR	g20749	BLASTN	809	2e-30	70	Pea PSU2 gene for U2 snRNA
19644	GM_M49_A2_A04_MR	g1666236	BLASTX	172	7e-12	29	(U76261) unknown [Hordeum vulgare]
19645	GM_M49_A2_A05_MR	g18559	BLASTN	686	2e-34	79	G.max gene for catalase
19646	GM_M49_A2_A05_T7	g3777527	BLASTX	712	2e-68	95	(AF053008) gag-pol polyprotein [Glycine max]
19647	GM_M49_A2_A07_MR	g3097320	BLASTN	1317	1e-52	84	Glycine max gene for Bd 30K, complete cds
19648	GM_M49_A2_A09_MR	g3702722	BLASTN	525	1e-16	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]
19649	GM_M49_A2_A12_MR	g3036785	BLASTN	354	6e-09	62	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/l,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19650	GM_M49_A2_B01_MR	g507910	BLASTN	642	2e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19651	GM_M49_A2_B03_MR	g3319345	BLASTX	221	3e-16	38	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
19652	GM_M49_A2_B08_T7	g4063760	BLASTX	371	4e-32	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19653	GM_M49_A2_B11_T7	g3021343	BLASTN	961	2e-37	76	Cicer arietinum mRNA for hypothetical protein homologous to EST B23019
19654	GM_M49_A2_C01_MR	g2791937	BLASTX	345	1e-30	73	(AJ001200) reverse transcriptase [Alstroemeria aurea]
19655	GM_M49_A2_C04_MR	g3695395	BLASTX	128	7e-09	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
19656	GM_M49_A2_C05_MR	g2522227	BLASTX	180	5e-13	60	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19657	GM_M49_A2_C05_T7	g1769899	BLASTX	213	1e-16	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19658	GM_M49_A2_C10_T7	g1769898	BLASTX	152	4e-09	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19659	GM_M49_A2_D03_T7	g2522228	BLASTX	270	1e-22	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
19660	GM_M49_A2_D04_MR	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19661	GM_M49_A2_D04_T7	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19662	GM_M49_A2_D06_T7	g3142328	BLASTN	1229	9e-49	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19663	GM_M49_A2_D09_T7	g2511696	BLASTN	717	8e-26	83	Phaseolus vulgaris Moldavian encoding asparagine-specific endopeptidase precursor (clone cp6b)
19664	GM_M49_A2_D10_MR	g507910	BLASTN	349	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19665	GM_M49_A2_E01_T7	g2443320	BLASTX	281	2e-22	45	(D85597) polyprotein [Oryza australiensis]
19666	GM_M49_A2_E02_MR	g507910	BLASTN	471	1e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19667	GM_M49_A2_E06_MR	g507910	BLASTN	568	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19668	GM_M49_A2_E07_T7	g3097320	BLASTN	348	1e-08	64	Glycine max gene for Bd 30K, complete cds
19669	GM_M49_A2_E08_MR	g2995405	BLASTX	409	2e-36	59	(Y12432) polyprotein [Ananas comosus]
19670	GM_M49_A2_E11_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19671	GM_M49_A2_E11_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19672	GM_M49_A2_F01_MR	g3033389	BLASTX	221	3e-16	43	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
19673	GM_M49_A2_F02_MR	g2388571	BLASTX	186	1e-23	70	(AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb X98321). [Arabidopsis thaliana] gi 2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]
19674	GM_M49_A2_F02_T7	g100484	BLASTX	384	5e-34	54	hypothetical protein - garden snapdragon
19675	GM_M49_A2_F03_T7	g3142328	BLASTN	1060	4e-41	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19676	GM_M49_A2_F08_T7	g2997694	BLASTX	120	2e-11	38	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
19677	GM_M49_A2_F12_T7	g3645899	BLASTX	378	6e-33	52	(U68408) 5' end not determined experimentally [Zea mays]
19678	GM_M49_A2_G03_MR	g3142328	BLASTN	1173	3e-46	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19679	GM_M49_A2_G07_T7	g434060	BLASTN	531	4e-17	73	Soybean DNA for basic 7S globulin, complete cds
19680	GM_M49_A2_G09_T7	g2961349	BLASTX	171	7e-11	51	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
19681	GM_M49_A2_G11_T7	g2914703	BLASTX	159	3e-11	57	(AC003974) unknown protein [Arabidopsis thaliana]
19682	GM_M49_A2_G12_MR	g2760839	BLASTX	349	2e-30	62	(AC003105) putative receptor kinase [Arabidopsis thaliana]
19683	GM_M49_A2_H06_MR	g3777527	BLASTX	624	6e-59	86	(AF053008) gag-pol polyprotein [Glycine max]
19684	GM_M49_A2_H07_T7	g3367647	BLASTX	259	4e-26	56	(Y17298) enolase [Cunninghamella elegans]
19685	GM_M49_A2_H12_MR	g18695	BLASTN	500	8e-16	75	Soybean nodulin 22 gene
19686	GM_M49_B1_A04_T7	g3924609	BLASTX	301	3e-32	60	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
19687	GM_M49_B1_A05_T7	g18559	BLASTN	387	2e-10	67	G.max gene for catalase
19688	GM_M49_B1_A06_MR	g2951945	BLASTN	378	5e-10	61	Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence [Homo sapiens]
19689	GM_M49_B1_A10_MR	g507910	BLASTN	509	2e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19690	GM_M49_B1_B01_T7	g3522943	BLASTX	201	1e-22	58	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
19691	GM_M49_B1_B02_MR	g4063760	BLASTX	271	2e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19692	GM_M49_B1_B02_T7	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
19693	GM_M49_B1_B06_MR	g4063760	BLASTX	208	1e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19694	GM_M49_B1_B08_MR	g18559	BLASTN	351	7e-09	63	G.max gene for catalase
19695	GM_M49_B1_B10_MR	g18660	BLASTN	644	3e-22	76	G.max hsp22 gene for low MW heat shock protein
19696	GM_M49_B1_B12_T7	g2511697	BLASTX	292	1e-24	77	(Z99956) asparagine-specific endopeptidase precursor [Phaseolus vulgaris]
19697	GM_M49_B1_C02_T7	g2129746	BLASTX	216	5e-17	78	SUPERMAN protein - Arabidopsis thaliana gi 1079669 (U38946) SUPERMAN [Arabidopsis thaliana] gi 1585427 prf 2124420A SUPERMAN gene [Arabidopsis thaliana]
19698	GM_M49_B1_C07_MR	g3947733	BLASTX	163	2e-10	34	(AJ009719) NL25 [Solanum tuberosum]
19699	GM_M49_B1_C12_T7	g3142328	BLASTN	1171	4e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19700	GM_M49_B1_D01_MR	g3142328	BLASTN	1122	7e-44	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19701	GM_M49_B1_D02_T7	g3142328	BLASTN	1156	2e-45	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19702	GM_M49_B1_D03_T7	g1666236	BLASTX	212	2e-16	30	(U76261) unknown [Hordeum vulgare]
19703	GM_M49_B1_D06_T7	g2522228	BLASTX	499	5e-47	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
19704	GM_M49_B1_D12_MR	g3928116	BLASTN	388	2e-10	66	, complete sequence [Homo sapiens]
19705	GM_M49_B1_E03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19706	GM_M49_B1_E11_MR	g158813	BLASTN	428	4e-13	67	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
19707	GM_M49_B1_E11_T7	g3645899	BLASTX	172	8e-25	56	(U68408) 5' end not determined experimentally [Zea mays]
19708	GM_M49_B1_F01_MR	g4063756	BLASTN	428	3e-12	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19709	GM_M49_B1_F01_T7	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
19710	GM_M49_B1_F02_T7	g3142328	BLASTN	653	1e-22	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19711	GM_M49_B1_F03_T7	g1076509	BLASTX	183	7e-22	72	chloroplast RNA binding protein - kidney bean gi 558629 (X82030) chloroplast RNA binding protein [Phaseolus vulgaris]
19712	GM_M49_B1_F05_MR	g18660	BLASTN	590	9e-20	75	G.max hsp22 gene for low MW heat shock protein
19713	GM_M49_B1_F12_MR	g1769898	BLASTX	173	2e-14	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19714	GM_M49_B1_F12_T7	g2213582	BLASTX	137	9e-14	57	(AC000348) T7N9.2 [Arabidopsis thaliana]
19715	GM_M49_B1_G01_T7	g535454	BLASTX	102	1e-09	48	(U13940) cysteine proteinase [Alnus glutinosa]
19716	GM_M49_B1_G03_MR	g4063760	BLASTX	311	1e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19717	GM_M49_B1_G09_MR	g2462058	BLASTX	118	4e-11	50	(Y13389) reverse transcriptase [Antirrhinum majus]
19718	GM_M49_B1_G09_T7	g2864621	BLASTX	188	3e-13	42	hypothetical protein [Arabidopsis thaliana]
19719	GM_M49_B1_G10_T7	g3002819	BLASTX	122	9e-24	74	(AF041852) RPB140 [Chloranthus spicatus]
19720	GM_M49_B1_G12_T7	g2864621	BLASTX	165	9e-11	40	hypothetical protein [Arabidopsis thaliana]
19721	GM_M49_B1_H04_MR	g3142328	BLASTN	1050	1e-40	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19722	GM_M49_B1_H05_T7	g99755	BLASTX	375	3e-35	54	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
19723	GM_M49_B1_H09_MR	g3645899	BLASTX	168	6e-15	44	(U68408) 5' end not determined experimentally [Zea mays]
19724	GM_M50_A1_A01_MR	g18559	BLASTN	753	4e-27	76	G.max gene for catalase
19725	GM_M50_A1_A02_MR	g3649752	BLASTN	350	9e-09	66	Plasmodium falciparum MAL3P3, complete sequence [Plasmodium falciparum]
19726	GM_M50_A1_A05_T7	g3334667	BLASTX	253	3e-20	41	(Y10493) putative cytochrome P450 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19727	GM_M50_A1_A06_T7	g507910	BLASTN	365	7e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19728	GM_M50_A1_A09_MR	g4063760	BLASTX	274	5e-23	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19729	GM_M50_A1_B01_T7	g3777527	BLASTX	202	6e-14	34	(AF053008) gag-pol polyprotein [Glycine max]
19730	GM_M50_A1_B03_MR	g99922	BLASTX	496	1e-46	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19731	GM_M50_A1_B04_T7	g1167523	BLASTX	373	3e-32	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19732	GM_M50_A1_B06_MR	g2245044	BLASTX	336	5e-28	59	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
19733	GM_M50_A1_B10_MR	g4038056	BLASTX	286	3e-23	39	(AC005897) putative transposon [Arabidopsis thaliana]
19734	GM_M50_A1_B10_T7	g3097320	BLASTN	1186	1e-46	78	Glycine max gene for Bd 30K, complete cds
19735	GM_M50_A1_B12_T7	g507910	BLASTN	581	1e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19736	GM_M50_A1_C04_T7	g3097320	BLASTN	784	2e-28	73	Glycine max gene for Bd 30K, complete cds
19737	GM_M50_A1_C06_T7	g1769898	BLASTX	395	1e-35	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19738	GM_M50_A1_D04_MR	g18559	BLASTN	588	5e-25	80	G.max gene for catalase
19739	GM_M50_A1_E03_T7	g507910	BLASTN	447	1e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19740	GM_M50_A1_E08_T7	g3386611	BLASTX	139	1e-13	53	(AC004665) unknown protein [Arabidopsis thaliana]
19741	GM_M50_A1_F01_T7	g3645899	BLASTX	208	7e-15	38	(U68408) 5' end not determined experimentally [Zea mays]
19742	GM_M50_A1_F05_MR	g4038056	BLASTX	217	7e-16	36	(AC005897) putative transposon [Arabidopsis thaliana]
19743	GM_M50_A1_F09_MR	g507910	BLASTN	358	1e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19744	GM_M50_A1_F10_MR	g3777527	BLASTX	204	4e-14	42	(AF053008) gag-pol polyprotein [Glycine max]
19745	GM_M50_A1_G01_T7	g3142328	BLASTN	1281	4e-51	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19746	GM_M50_A1_G03_MR	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19747	GM_M50_A1_G06_MR	g3645899	BLASTX	154	1e-20	44	(U68408) 5' end not determined experimentally [Zea mays]
19748	GM_M50_A1_G08_MR	g2129618	BLASTX	176	2e-11	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19749	GM_M50_A1_G08_T7	g629693	BLASTX	149	3e-09	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19750	GM_M50_A1_G09_T7	g2462058	BLASTX	259	1e-21	51	(Y13389) reverse transcriptase [Antirrhinum majus]
19751	GM_M50_A1_G11_T7	g1142701	BLASTN	1422	6e-58	87	Glycine max satellite STR120-A.3.
19752	GM_M50_A1_G12_MR	g99922	BLASTX	243	7e-20	58	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19753	GM_M50_A1_H01_T7	g1167523	BLASTX	192	6e-13	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19754	GM_M50_A1_H05_MR	g507910	BLASTN	490	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19755	GM_M50_A1_H09_MR	g507910	BLASTN	601	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19756	GM_M50_A1_H09_T7	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19757	GM_M50_A1_H10_MR	g505129	BLASTN	352	6e-09	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19758	GM_M50_A1_H12_T7	g18559	BLASTN	895	2e-33	75	G.max gene for catalase
19759	GM_M50_A2_A01_MR	g3097320	BLASTN	458	1e-13	71	Glycine max gene for Bd 30K, complete cds
19760	GM_M50_A2_A08_MR	g3097320	BLASTN	381	3e-10	72	Glycine max gene for Bd 30K, complete cds
19761	GM_M50_A2_A10_T7	g905361	BLASTX	149	9e-09	83	(U22103) gag-protease polyprotein [Glycine max]
19762	GM_M50_A2_B05_T7	g531389	BLASTX	373	3e-32	47	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
19763	GM_M50_A2_B06_MR	g1167523	BLASTX	105	3e-12	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19764	GM_M50_A2_C12_T7	g130582	BLASTX	267	6e-21	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19765	GM_M50_A2_D03_T7	g1769897	BLASTX	156	1e-09	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19766	GM_M50_A2_D07_MR	g4038056	BLASTX	185	3e-14	38	(AC005897) putative transposon [Arabidopsis thaliana]
19767	GM_M50_A2_D12_MR	g2262107	BLASTX	156	2e-17	96	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
19768	GM_M50_A2_E11_T7	g3789709	BLASTN	374	7e-10	65	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
19769	GM_M50_A2_E12_T7	g3777527	BLASTX	257	9e-20	40	(AF053008) gag-pol polyprotein [Glycine max]
19770	GM_M50_A2_F01_T7	g100484	BLASTX	395	3e-35	55	hypothetical protein - garden snapdragon
19771	GM_M50_A2_F04_T7	g2244915	BLASTX	239	3e-18	39	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
19772	GM_M50_A2_F06_T7	g3777526	BLASTN	607	2e-20	70	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
19773	GM_M50_A2_F12_MR	g2244915	BLASTX	183	3e-12	33	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
19774	GM_M50_A2_G01_MR	g629693	BLASTX	161	3e-16	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19775	GM_M50_A2_G02_MR	g2443320	BLASTX	153	9e-09	38	(D85597) polyprotein [Oryza australiensis]
19776	GM_M50_A2_G04_MR	g2995405	BLASTX	169	1e-10	40	(Y12432) polyprotein [Ananas comosus]
19777	GM_M50_A2_G04_T7	g3810596	BLASTX	293	6e-24	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19778	GM_M50_A2_G05_MR	g148071	BLASTX	148	8e-10	44	(M54881) thioredoxin [Escherichia coli]
19779	GM_M50_A2_G07_MR	g507910	BLASTN	498	7e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19780	GM_M50_A2_G08_MR	g1217967	BLASTX	184	2e-17	52	(X96431) high affinity sulphate transporter [Hordeum vulgare]
19781	GM_M50_A2_G12_MR	g1769898	BLASTX	474	2e-44	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19782	GM_M50_A2_G12_T7	g100488	BLASTX	102	9e-10	50	TNP2 protein - garden snapdragon
19783	GM_M50_A2_H06_T7	g2462936	BLASTX	351	3e-31	53	(Y12321) open reading frame 2 [Brassica oleracea]
19784	GM_M50_A2_H07_T7	g18559	BLASTN	817	5e-30	72	G.max gene for catalase
19785	GM_M50_A2_H09_MR	g3426334	BLASTN	466	4e-14	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19786	GM_M50_B1_A03_MR	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19787	GM_M50_B1_A03_T7	g507910	BLASTN	439	3e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19788	GM_M50_B1_A07_MR	g507910	BLASTN	360	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19789	GM_M50_B1_A07_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19790	GM_M50_B1_A08_MR	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19791	GM_M50_B1_A08_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19792	GM_M50_B1_A10_MR	g2129613	BLASTX	146	4e-10	58	homeotic protein BEL1 - Arabidopsis thaliana gi 1122533 (U39944) BELL1 [Arabidopsis thaliana]
19793	GM_M50_B1_A10_T7	g4115365	BLASTX	170	1e-10	36	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
19794	GM_M50_B1_B01_T7	g3142328	BLASTN	1482	3e-60	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19795	GM_M50_B1_B04_MR	g4140712	BLASTX	451	7e-45	55	(AF110183) putative integrase [Oryza sativa]
19796	GM_M50_B1_B05_T7	g2995405	BLASTX	396	4e-35	54	(Y12432) polyprotein [Ananas comosus]
19797	GM_M50_B1_B07_MR	g18559	BLASTN	983	2e-37	74	G.max gene for catalase
19798	GM_M50_B1_B08_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19799	GM_M50_B1_D04_T7	g2429543	BLASTX	188	1e-12	48	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
19800	GM_M50_B1_D08_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19801	GM_M50_B1_D08_T7	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19802	GM_M50_B1_E02_MR	g2335097	BLASTX	167	2e-10	36	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
19803	GM_M50_B1_E03_MR	g507910	BLASTN	459	4e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19804	GM_M50_B1_E06_T7	g505129	BLASTN	357	3e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19805	GM_M50_B1_E07_MR	g3777527	BLASTX	514	3e-47	85	(AF053008) gag-pol polyprotein [Glycine max]

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19806	GM_M50_B1_E10_T7	g3386534	BLASTX	351	2e-33	57	(AF078934) mariner transposase [Glycine max]
19807	GM_M50_B1_E11_MR	g507910	BLASTN	371	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19808	GM_M50_B1_E11_T7	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19809	GM_M50_B1_E12_MR	g2245113	BLASTX	152	3e-09	71	(Z97343) glycerol-3-phosphate permease homolog [Arabidopsis thaliana]
19810	GM_M50_B1_E12_T7	g2245126	BLASTN	371	1e-09	65	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.
19811	GM_M50_B1_F01_MR	g4063760	BLASTX	255	9e-20	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19812	GM_M50_B1_F01_T7	g2995405	BLASTX	253	9e-20	44	(Y12432) polyprotein [Ananas comosus]
19813	GM_M50_B1_F08_MR	g180902	BLASTN	506	8e-17	63	Human variable number tandem repeat (VNTR) region, allele 14R2 3' to collagen type II (COL2A1) gene.
19814	GM_M50_B1_F09_T7	g2462134	BLASTX	247	1e-19	37	(Y13368) reverse transcriptase [Beta vulgaris]
19815	GM_M50_B1_F10_MR	g507910	BLASTN	647	1e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19816	GM_M50_B1_F10_T7	g507910	BLASTN	477	6e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19817	GM_M50_B1_F11_MR	g905361	BLASTX	220	2e-16	35	(U22103) gag-protease polyprotein [Glycine max]
19818	GM_M50_B1_F12_MR	g507910	BLASTN	588	6e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19819	GM_M50_B1_G06_T7	g3283026	BLASTX	266	3e-21	41	putative transposase [Arabidopsis thaliana]
19820	GM_M50_B1_G07_T7	g3142379	BLASTX	284	6e-24	61	(AF053008) envelope-like [Glycine max]
19821	GM_M50_B1_G08_MR	g4153865	BLASTN	368	1e-09	62	Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence [Homo sapiens]
19822	GM_M50_B1_H02_MR	g2443320	BLASTX	170	1e-10	40	(D85597) polyprotein [Oryza australiensis]
19823	GM_M50_B1_H03_T7	g905361	BLASTX	439	2e-40	96	(U22103) gag-protease polyprotein [Glycine max]
19824	GM_M50_B1_H04_MR	g18559	BLASTN	399	5e-11	69	G.max gene for catalase
19825	GM_M50_B1_H05_T7	g3142328	BLASTN	752	4e-27	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19826	GM_M50_B1_H09_MR	g4063756	BLASTN	548	1e-17	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19827	GM_M50_B1_H10_T7	g3142328	BLASTN	981	2e-37	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19828	GM_M50_B2_A01_T7	g3645899	BLASTX	347	1e-29	50	(U68408) 5' end not determined experimentally [Zea mays]
19829	GM_M50_B2_A02_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19830	GM_M50_B2_A03_T7	g3176693	BLASTN	377	5e-10	63	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]
19831	GM_M50_B2_A07_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19832	GM_M50_B2_A09_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19833	GM_M50_B2_A11_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19834	GM_M50_B2_B04_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19835	GM_M50_B2_B06_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19836	GM_M50_B2_B11_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19837	GM_M50_B2_B12_T7	g4049353	BLASTX	141	4e-17	57	(AL034567) putative protein [Arabidopsis thaliana]
19838	GM_M50_B2_C01_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19839	GM_M50_B2_C03_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19840	GM_M50_B2_C05_T7	g18695	BLASTN	348	8e-09	70	Soybean nodulin 22 gene
19841	GM_M50_B2_C08_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19842	GM_M50_B2_C08_T7	g18559	BLASTN	656	1e-22	71	G.max gene for catalase
19843	GM_M50_B2_C10_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19844	GM_M50_B2_D02_T7	g507910	BLASTN	477	6e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19845	GM_M50_B2_D03_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19846	GM_M50_B2_D03_T7	g4092471	BLASTN	413	1e-11	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
19847	GM_M50_B2_D04_T7	g1769897	BLASTX	242	9e-37	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19848	GM_M50_B2_D05_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19849	GM_M50_B2_D07_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19850	GM_M50_B2_D11_T7	g169974	BLASTN	415	8e-12	64	Glycine max vspA gene, complete cds.
19851	GM_M50_B2_E01_T7	g2464905	BLASTX	225	6e-18	58	(Z99708) minor allergen [Arabidopsis thaliana]
19852	GM_M50_B2_E02_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19853	GM_M50_B2_E07_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19854	GM_M50_B2_E09_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19855	GM_M50_B2_E11_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19856	GM_M50_B2_E11_T7	g2341043	BLASTX	208	5e-24	74	(AC000104) Strong similarity to Arabidopsis REV3C (gb X62461). [Arabidopsis thaliana]
19857	GM_M50_B2_F01_T7	g2995405	BLASTX	361	3e-31	50	(Y12432) polyprotein [Ananas comosus]
19858	GM_M50_B2_F04_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19859	GM_M50_B2_F06_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19860	GM_M50_B2_F10_T7	g507910	BLASTN	455	6e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19861	GM_M50_B2_F11_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19862	GM_M50_B2_G01_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19863	GM_M50_B2_G03_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19864	GM_M50_B2_G08_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19865	GM_M50_B2_G10_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19866	GM_M50_B2_G12_T7	g2058281	BLASTN	395	4e-11	75	A.thaliana mRNA for AtRanBP1a protein
19867	GM_M50_B2_H03_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19868	GM_M50_B2_H05_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19869	GM_M50_B2_H07_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19870	GM_M50_B2_H12_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19871	SB_M01_A1_A12_MF	g1769898	BLASTX	111	4e-13	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19872	SB_M01_A1_E10_MF	g3142328	BLASTN	919	1e-34	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19873	SB_M01_A1_E12_MF	g507910	BLASTN	397	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19874	SB_M08_A1_A12_MF	g4049332	BLASTN	471	3e-14	75	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
19875	SB_M08_A1_B03_MR	g3142328	BLASTN	445	4e-13	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19876	SB_M08_A1_B10_MR	g3777527	BLASTX	323	3e-35	87	(AF053008) gag-pol polyprotein [Glycine max]
19877	SB_M08_A1_B12_MF	g4092471	BLASTN	424	4e-12	72	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
19878	SB_M08_A1_C08_MR	g2828327	BLASTN	416	1e-12	66	Lycopersicon esculentum cv Red River unknown sequence PCR random amplified RAPD band 10
19879	SB_M08_A1_D04_MR	g507910	BLASTN	524	5e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19880	SB_M08_A1_D07_MF	g2464905	BLASTX	234	6e-19	58	(Z99708) minor allergen [Arabidopsis thaliana]
19881	SB_M08_A1_D12_MF	g2642431	BLASTX	192	7e-13	29	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
19882	SB_M08_A1_E06_MF	g1769898	BLASTX	241	1e-18	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19883	SB_M08_A1_E06_MR	g2522227	BLASTX	234	6e-19	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19884	SB_M08_A1_E12_MF	g18559	BLASTN	565	1e-18	69	G.max gene for catalase
19885	SB_M08_A1_F12_MR	g1575536	BLASTX	163	6e-10	68	(U65533) regulator of nonsense transcript stability [Homo sapiens]
19886	SB_M08_A1_G04_MF	g4063760	BLASTX	239	4e-18	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19887	SB_M08_A1_G04_MR	g507910	BLASTN	399	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19888	SB_M08_A1_G10_MF	g2996647	BLASTN	377	5e-10	61	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
19889	SB_M08_A1_G12_MR	g3687234	BLASTX	228	7e-17	58	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
19890	SB_M08_A1_H08_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19891	SB_M08_A1_H11_MR	g18559	BLASTN	750	6e-27	75	G.max gene for catalase
19892	SB_M08_A1_H12_MR	g4063760	BLASTX	180	9e-12	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19893	SB_M08_A2_A08_MF	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19894	SB_M08_A2_A10_MF	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19895	SB_M08_A2_B01_MF	g2864621	BLASTX	137	5e-17	39	hypothetical protein [Arabidopsis thaliana]
19896	SB_M08_A2_B08_MF	g3777527	BLASTX	641	9e-61	92	(AF053008) gag-pol polyprotein [Glycine max]
19897	SB_M08_A2_B10_MF	g18559	BLASTN	897	1e-33	78	G.max gene for catalase
19898	SB_M08_A2_B11_MF	g18559	BLASTN	943	1e-35	76	G.max gene for catalase
19899	SB_M08_A2_C07_MF	g3337395	BLASTN	420	6e-12	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
19900	SB_M08_A2_E02_MF	g407858	BLASTN	374	6e-10	65	P.falciparum (FCR3) cpn60 gene.
19901	SB_M08_A2_E11_MF	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19902	SB_M08_A2_F03_MF	g2443320	BLASTX	145	3e-12	51	(D85597) polyprotein [Oryza australiensis]
19903	SB_M08_A2_G02_MF	g4063756	BLASTN	470	3e-14	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19904	SB_M08_A2_G08_MF	g3426334	BLASTN	352	6e-09	59	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19905	SB_M08_A2_H05_MF	g3600062	BLASTN	367	1e-09	61	Arabidopsis thaliana BAC T25C13
19906	SB_M08_A2_H08_MF	g507910	BLASTN	651	8e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19907	SB_M08_B1_A04_MF	g507910	BLASTN	755	2e-27	92	Glycine max BSR-101 satellite SB92 genomic sequence.
19908	SB_M08_B1_A06_MF	g3702339	BLASTX	219	4e-17	54	(AC005397) unknown protein [Arabidopsis thaliana]
19909	SB_M08_B1_A11_MF	g3142379	BLASTX	216	4e-18	47	(AF053008) envelope-like [Glycine max]
19910	SB_M08_B1_B01_MF	g505129	BLASTN	358	3e-09	67	Winged bean DNA. Kunitz chymotrypsin inhibitor-3 gene homologous region
19911	SB_M08_B1_B09_MF	g2864621	BLASTX	95	7e-09	36	hypothetical protein [Arabidopsis thaliana]
19912	SB_M08_B1_C06_MF	g1142699	BLASTN	1107	1e-43	81	Glycine max satellite STR120-A 1
19913	SB_M08_B1_C11_MF	g1666236	BLASTX	151	2e-09	27	(U76261) unknown [Hordeum vulgare]
19914	SB_M08_B1_D12_MF	g1431738	BLASTN	727	4e-26	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
19915	SB_M08_B1_E04_MF	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19916	SB_M08_B1_F04_MF	g4063760	BLASTX	371	4e-32	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19917	SB_M08_B1_F12_MF	g905361	BLASTX	712	1e-69	95	(U22103) gag-protease polyprotein [Glycine max]
19918	SB_M08_B1_G01_MF	g1769897	BLASTX	225	4e-17	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19919	SB_M08_B1_G03_MF	g3777526	BLASTN	1328	4e-53	88	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
19920	SB_M08_B1_H05_MF	g632064	BLASTX	170	4e-12	37	hypothetical protein - wheat gi 530779 (X79130) Triticum sp. (pAWJL3) leucine rich repeat region mRNA [Triticum aestivum]
19921	SB_M08_B1_H07_MF	g3269286	BLASTX	154	1e-09	55	(AI.030978) putative protein [Arabidopsis thaliana]
19922	SB_M08_B1_H10_MF	g3645899	BLASTX	211	4e-15	52	(U68408) 5' end not determined experimentally [Zea mays]
19923	SB_M08_B2_A07_MR	g4063756	BLASTN	375	7e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19924	SB_M08_B2_A09_MR	g3142328	BLASTN	421	5e-12	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19925	SB_M08_B2_B08_MR	g3142328	BLASTN	1829	3e-76	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19926	SB_M08_B2_C09_MR	g2960057	BLASTN	380	4e-10	66	Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19927	SB_M08_B2_D08_MR	g2252828	BLASTX	193	1e-14	37	(AF013293) No definition line found [Arabidopsis thaliana]
19928	SB_M08_B2_D10_MR	g2462058	BLASTX	238	2e-21	41	(Y13389) reverse transcriptase [Antirrhinum majus]
19929	SB_M08_B2_E08_MR	g4165018	BLASTX	155	1e-13	66	(D89053) Acyl-CoA synthetase 3 [Homo sapiens]
19930	SB_M08_B2_F07_MR	g2979574	BLASTN	356	5e-09	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
19931	SB_M08_B2_G10_MR	g3845197	BLASTN	371	1e-09	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
19932	SB_M08_B2_H06_MR	g1091678	BLASTX	266	3e-21	37	activator-like transposable element [Pennisetum glaucum]
19933	SB_M08_B2_H08_MR	g3377848	BLASTX	264	6e-22	47	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
19934	SB_M09_A1_A04_MR	g629693	BLASTX	458	1e-42	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19935	SB_M09_A1_A05_MR	g507910	BLASTN	614	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19936	SB_M09_A1_A05_T7	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19937	SB_M09_A1_A06_MR	g4063760	BLASTX	171	1e-13	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19938	SB_M09_A1_A08_MR	g2522228	BLASTX	516	8e-49	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
19939	SB_M09_A1_A09_T7	g3777527	BLASTX	623	8e-59	86	(AF053008) gag-pol polyprotein [Glycine max]
19940	SB_M09_A1_A10_MR	g507910	BLASTN	605	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19941	SB_M09_A1_A10_T7	g4063760	BLASTX	226	1e-16	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19942	SB_M09_A1_A11_T7	g4063760	BLASTX	191	7e-13	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19943	SB_M09_A1_B06_T7	g4063760	BLASTX	366	1e-31	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19944	SB_M09_A1_B07_MR	g3264544	BLASTN	459	1e-13	63	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
19945	SB_M09_A1_B08_T7	g100484	BLASTX	314	2e-26	50	hypothetical protein - garden snapdragon
19946	SB_M09_A1_C04_MR	g3645899	BLASTX	271	2e-21	56	(U68408) 5' end not determined experimentally [Zea mays]
19947	SB_M09_A1_C06_T7	g2160782	BLASTX	500	4e-47	62	(AF001505) putative ammonium transporter OsAMT1p [Oryza sativa]
19948	SB_M09_A1_C07_T7	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19949	SB_M09_A1_C09_MR	g2924341	BLASTN	497	1e-15	63	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes
19950	SB_M09_A1_C11_MR	g4063760	BLASTX	175	3e-11	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19951	SB_M09_A1_C11_T7	g3869065	BLASTN	400	5e-11	63	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
19952	SB_M09_A1_D02_MR	g507910	BLASTN	381	1e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19953	SB_M09_A1_D04_T7	g18559	BLASTN	944	9e-36	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19954	SB_M09_A1_D07_MR	g3319372	BLASTX	274	9e-22	43	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
19955	SB_M09_A1_D07_T7	g2522227	BLASTX	206	5e-16	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19956	SB_M09_A1_D10_MR	g100484	BLASTX	329	5e-28	48	hypothetical protein - garden snapdragon
19957	SB_M09_A1_E03_MR	g2129618	BLASTX	168	1e-10	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19958	SB_M09_A1_E07_MF	g3777527	BLASTX	692	3e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
19959	SB_M09_A1_E08_MF	g3097320	BLASTN	634	1e-21	73	Glycine max gene for Bd 30K, complete cds
19960	SB_M09_A1_F03_MR	g3319366	BLASTX	122	6e-10	53	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
19961	SB_M09_A1_F06_MF	g507910	BLASTN	373	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19962	SB_M09_A1_F06_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19963	SB_M09_A1_F07_MF	g905361	BLASTX	654	2e-63	96	(U22103) gag-protease polyprotein [Glycine max]
19964	SB_M09_A1_F08_MR	g2522228	BLASTX	328	7e-29	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
19965	SB_M09_A1_F10_MR	g18559	BLASTN	387	2e-10	76	G.max gene for catalase
19966	SB_M09_A1_G01_MR	g3264544	BLASTN	471	3e-14	67	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
19967	SB_M09_A1_G04_MR	g4115365	BLASTX	298	3e-24	61	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
19968	SB_M09_A1_G06_MF	g3777527	BLASTX	310	2e-25	45	(AF053008) gag-pol polyprotein [Glycine max]
19969	SB_M09_A1_G08_MR	g4063760	BLASTX	450	1e-40	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19970	SB_M09_A1_G11_MR	g905361	BLASTX	583	7e-56	84	(U22103) gag-protease polyprotein [Glycine max]
19971	SB_M09_A1_G12_MF	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
19972	SB_M09_A1_H03_MF	g1658457	BLASTX	416	3e-38	78	(U75248) reverse transcriptase [Gossypium barbadense]
19973	SB_M09_A1_H05_MR	g3426334	BLASTN	488	4e-15	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19974	SB_M09_A1_H07_MR	g4063760	BLASTX	174	8e-14	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19975	SB_M09_A1_H10_MR	g1666236	BLASTX	203	2e-15	31	(U76261) unknown [Hordeum vulgare]
19976	SB_M09_A1_H12_MR	g3810596	BLASTX	152	9e-16	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19977	SB_M09_A2_A01_MR	g3645899	BLASTX	159	1e-09	49	(U68408) 5' end not determined experimentally [Zea mays]
19978	SB_M09_A2_A03_MR	g3645899	BLASTX	163	5e-10	48	(U68408) 5' end not determined experimentally [Zea mays]
19979	SB_M09_A2_A04_MR	g2342681	BLASTX	384	9e-34	59	(AC000106) F7G19.9 [Arabidopsis thaliana]
19980	SB_M09_A2_A05_T7	g18559	BLASTN	805	2e-29	73	G.max gene for catalase
19981	SB_M09_A2_A07_MR	g1732513	BLASTX	192	2e-14	70	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	% Ident	Description
19982	SB_M09_A2_A07_T7	g18559	BLASTN	896	1e-33	75	G.max gene for catalase
19983	SB_M09_A2_B01_T7	g4063760	BLASTX	178	1e-11	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19984	SB_M09_A2_B03_MR	g3080376	BLASTX	171	4e-11	41	(AL022580) putative protein [Arabidopsis thaliana]
19985	SB_M09_A2_B07_MR	g100484	BLASTX	354	9e-31	51	hypothetical protein - garden snapdragon
19986	SB_M09_A2_B07_T7	g18559	BLASTN	590	1e-19	78	G.max gene for catalase
19987	SB_M09_A2_C08_T7	g3097320	BLASTN	710	4e-25	77	Glycine max gene for Bd 30K, complete cds
19988	SB_M09_A2_D02_T7	g4063760	BLASTX	173	5e-11	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19989	SB_M09_A2_D12_MR	g4063760	BLASTX	257	6e-20	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19990	SB_M09_A2_E05_MR	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19991	SB_M09_A2_E07_MR	g3080353	BLASTX	165	3e-11	66	(AL022580) cytochrome P450 [Arabidopsis thaliana]
19992	SB_M09_A2_F01_MF	g2764526	BLASTN	380	4e-10	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19993	SB_M09_A2_F05_MR	g1769898	BLASTX	311	3e-26	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19994	SB_M09_A2_F07_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19995	SB_M09_A2_G07_MF	g4063760	BLASTX	175	3e-11	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19996	SB_M09_A2_G07_MR	g3777527	BLASTX	200	3e-21	64	(AF053008) gag-pol polyprotein [Glycine max]
19997	SB_M09_A2_G10_MR	g905361	BLASTX	337	4e-29	78	(U22103) gag-protease polyprotein [Glycine max]
19998	SB_M09_A2_H01_MF	g3452231	BLASTN	353	6e-09	65	Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds
19999	SB_M09_A2_H06_MF	g507910	BLASTN	483	3e-15	80	Glycine max BSR-101 satellite SB92 genomic sequence.
20000	SB_M09_A2_H07_MR	g3980397	BLASTX	156	5e-10	53	(AC004561) putative protein phosphatase 2C [Arabidopsis thaliana]
20001	SB_M09_B2_A04_MF	g4063760	BLASTX	260	3e-20	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
20002	SB_M09_B2_A05_MF	g3953462	BLASTX	144	7e-09	27	(AC002328) F20N2.7 [Arabidopsis thaliana]
20003	SB_M09_B2_A09_MF	g3142328	BLASTN	951	4e-36	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20004	SB_M09_B2_A10_MF	g505129	BLASTN	391	1e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
20005	SB_M09_B2_A10_MR	g3142328	BLASTN	686	4e-24	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20006	SB_M09_B2_A11_MF	g3077640	BLASTX	324	2e-28	59	(AJ223151) O-methyltransferase [Prunus dulcis]
20007	SB_M09_B2_A12_MF	g2852684	BLASTX	220	3e-16	40	(AF017751) resistance protein candidate [Lactuca sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
20008	SB_M09_B2_A12_MR	g13767	BLASTN	339	3e-09	59	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
20009	SB_M09_B2_B04_MF	g1707007	BLASTX	153	4e-09	33	(U78721) hypothetical protein [Arabidopsis thaliana]
20010	SB_M09_B2_B04_MR	g905361	BLASTX	215	7e-16	31	(U22103) gag-protease polyprotein [Glycine max]
20011	SB_M09_B2_B07_MF	g2129618	BLASTX	225	1e-16	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
20012	SB_M09_B2_B08_MF	g1769898	BLASTX	179	5e-12	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
20013	SB_M09_B2_C03_MR	g2497540	BLASTX	333	2e-29	55	PYRUVATE KINASE, CHLOROPLAST ISOZYME G
20014	SB_M09_B2_C06_MR	g3142328	BLASTN	827	2e-30	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20015	SB_M09_B2_C07_MR	g507910	BLASTN	655	6e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
20016	SB_M09_B2_C08_MF	g3122625	BLASTX	211	2e-26	89	PROBABLE 26S PROTEASE REGULATORY SUBUNIT S10B gi 2394434 (AF024493) strong similarity to the AAA family of ATPases [Caenorhabditis elegans]
20017	SB_M09_B2_C09_MR	g13096	BLASTN	369	1e-09	65	Leishmania tarentolae maxicircle DNA fragment
20018	SB_M09_B2_D02_MF	g1142703	BLASTN	288	4e-12	75	Glycine max satellite STR120-B.1.
20019	SB_M09_B2_D03_MR	g2541876	BLASTX	228	2e-17	43	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
20020	SB_M09_B2_D07_MF	g3777527	BLASTX	598	4e-56	86	(AF053008) gag-pol polyprotein [Glycine max]
20021	SB_M09_B2_D07_MR	g576756	BLASTN	235	3e-11	62	Myrmecia pilosula HI87-133 mitochondrion cytochrome b gene, partial cds.
20022	SB_M09_B2_D12_MR	g100484	BLASTX	150	3e-18	42	hypothetical protein - garden snapdragon
20023	SB_M09_B2_E03_MR	g2443320	BLASTX	117	9e-12	42	(D85597) polyprotein [Oryza australiensis]
20024	SB_M09_B2_E04_MF	g100484	BLASTX	348	4e-30	53	hypothetical protein - garden snapdragon
20025	SB_M09_B2_E06_MR	g100484	BLASTX	332	2e-28	59	hypothetical protein - garden snapdragon
20026	SB_M09_B2_E07_MF	g1272349	BLASTX	238	9e-19	47	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
20027	SB_M09_B2_E07_MR	g3777527	BLASTX	250	5e-19	42	(AF053008) gag-pol polyprotein [Glycine max]
20028	SB_M09_B2_E08_MR	g100484	BLASTX	335	1e-28	60	hypothetical protein - garden snapdragon
20029	SB_M09_B2_E12_MF	g4006831	BLASTX	104	6e-12	38	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
20030	SB_M09_B2_F03_MF	g507910	BLASTN	339	1e-08	68	Glycine max BSR-101 satellite SB92 genomic sequence.
20031	SB_M09_B2_F04_MF	g2129618	BLASTX	172	5e-11	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
20032	SB_M09_B2_F07_MR	g2982253	BLASTX	201	2e-15	78	(AF051209) CROC-1-like protein [Picea mariana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
20033	SB_M09_B2_F11_MR	g3068704	BLASTX	304	4e-25	44	(AF049236) unknown [Arabidopsis thaliana]
20034	SB_M09_B2_G01_MR	g2522228	BLASTX	339	4e-30	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
20035	SB_M09_B2_G03_MF	g2995405	BLASTX	334	2e-28	58	(Y12432) polyprotein [Ananas comosus]
20036	SB_M09_B2_G03_MR	g2129618	BLASTX	173	4e-11	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
20037	SB_M09_B2_G04_MR	g2995405	BLASTX	397	6e-37	65	(Y12432) polyprotein [Ananas comosus]
20038	SB_M09_B2_G08_MR	g2244802	BLASTX	205	1e-15	31	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
20039	SB_M09_B2_H01_MF	g603866	BLASTN	394	6e-11	71	N.tabacum mRNA for L-Glutamate:tRNA-Glu ligase
20040	SB_M09_B2_H04_MF	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
20041	SB_M09_B2_H04_MR	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20042	SB_M09_B2_H08_MR	g1313966	BLASTX	131	3e-11	44	(Z72425) major allergen Mal d 1 [Malus domestica]
20043	SB_M09_B2_H12_MR	g3645899	BLASTX	217	1e-15	41	(U68408) 5' end not determined experimentally [Zea mays]
20044	SB_M11_B1_A10_MF	g1167523	BLASTX	261	3e-20	49	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
20045	SB_M11_B1_B04_MF	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20046	SB_M11_B1_C08_MF	g507910	BLASTN	362	9e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
20047	SB_M11_B1_D06_MF	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
20048	SB_M11_B1_D07_MF	g1769899	BLASTX	157	9e-11	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
20049	SB_M11_B1_E06_MF	g3426334	BLASTN	585	2e-19	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
20050	SB_M11_B1_F11_MF	g2586082	BLASTX	218	4e-21	56	(U72725) retrofit [Oryza longistaminata]
20051	SB_M11_B2_C03_MR	g2462058	BLASTX	213	1e-16	55	(Y13389) reverse transcriptase [Antirrhinum majus]
20052	SB_M11_B2_C12_MR	g2288997	BLASTX	229	2e-21	77	(AC002335) hypothetical protein [Arabidopsis thaliana]
20053	SB_M11_B2_D01_MR	g3142328	BLASTN	1026	2e-39	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20054	SB_M11_B2_D07_MR	g507910	BLASTN	461	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
20055	SB_M11_B2_E02_MR	g905361	BLASTX	156	2e-09	70	(U22103) gag-protease polyprotein [Glycine max]
20056	SB_M11_B2_E04_MR	g507910	BLASTN	411	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
20057	SB_M11_B2_E10_MR	g3142328	BLASTN	530	5e-17	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20058	SB_M11_B2_F04_MR	g3810596	BLASTX	220	4e-16	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
20059	SB_M11_B2_F06_MR	g2995405	BLASTX	174	2e-26	64	(Y12432) polyprotein [Ananas comosus]
20060	SB_M11_B2_H02_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20061	SB_M11_B2_H03_MR	g2623990	BLASTX	121	2e-11	64	(Y13156) ferrochelatase [Arabidopsis thaliana]
20062	SB_M11_B2_H09_MR	g2344894	BLASTX	227	7e-18	48	(AC002388) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
20063	SB_M11_B2_H10_MR	g507910	BLASTN	405	1e-11	83	Glycine max BSR-101 satellite SB92 genomic sequence.
20064	SB_M11_B2_H12_MR	g2921625	BLASTN	544	1e-17	73	Lupinus luteus leghemoglobin (LbI) gene, complete cds
20065	SB_M12_B1_A03_MR	g507910	BLASTN	343	7e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
20066	SB_M12_B1_A07_MR	g3142328	BLASTN	729	5e-26	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20067	SB_M12_B1_B08_MF	g2462936	BLASTX	347	7e-31	56	(Y12321) open reading frame 2 [Brassica oleracea]
20068	SB_M12_B1_B10_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
20069	SB_M12_B1_E03_MR	g2995405	BLASTX	431	7e-39	63	(Y12432) polyprotein [Ananas comosus]
20070	SB_M12_B1_E05_MR	g18559	BLASTN	601	3e-20	74	G.max gene for catalase
20071	SB_M12_B1_E07_MF	g3377855	BLASTX	294	2e-29	70	(AF076274) contains similarity to reverse tranciptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
20072	SB_M12_B1_F01_MR	g4063760	BLASTX	418	4e-37	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
20073	SB_M12_B1_F08_MF	g3650039	BLASTX	205	9e-15	52	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
20074	SB_M12_B1_F08_MR	g3097320	BLASTN	349	9e-09	61	Glycine max gene for Bd 30K, complete cds
20075	SB_M12_B1_F09_MF	g2522228	BLASTX	353	2e-31	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
20076	SB_M12_B1_F09_MR	g3420042	BLASTN	355	5e-09	59	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]
20077	SB_M12_B1_G04_MR	g2997694	BLASTX	175	1e-12	34	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
20078	SB_M12_B1_G08_MF	g3550435	BLASTN	412	1e-11	62	Hordeum vulgare Hotr1 gene
20079	SB_M12_B1_G08_MR	g4063760	BLASTX	230	5e-17	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
20080	SB_M12_B1_G11_MF	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20081	SB_M12_B1_H06_MR	g507910	BLASTN	386	8e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
20082	SB_M12_B1_H09_MR	g4106406	BLASTN	397	9e-12	62	Sorghum bicolor centromere specific element pHind22, complete sequence

Table Headings

Seq no.

Provides the SEQ ID NO. for the listed sequences.

Clone ID

The clone ID number refers to the particular clone in the PhytoSeq database.

NCBI gi

Each sequence in the GenBank public database is arbitrarily assigned a unique NCBI gi (National Center for Biotechnology Information GenBank Identifier) number. In this table, the NCBI gi number which is associated (in the same row) with a given clone refers to the particular GenBank sequence which is used in the sequence comparison.

Method

The entry in the "Method" column of the table refers to the type of BLAST search that is used for the sequence comparison.

Score

Each entry in the "Score" column of the table refers to the BLAST score that is generated by sequence comparison of the designated clone with the designated GenBank sequence using the designated BLAST method.

P-Value

The entries in the P-Value column refer to the probability that such matches occur by chance.

% Ident

The entries in the "% Ident" column of the table refer to the percentage of identically matched nucleotides (or residues) that exist along the length of that portion of the sequences which is aligned by the BLAST comparison to generate the statistical scores presented.

Description

A description of the database entry referenced in the "NCBI gi" column. Sequences were analyzed by BLASTX against the non-redundant protein database maintained by NCBI, and a description of the top hit is provided.